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<b>(21) International Application Number:</b> PCT/US99/25031 <b>(22) International Filing Date:</b> 27 October 1999 (27.10.99)  <b>(30) Priority Data:</b> 60/105,971 28 October 1998 (28.10.98) US  <b>(71) Applicant (for all designated States except US):</b> HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> NI, Jian [CN/US]; 5502 Manorfield Road, Rockville, MD 20853 (US). RUBEN, Steven, M. [US/US]; 18525 Heritage Hills Drive, Olney, MD 20832 (US). OLSEN, Henrik, S. [DK/US]; 182 Kendrick Place #24, Gaithersburg, MD 20878 (US). YOUNG, Paul, E. [US/US]; 122 Beckwith Street, Gaithersburg, MD 20878 (US). KENNY, Joseph, J. [US/US]; 10804 Show Pony Place, Damascus, MD 20872 (US). MOORE, Paul, A. [GB/US]; 19005 Leatherbark Drive, Germantown, MD 20874 (US). WEI, Ying-Fei [CN/US]; 242 Gravatt Drive, Berkeley, CA 94705 (US). GREENE, John, M. [US/US]; 872 Diamond Drive, Gaithersburg, MD 20878 (US).		<b>(74) Agents:</b> HOOVER, Kenley, K. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).  <b>(81) Designated States:</b> AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i>
<b>(54) Title:</b> 12 HUMAN SECRETED PROTEINS		
<b>(57) Abstract</b>  The present invention relates to 12 novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.		

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## 12 Human Secreted Proteins

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### *Field of the Invention*

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and their production.

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### *Background of the Invention*

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or  
15 organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum  
20 (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

Proteins targeted to the ER by a signal sequence can be released into the  
25 extracellular space as a secreted protein. For example, vesicles containing secreted

proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell  
5 membrane can also be secreted into the extracellular space by proteolytic cleavage of a “linker” holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include the commercially valuable human insulin, interferon, Factor VIII, human growth  
10 hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using secreted proteins or the genes that encode them.

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### *Summary of the Invention*

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies,  
20 and recombinant and synthetic methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders and conditions related to the polypeptides and polynucleotides, and therapeutic methods for treating such disorders and conditions. The invention further relates to screening methods for identifying binding partners of the polypeptides.

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### *Detailed Description*

#### **Definitions**

5 The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

20 In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

25

In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous

nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5 kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table XIII, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained

in SEQ ID NO:X, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20  $\mu$ g/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M  $\text{NaH}_2\text{PO}_4$ ; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

5           The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-  
10       stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for  
15       other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

          The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may  
20       contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide,  
25       including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given

polypeptide may contain many types of modifications. Polypeptides may be branched ,  
for example, as a result of ubiquitination, and they may be cyclic, with or without  
branching. Cyclic, branched, and branched cyclic polypeptides may result from  
posttranslation natural processes or may be made by synthetic methods. Modifications  
5 include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of  
flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or  
nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent  
attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation,  
demethylation, formation of covalent cross-links, formation of cysteine, formation of  
10 pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation,  
hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic  
processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-  
RNA mediated addition of amino acids to proteins such as arginylation, and  
ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR  
15 PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York  
(1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B.  
C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth  
Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y"  
20 refers to a polypeptide sequence, both sequences identified by an integer specified in  
Table XIII.

"A polypeptide having biological activity" refers to polypeptides exhibiting  
activity similar, but not necessarily identical to, an activity of a polypeptide of the  
present invention, including mature forms, as measured in a particular biological assay,  
25 with or without dose dependency. In the case where dose dependency does exist, it need  
not be identical to that of the polypeptide, but rather substantially similar to the dose-  
dependence in a given activity as compared to the polypeptide of the present invention

(i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

5

### **Polynucleotides and Polypeptides of the Invention**

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 1**

10           The translation product of this gene shares sequence homology with a protein from *Xenopus laevis* that is described as upregulated in response to thyroid hormone in tadpoles, and is thought to be important in the tail resorption process during *Xenopus laevis* metamorphosis (See Proc. Natl. Acad. Sci. USA (1996 Mar. 5):93(5):1924-9, which is herein incorporated by reference). In addition, translation product of this gene

15           shares sequence homology with a recently described group of proteins, called hedgehog interacting proteins (HIPs) (See International Publication No. WO98/12326, which is herein incorporated by reference). These proteins bind to hedgehog polypeptides such as Shh and Dhh with high affinity (K<sub>d</sub> approx. 1 nM). HIPs exhibit spatially and temporally

20           restricted expression domains indicative of important roles in hedgehog-mediated induction. They regulate differentiation of neuronal cells, regulate survival of differentiated neuronal cells, proliferation of chondrocytes, proliferation of testicular germ line cells and/or expression of patched or hedgehog genes. The biological activity of this polypeptide is assayed by techniques known in the art, otherwise disclosed herein and as described in International Publication No. WO98/12326, which is herein

25           incorporated by reference.

          Preferred polypeptides of the invention comprise the following amino acid sequence:

MLRTSTPNLCGGLHCRAPWLSSGILCLCLIFLLGQVGLLQGHPQCLDYGPPFQPP  
 LHLEFCSDYESFGCCDQHKDRRIAARYWDIMEYFDLKRHELCDYIKDILCQEC  
 SPYAAHLYDAENTQTPLRNLPGLCSDYCSAFHSNCHSAISLLTNDRGLQESHGRD  
 GTRFCHLLDLPDKDYCFPNVLRNDYLNRLHGMVAQDPQGCLQLCLSEVANGLR  
 5 NPVSMVHAGDGTTHRFFVAEQVG VVWVYLPDGSRL EQPFLDLKNIVLTTPWIGD  
 ERGFLGLAFHPKFRHNRFYIYYSCLDKKKVEKIRISEMKVSRADPNKADLKSER  
 VILEIEEPASNHNGGQLLFGLDGYMYIFTGDGGQAGDPFGLFGNAQNKSSLLGK  
 VLRIDVNRAGSHGKRYRVPNDPNFVSEPGAHPAIYAYGIRNMWRCVDRGDPIT  
 RQGRGRIFCGDVGQNRFEEDLILKGGNYGWRAKEGFACYDKKLCHNASLDDV  
 10 LPIYAYGHAVGKSVTGGYVYRGCEPNLNGLYIFGDFMSGRLMALQEDRKNKK  
 WKKQDLCLGSTTSCAFPLISTHSHKFIISFAEDEAGELYFLATSYPAYAPRGSIIK  
 FVDPSRRAPPGKCKYKPVVVRTKSKRIPFRPLAKTVLDLLKEQSEKAARKSSSAT  
 LASGPAQGLSEKGSSKKLASPTSSKNTLRGPGTKKKARVGPHVRQGKRRKSLKS  
 HSGRMPSAEQKRAGRSLP (SEQ ID NO: 47). Also preferred are polypeptides  
 15 comprising the mature polypeptide which is predicted to consist of residues 42-724 of the  
 foregoing sequence, and biologically active fragments of the mature polypeptide.

Figures 1A-C show the nucleotide (SEQ ID NO:11) and deduced amino acid  
 sequence (SEQ ID NO:29) of this protein.

Figure 2 shows the regions of similarity between the amino acid sequences of  
 20 SEQ ID NO:29, the *Xenopus laevis* tail resorption protein (gi|1234787) (SEQ ID  
 NO:48), and the Hedgehog Interacting Protein ("HIP"; gi|AAD31172.1) (SEQ ID  
 NO:49).

Figure 3 shows an analysis of the amino acid sequence of SEQ ID NO: 29.  
 Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic  
 25 regions; flexible regions; antigenic index and surface probability are shown.

Northern analysis indicates that a 2.5-3.0 kb transcript of this gene is expressed  
 primarily in testes tissue and A549 lung carcinoma tissue, but interestingly is absent from

normal lung tissue. This gene is also expressed in osteoarthritis tissue and human fetal tissues.

The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding the polypeptide having the amino acid sequence shown in  
5 Figures 1A-C (SEQ ID NO:29), which was determined by sequencing a cloned cDNA. The nucleotide sequence shown in Figures 1A-C (SEQ ID NO:11) was obtained by sequencing a cloned cDNA, which was deposited on Nov. 17, 1998 at the American Type Culture Collection, and given Accession Number 203484. The deposited gene is inserted in the pSport plasmid (Life Technologies, Rockville, MD) using the SalI/NotI  
10 restriction endonuclease cleavage sites.

The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated DNA molecule having the nucleotide sequence of the deposited cDNA or the nucleotide sequence shown in SEQ ID NO:11 is intended DNA fragments at least about 15nt, and more preferably at least about  
15 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length which are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-1500 nt in length are also useful according to the present invention, as are fragments corresponding to most, if not all, of the nucleotide sequence of the deposited cDNA or as shown in SEQ ID NO:11. By a fragment at least 20 nt in  
20 length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of the deposited cDNA or the nucleotide sequence as shown in SEQ ID NO:11. In this context "about" includes the particularly recited size, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Representative examples of polynucleotide fragments of the invention include,  
25 for example, fragments that comprise, or alternatively, consist of, a sequence from about nucleotide 1 to about 50, from about 51 to about 100, from about 101 to about 150, from about 151 to about 200, from about 201 to about 250, from about 251 to about 300, from



about 301 to about 350, from about 351 to about 400, from about 401 to about 450, from about 451 to about 500, and from about 501 to about 550, and from about 551 to about 570 of SEQ ID NO:11, or the complementary strand thereto, or the cDNA contained in the deposited gene. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. In additional embodiments, the polynucleotides of the invention encode functional attributes of the corresponding protein.

Preferred embodiments of the invention in this regard include fragments that comprise alpha-helix and alpha-helix forming regions ("alpha-regions"), beta-sheet and beta-sheet forming regions ("beta-regions"), turn and turn-forming regions ("turn-regions"), coil and coil-forming regions ("coil-regions"), hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions and high antigenic index regions. The data representing the structural or functional attributes of the protein set forth in Figure 3 and/or Table I, as described above, was generated using the various modules and algorithms of the DNA\*STAR set on default parameters. In a preferred embodiment, the data presented in columns VIII, IX, XIII, and XIV of Table I can be used to determine regions of the protein which exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or XIV by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Certain preferred regions in these regards are set out in Figure 3, but may, as shown in Table I, be represented or identified by using tabular representations of the data presented in Figure 3. The DNA\*STAR computer algorithm used to generate Figure 3 (set on the original default parameters) was used to present the data in Figure 3 in a tabular format (See Table I). The tabular format of the data in Figure 3 is used to easily

determine specific boundaries of a preferred region. The above-mentioned preferred regions set out in Figure 3 and in Table I include, but are not limited to, regions of the aforementioned types identified by analysis of the amino acid sequence set out in Figures 1A-C (SEQ ID NO:29). As set out in Figure 3 and in Table I, such preferred regions

5 include Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and Hopp-Woods hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schulz flexible regions, Jameson-Wolf regions of high antigenic index and Emini surface-forming regions. Even if deletion of one or more amino acids from the

10 N-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, etc.) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the

15 complete or mature polypeptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic

20 activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence shown in Figures 1A-C, up to the alanine residue at position number 524 and polynucleotides

25 encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues n1-524 of Figures 1A-C, where n1 is an integer from 1 to 524 corresponding to the position of the amino acid residue in Figures

1A-C (which is identical to the sequence shown as SEQ ID NO:29). N-terminal deletions of the polypeptide of the invention shown as SEQ ID NO:29 include polypeptides comprising the amino acid sequence of residues: V-2 to P-529; A-3 to P-529; Q-4 to P-529; D-5 to P-529; P-6 to P-529; Q-7 to P-529; G-8 to P-529; C-9 to P-529; L-10 to P-529; Q-11 to P-529; L-12 to P-529; C-13 to P-529; L-14 to P-529; S-15 to P-529; E-16 to P-529; V-17 to P-529; A-18 to P-529; N-19 to P-529; G-20 to P-529; L-21 to P-529; R-22 to P-529; N-23 to P-529; P-24 to P-529; V-25 to P-529; S-26 to P-529; M-27 to P-529; V-28 to P-529; H-29 to P-529; A-30 to P-529; G-31 to P-529; D-32 to P-529; G-33 to P-529; T-34 to P-529; H-35 to P-529; R-36 to P-529; F-37 to P-529; F-38 to P-529; V-39 to P-529; A-40 to P-529; E-41 to P-529; Q-42 to P-529; V-43 to P-529; G-44 to P-529; V-45 to P-529; V-46 to P-529; W-47 to P-529; V-48 to P-529; Y-49 to P-529; L-50 to P-529; P-51 to P-529; D-52 to P-529; G-53 to P-529; S-54 to P-529; R-55 to P-529; L-56 to P-529; E-57 to P-529; Q-58 to P-529; P-59 to P-529; F-60 to P-529; L-61 to P-529; D-62 to P-529; L-63 to P-529; K-64 to P-529; N-65 to P-529; I-66 to P-529; V-67 to P-529; L-68 to P-529; T-69 to P-529; T-70 to P-529; P-71 to P-529; W-72 to P-529; I-73 to P-529; G-74 to P-529; D-75 to P-529; E-76 to P-529; R-77 to P-529; G-78 to P-529; F-79 to P-529; L-80 to P-529; G-81 to P-529; L-82 to P-529; A-83 to P-529; F-84 to P-529; H-85 to P-529; P-86 to P-529; K-87 to P-529; F-88 to P-529; R-89 to P-529; H-90 to P-529; N-91 to P-529; R-92 to P-529; K-93 to P-529; F-94 to P-529; Y-95 to P-529; I-96 to P-529; Y-97 to P-529; Y-98 to P-529; S-99 to P-529; C-100 to P-529; L-101 to P-529; D-102 to P-529; K-103 to P-529; K-104 to P-529; K-105 to P-529; V-106 to P-529; E-107 to P-529; K-108 to P-529; I-109 to P-529; R-110 to P-529; I-111 to P-529; S-112 to P-529; E-113 to P-529; M-114 to P-529; K-115 to P-529; V-116 to P-529; S-117 to P-529; R-118 to P-529; A-119 to P-529; D-120 to P-529; P-121 to P-529; N-122 to P-529; K-123 to P-529; A-124 to P-529; D-125 to P-529; L-126 to P-529; K-127 to P-529; S-128 to P-529; E-129 to P-529; R-130 to P-529; V-131 to P-529; I-132 to P-529; L-133 to P-529; E-134 to P-529; I-135 to P-529; E-136 to P-529; E-137 to P-529; P-138 to P-529;

A-139 to P-529; S-140 to P-529; N-141 to P-529; H-142 to P-529; N-143 to P-529; G-144 to P-529; G-145 to P-529; Q-146 to P-529; L-147 to P-529; L-148 to P-529; F-149 to P-529; G-150 to P-529; L-151 to P-529; D-152 to P-529; G-153 to P-529; Y-154 to P-529; M-155 to P-529; Y-156 to P-529; I-157 to P-529; F-158 to P-529; T-159 to P-529;  
5 G-160 to P-529; D-161 to P-529; G-162 to P-529; G-163 to P-529; Q-164 to P-529; A-165 to P-529; G-166 to P-529; D-167 to P-529; P-168 to P-529; F-169 to P-529; G-170 to P-529; L-171 to P-529; F-172 to P-529; G-173 to P-529; N-174 to P-529; A-175 to P-529; Q-176 to P-529; N-177 to P-529; K-178 to P-529; S-179 to P-529; S-180 to P-529; L-181 to P-529; L-182 to P-529; G-183 to P-529; K-184 to P-529; V-185 to P-529; L-186 to P-529; R-187 to P-529; I-188 to P-529; D-189 to P-529; V-190 to P-529; N-191 to P-529; R-192 to P-529; A-193 to P-529; G-194 to P-529; S-195 to P-529; H-196 to P-529; G-197 to P-529; K-198 to P-529; R-199 to P-529; Y-200 to P-529; R-201 to P-529; V-202 to P-529; P-203 to P-529; S-204 to P-529; D-205 to P-529; N-206 to P-529; P-207 to P-529; F-208 to P-529; V-209 to P-529; S-210 to P-529; E-211 to P-529; P-212 to P-529; G-213 to P-529; A-214 to P-529; H-215 to P-529; P-216 to P-529; A-217 to P-529;  
15 I-218 to P-529; Y-219 to P-529; A-220 to P-529; Y-221 to P-529; G-222 to P-529; I-223 to P-529; R-224 to P-529; N-225 to P-529; M-226 to P-529; W-227 to P-529; R-228 to P-529; C-229 to P-529; A-230 to P-529; V-231 to P-529; D-232 to P-529; R-233 to P-529; G-234 to P-529; D-235 to P-529; P-236 to P-529; I-237 to P-529; T-238 to P-529;  
20 R-239 to P-529; Q-240 to P-529; G-241 to P-529; R-242 to P-529; G-243 to P-529; R-244 to P-529; I-245 to P-529; F-246 to P-529; C-247 to P-529; G-248 to P-529; D-249 to P-529; V-250 to P-529; G-251 to P-529; Q-252 to P-529; N-253 to P-529; R-254 to P-529; F-255 to P-529; E-256 to P-529; E-257 to P-529; V-258 to P-529; D-259 to P-529; L-260 to P-529; I-261 to P-529; L-262 to P-529; K-263 to P-529; G-264 to P-529; G-265 to P-529; N-266 to P-529; Y-267 to P-529; G-268 to P-529; W-269 to P-529; R-270 to P-529; A-271 to P-529; K-272 to P-529; E-273 to P-529; G-274 to P-529; F-275 to P-529; A-276 to P-529; C-277 to P-529; Y-278 to P-529; D-279 to P-529; K-280 to P-529; K-

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10 529; S-471 to P-529; K-472 to P-529; K-473 to P-529; L-474 to P-529; A-475 to P-529; S-476 to P-529; P-477 to P-529; T-478 to P-529; S-479 to P-529; S-480 to P-529; K-481 to P-529; N-482 to P-529; T-483 to P-529; L-484 to P-529; R-485 to P-529; G-486 to P-529; P-487 to P-529; G-488 to P-529; T-489 to P-529; K-490 to P-529; K-491 to P-529; K-492 to P-529; A-493 to P-529; R-494 to P-529; V-495 to P-529; G-496 to P-529; P-  
15 497 to P-529; H-498 to P-529; V-499 to P-529; R-500 to P-529; Q-501 to P-529; G-502 to P-529; K-503 to P-529; R-504 to P-529; R-505 to P-529; K-506 to P-529; S-507 to P-529; L-508 to P-529; K-509 to P-529; S-510 to P-529; H-511 to P-529; S-512 to P-529; G-513 to P-529; R-514 to P-529; M-515 to P-529; R-516 to P-529; P-517 to P-529; S-518 to P-529; A-519 to P-529; E-520 to P-529; Q-521 to P-529; K-522 to P-529; R-523  
20 to P-529; A-524 to P-529; of SEQ ID NO:29. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities (e.g., ability  
25 to illicit mitogenic activity, induce differentiation of normal or malignant cells, bind to EGF receptors, etc.)), may still be retained. For example the ability to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally

will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the polypeptide shown in Figures 1A-C, up to the glutamine residue at position number 7, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues 1-m1 of Figures 1A-C, where m1 is an integer from 7 to 528 corresponding to the position of the amino acid residue in Figures 1A-C. Moreover, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of C-terminal deletions of the polypeptide of the invention shown as SEQ ID NO:29 include polypeptides comprising the amino acid sequence of residues: M-1 to L-528; M-1 to S-527; M-1 to R-526; M-1 to G-525; M-1 to A-524; M-1 to R-523; M-1 to K-522; M-1 to Q-521; M-1 to E-520; M-1 to A-519; M-1 to S-518; M-1 to P-517; M-1 to R-516; M-1 to M-515; M-1 to R-514; M-1 to G-513; M-1 to S-512; M-1 to H-511; M-1 to S-510; M-1 to K-509; M-1 to L-508; M-1 to S-507; M-1 to K-506; M-1 to R-505; M-1 to R-504; M-1 to K-503; M-1 to G-502; M-1 to Q-501; M-1 to R-500; M-1 to V-499; M-1 to H-498; M-1 to P-497; M-1 to G-496; M-1 to V-495; M-1 to R-494; M-1 to A-493; M-1 to K-492; M-1 to K-491; M-1 to K-490; M-1 to T-489; M-1 to G-488; M-1 to P-487; M-1 to G-486; M-1 to R-485; M-1 to L-484; M-1 to T-483; M-1 to N-482; M-1 to K-481; M-1 to S-480; M-1 to S-479; M-1 to T-478; M-1 to P-477; M-1 to S-476; M-1 to A-475; M-1 to L-474; M-1 to K-473; M-1 to K-472; M-1 to S-471; M-1 to S-470; M-1 to

G-469; M-1 to K-468; M-1 to E-467; M-1 to S-466; M-1 to L-465; M-1 to G-464; M-1 to Q-463; M-1 to A-462; M-1 to P-461; M-1 to G-460; M-1 to S-459; M-1 to A-458; M-1 to L-457; M-1 to T-456; M-1 to A-455; M-1 to S-454; M-1 to S-453; M-1 to S-452; M-1 to K-451; M-1 to R-450; M-1 to A-449; M-1 to A-448; M-1 to K-447; M-1 to E-446;  
5 M-1 to S-445; M-1 to Q-444; M-1 to E-443; M-1 to K-442; M-1 to L-441; M-1 to L-440; M-1 to D-439; M-1 to L-438; M-1 to V-437; M-1 to T-436; M-1 to K-435; M-1 to A-434; M-1 to L-433; M-1 to P-432; M-1 to R-431; M-1 to F-430; M-1 to P-429; M-1 to I-428; M-1 to R-427; M-1 to K-426; M-1 to S-425; M-1 to K-424; M-1 to T-423; M-1 to R-422; M-1 to V-421; M-1 to P-420; M-1 to V-419; M-1 to P-418; M-1 to K-417; M-1 to Y-416; M-1 to K-415; M-1 to C-414; M-1 to K-413; M-1 to G-412; M-1 to P-411; M-1 to P-410; M-1 to A-409; M-1 to R-408; M-1 to R-407; M-1 to S-406; M-1 to P-405; M-1 to D-404; M-1 to V-403; M-1 to F-402; M-1 to K-401; M-1 to Y-400; M-1 to I-399; M-1 to S-398; M-1 to G-397; M-1 to R-396; M-1 to P-395; M-1 to A-394; M-1 to Y-393; M-1 to A-392; M-1 to S-391; M-1 to P-390; M-1 to Y-389; M-1 to S-388; M-1 to T-387; M-1 to A-386; M-1 to L-385; M-1 to F-384; M-1 to Y-383; M-1 to L-382; M-1 to E-381; M-1 to G-380; M-1 to A-379; M-1 to E-378; M-1 to D-377; M-1 to E-376; M-1 to A-375; M-1 to F-374; M-1 to S-373; M-1 to I-372; M-1 to I-371; M-1 to F-370; M-1 to K-369; M-1 to S-368; M-1 to H-367; M-1 to T-366; M-1 to S-365; M-1 to I-364; M-1 to L-363; M-1 to G-362; M-1 to P-361; M-1 to F-360; M-1 to A-359; M-1 to C-358; M-1 to S-357; M-1 to T-356; M-1 to T-355; M-1 to S-354; M-1 to G-353; M-1 to L-352; M-1 to C-351; M-1 to L-350; M-1 to D-349; M-1 to Q-348; M-1 to K-347; M-1 to K-346; M-1 to W-345; M-1 to K-344; M-1 to K-343; M-1 to N-342; M-1 to K-341; M-1 to R-340; M-1 to D-339; M-1 to E-338; M-1 to Q-337; M-1 to L-336; M-1 to A-335; M-1 to M-334; M-1 to L-333; M-1 to R-332; M-1 to G-331; M-1 to S-330; M-1 to M-329; M-1 to F-328; M-1 to D-327; M-1 to G-326; M-1 to F-325; M-1 to I-324; M-1 to Y-323; M-1 to L-322; M-1 to G-321; M-1 to N-320; M-1 to L-319; M-1 to N-318; M-1 to P-317; M-1 to S-316; M-1 to E-315; M-1 to C-314; M-1 to G-313; M-1 to R-312; M-1 to Y-311; M-



1 to V-310; M-1 to Y-309; M-1 to G-308; M-1 to G-307; M-1 to T-306; M-1 to V-305;  
M-1 to S-304; M-1 to K-303; M-1 to G-302; M-1 to V-301; M-1 to A-300; M-1 to H-  
299; M-1 to G-298; M-1 to Y-297; M-1 to A-296; M-1 to Y-295; M-1 to I-294; M-1 to  
P-293; M-1 to L-292; M-1 to V-291; M-1 to D-290; M-1 to D-289; M-1 to L-288; M-1  
5 to S-287; M-1 to A-286; M-1 to N-285; M-1 to H-284; M-1 to C-283; M-1 to L-282; M-  
1 to K-281; M-1 to K-280; M-1 to D-279; M-1 to Y-278; M-1 to C-277; M-1 to A-276;  
M-1 to F-275; M-1 to G-274; M-1 to E-273; M-1 to K-272; M-1 to A-271; M-1 to R-  
270; M-1 to W-269; M-1 to G-268; M-1 to Y-267; M-1 to N-266; M-1 to G-265; M-1 to  
G-264; M-1 to K-263; M-1 to L-262; M-1 to I-261; M-1 to L-260; M-1 to D-259; M-1 to  
10 V-258; M-1 to E-257; M-1 to E-256; M-1 to F-255; M-1 to R-254; M-1 to N-253; M-1 to  
Q-252; M-1 to G-251; M-1 to V-250; M-1 to D-249; M-1 to G-248; M-1 to C-247; M-1  
to F-246; M-1 to I-245; M-1 to R-244; M-1 to G-243; M-1 to R-242; M-1 to G-241; M-1  
to Q-240; M-1 to R-239; M-1 to T-238; M-1 to I-237; M-1 to P-236; M-1 to D-235; M-1  
to G-234; M-1 to R-233; M-1 to D-232; M-1 to V-231; M-1 to A-230; M-1 to C-229; M-  
15 1 to R-228; M-1 to W-227; M-1 to M-226; M-1 to N-225; M-1 to R-224; M-1 to I-223;  
M-1 to G-222; M-1 to Y-221; M-1 to A-220; M-1 to Y-219; M-1 to I-218; M-1 to A-  
217; M-1 to P-216; M-1 to H-215; M-1 to A-214; M-1 to G-213; M-1 to P-212; M-1 to  
E-211; M-1 to S-210; M-1 to V-209; M-1 to F-208; M-1 to P-207; M-1 to N-206; M-1 to  
D-205; M-1 to S-204; M-1 to P-203; M-1 to V-202; M-1 to R-201; M-1 to Y-200; M-1  
20 to R-199; M-1 to K-198; M-1 to G-197; M-1 to H-196; M-1 to S-195; M-1 to G-194; M-  
1 to A-193; M-1 to R-192; M-1 to N-191; M-1 to V-190; M-1 to D-189; M-1 to I-188;  
M-1 to R-187; M-1 to L-186; M-1 to V-185; M-1 to K-184; M-1 to G-183; M-1 to L-  
182; M-1 to L-181; M-1 to S-180; M-1 to S-179; M-1 to K-178; M-1 to N-177; M-1 to  
Q-176; M-1 to A-175; M-1 to N-174; M-1 to G-173; M-1 to F-172; M-1 to L-171; M-1  
25 to G-170; M-1 to F-169; M-1 to P-168; M-1 to D-167; M-1 to G-166; M-1 to A-165; M-  
1 to Q-164; M-1 to G-163; M-1 to G-162; M-1 to D-161; M-1 to G-160; M-1 to T-159;  
M-1 to F-158; M-1 to I-157; M-1 to Y-156; M-1 to M-155; M-1 to Y-154; M-1 to G-

153; M-1 to D-152; M-1 to L-151; M-1 to G-150; M-1 to F-149; M-1 to L-148; M-1 to  
L-147; M-1 to Q-146; M-1 to G-145; M-1 to G-144; M-1 to N-143; M-1 to H-142; M-1  
to N-141; M-1 to S-140; M-1 to A-139; M-1 to P-138; M-1 to E-137; M-1 to E-136; M-1  
to I-135; M-1 to E-134; M-1 to L-133; M-1 to I-132; M-1 to V-131; M-1 to R-130; M-1  
5 to E-129; M-1 to S-128; M-1 to K-127; M-1 to L-126; M-1 to D-125; M-1 to A-124; M-  
1 to K-123; M-1 to N-122; M-1 to P-121; M-1 to D-120; M-1 to A-119; M-1 to R-118;  
M-1 to S-117; M-1 to V-116; M-1 to K-115; M-1 to M-114; M-1 to E-113; M-1 to S-  
112; M-1 to I-111; M-1 to R-110; M-1 to I-109; M-1 to K-108; M-1 to E-107; M-1 to V-  
106; M-1 to K-105; M-1 to K-104; M-1 to K-103; M-1 to D-102; M-1 to L-101; M-1 to  
10 C-100; M-1 to S-99; M-1 to Y-98; M-1 to Y-97; M-1 to I-96; M-1 to Y-95; M-1 to F-94;  
M-1 to K-93; M-1 to R-92; M-1 to N-91; M-1 to H-90; M-1 to R-89; M-1 to F-88; M-1  
to K-87; M-1 to P-86; M-1 to H-85; M-1 to F-84; M-1 to A-83; M-1 to L-82; M-1 to G-  
81; M-1 to L-80; M-1 to F-79; M-1 to G-78; M-1 to R-77; M-1 to E-76; M-1 to D-75; M-  
1 to G-74; M-1 to I-73; M-1 to W-72; M-1 to P-71; M-1 to T-70; M-1 to T-69; M-1 to L-  
15 68; M-1 to V-67; M-1 to I-66; M-1 to N-65; M-1 to K-64; M-1 to L-63; M-1 to D-62; M-  
1 to L-61; M-1 to F-60; M-1 to P-59; M-1 to Q-58; M-1 to E-57; M-1 to L-56; M-1 to R-  
55; M-1 to S-54; M-1 to G-53; M-1 to D-52; M-1 to P-51; M-1 to L-50; M-1 to Y-49; M-  
1 to V-48; M-1 to W-47; M-1 to V-46; M-1 to V-45; M-1 to G-44; M-1 to V-43; M-1 to  
Q-42; M-1 to E-41; M-1 to A-40; M-1 to V-39; M-1 to F-38; M-1 to F-37; M-1 to R-36;  
20 M-1 to H-35; M-1 to T-34; M-1 to G-33; M-1 to D-32; M-1 to G-31; M-1 to A-30; M-1  
to H-29; M-1 to V-28; M-1 to M-27; M-1 to S-26; M-1 to V-25; M-1 to P-24; M-1 to N-  
23; M-1 to R-22; M-1 to L-21; M-1 to G-20; M-1 to N-19; M-1 to A-18; M-1 to V-17;  
M-1 to E-16; M-1 to S-15; M-1 to L-14; M-1 to C-13; M-1 to L-12; M-1 to Q-11; M-1 to  
L-10; M-1 to C-9; M-1 to G-8; M-1 to Q-7; of SEQ ID NO:29. Polypeptides encoded by  
25 these polynucleotides are also encompassed by the invention.

Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental disorders, and degenerative disorders; osteoarthritis, and lung cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of developing tissues, cartilage, and bone, expression of this gene at significantly higher or lower levels is routinely detected in certain tissues or cell types (e.g. bone, lung, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred polypeptides of the present invention comprise immunogenic epitopes shown in SEQ ID NO: 29 as residues: Asp-52 to Glu-57, Arg-89 to Tyr-95, Asp-102 to Glu-107, Ser-117 to Ser-128, Glu-137 to Gly-145, Arg-192 to Arg-199, Val-231 to Gly-243, Val-250 to Glu-256, Arg-312 to Asn-318, Glu-338 to Asp-349, Pro-405 to Lys-417, Thr-423 to Ile-428, Lys-442 to Ser-453, Glu-467 to Ala-475, Thr-478 to Arg-494, Pro-497 to Arg-526. Polynucleotides encoding said polypeptides are also provided.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:11 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2595 of SEQ ID NO:11, b is an integer of 15 to 2609, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:11, and where b is greater than or equal to a + 14.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 2**

The translation product of this gene, sometimes referred to herein as TIDE (for  
 5 Ten Integrin Domains with EGF homology), shares sequence homology with integrins,  
 which are a superfamily of dimeric ab cell-surface glycoproteins that mediate the  
 adhesive functions of many cell types, enabling cells to interact with one another and  
 with the extracellular matrix (See Genomics 56, 169-178 (1999); all information and  
 references contained within this publication are hereby incorporated herein by reference).  
 10 Eight human integrin b subunits have been described to date, and in combination with the  
 12 known a subunits form a large family of heterodimeric cell surface receptors that  
 mediate cell adhesion to counter-receptors on neighboring cells, and to ECM proteins  
 (reviewed by Hynes, 1992). Integrin-ligand interactions are crucial for fundamental  
 biological processes such as cell migration and motility, and lymphocyte extravasation.

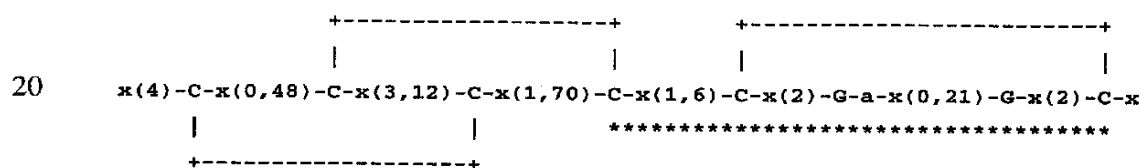
15 In another embodiment, polypeptides comprising the amino acid sequence of the  
 open reading frame upstream of the predicted signal peptide are contemplated by the  
 present invention. Specifically, polypeptides of the invention comprise the following  
 amino acid sequence:

TSTPPRAVPLPKSSQAAHQNRNCNSGWSPPASLGVRGSVCPAICWWHLS  
 20 LLPPPSVNPTLQKCSSPGAAQELSMRPPGFRNFLLLASSLLFAGLSAVPQSFSPSLR  
 SWPGAACRLSRAESERRCRAPGQPPGAALCHGRGRCDGVCICHVTEPGMFFGP  
 LCECHEWVCETYDGSTCAGHGKCDGKCKDQGWYGDACQYPTNCDLTKKK  
 SNQMCKNSQDIICSNAGTCHCGRCKCDNSDGSGLVYGKFCECDDRECIDDETEEI  
 CGGHGKCYCGNCYCKAGWHGDKCEFQCDITPWESKRRCTSPDGKICSNRGTCV  
 25 CGECTCHDVDPTGDWGDHGDTCEDERDCRAVYDRYSDDFCSGHGGQCNCGR  
 CDCKAGWYGKKCEHPQSCTLSAEEISIRKQCQSSDLPCSGRGKCECGKCTCYPPG  
 DRRVYGKTCECDDRRCEDLDGVVCGGHGTCSCGRVCVCERGWFGKLCQHPKRC

NMTEEQSKNLCESADGILCSGKGSCHCGKCICSAEEWYISGEFCDCDDRDCDKH  
DGLICTGNGICSCGNCECWDGWNGNACEI WLGSEYP (SEQ ID NO:50).

Polynucleotides encoding these polypeptides are also provided.

Included in this invention as preferred domains are EGF-like domain signature 1  
5 and 2 domains, which were identified using the ProSite analysis tool (Swiss Institute of  
Bioinformatics). A sequence of about thirty to forty amino-acid residues long found in  
the sequence of epidermal growth factor (EGF) has been shown [1 to 6] to be present, in  
a more or less conserved form, in a large number of other, mostly animal proteins. The  
functional significance of EGF domains in what appear to be unrelated proteins is not yet  
10 clear. However, a common feature is that these repeats are found in the extracellular  
domain of membrane-bound proteins or in proteins known to be secreted (exception:  
prostaglandin G/H synthase). The EGF domain includes six cysteine residues which have  
been shown (in EGF) to be involved in disulfide bonds. The main structure is a two-  
stranded beta-sheet followed by a loop to a C-terminal short two-stranded sheet.  
15 Subdomains between the conserved cysteines strongly vary in length as shown in the  
following schematic representation of the EGF-like domain:



'C': conserved cysteine involved in a disulfide bond. 'G': often conserved glycine 'a':  
25 often conserved aromatic amino acid '\*' : position of both patterns. 'x': any residue The  
region between the 5th and 6th cysteine contains two conserved glycines of which at  
least one is present in most EGF-like domains. The consensus pattern is as follows: C-x-  
C-x(5)-G-x(2)-C [The 3 C's are involved in disulfide bonds].

Preferred polypeptides of the invention comprise the following amino acid  
30 sequence: GKCDGKCKCDQGWDACQYPTNCDLTK (SEQ ID NO: 51),

GGHGKCYCGNCYCKAGWHGDKCEFQCDIT (SEQ ID NO:52),  
HGQCNCGRCDCKAGWYGKKCEHPQSCTLS (SEQ ID NO: 53),  
HGTCSGRCVCERGWFGKLCQHPRKCNMT (SEQ ID NO: 54),  
GNGICSCGNCECWDGWNGNACEIWLSEY (SEQ ID NO: 55), and  
5 ICGGHGKCYCGNCYCKAGWHGDKCEFQCDITPWESK (SEQ ID NO: 73).

Polynucleotides encoding these polypeptides are also provided.

Further preferred are polypeptides comprising the EGF-like domain signature 1 and 2 domains of the sequence referenced in Table I for this gene, and at least 5, 10, 15, 20, 25, 30, 50, or 75 additional contiguous amino acid residues of this referenced  
10 sequence. The additional contiguous amino acid residues is N-terminal or C- terminal to the EGF-like domain signature 1 and 2 domains.

Alternatively, the additional contiguous amino acid residues is both N-terminal and C-terminal to the EGF-like domain signature 1 and 2 domains, wherein the total N- and C-terminal contiguous amino acid residues equal the specified number. The above  
15 preferred polypeptide domain is characteristic of a signature specific to EGF-like domain 1 and 2 containing proteins. Based on the sequence similarity, the translation product of this gene is expected to share at least some biological activities with EGF-like containing proteins. Such activities are known in the art, some of which are described elsewhere herein.

20 Included in this invention as preferred domains are integrins beta chain cysteine-rich domains, which were identified using the ProSite analysis tool (Swiss Institute of Bioinformatics). Integrins [7,8] are a large family of cell surface receptors that mediate cell to cell as well as cell to matrix adhesion. Some integrins recognize the R-G-D sequence in their extracellular matrix protein ligand. Structurally, integrins consist of a  
25 dimer of an alpha and a beta chain. Each subunit has a large N-terminal extracellular domain followed by a transmembrane domain and a short C-terminal cytoplasmic region. Some receptors share a common beta chain while having different alpha chains. All the

integrin beta chains contain four repeats of a forty amino acid region in the C-terminal extremity of their extracellular domain. Each of the repeats contains eight cysteines. The consensus pattern is as follows: C-x-[GNQ]-x(1,3)-G-x-C-x-C-x(2)-C-x-C [The five C's are probably involved in disulfide bonds].

- 5 Preferred polypeptides of the invention comprise the following amino acid sequence: GPPGAALCHGRGRCDGVCICHVTEPGMFFGPLC (SEQ ID NO: 74), ETYDGSTCAGHGKCDGKCKCDQGWYGDACQYP (SEQ ID NO:58), MCKNSQDIICSNAGTCHCGRCKCDNSDGSLVYG (SEQ ID NO:59), IDDETEEICGGHGKCYCGNCYCKAGWHGDKC (SEQ ID NO:60),  
 10 KRRCTSPDGKICSNRGTCVCGECTCHDVDPTGDW (SEQ ID NO:61), DRYSDDFCSGHGQCNCGRCDCKAGWYGKKCEHPQ (SEQ ID NO:62), CQGSSDLPCSGRGKCECGKCTCYPPGDRRVYGK (SEQ ID NO:63), CEDLDGVVCGGHGTCSCGRVCERGWFGKLC (SEQ ID NO:64), SADGILCSGKGSCHCGKCICSAEEWYISGEFC (SEQ ID NO:65), and  
 15 CDKHDGLICTGNGICSCGNCECWDGWNGNACEI (SEQ ID NO: 66).

Polynucleotides encoding these polypeptides are also provided.

- Further preferred are polypeptides comprising the integrins beta chain cysteine-rich domain of the sequence referenced in Table XIII for this gene, and at least 5, 10, 15, 20, 25, 30, 50, or 75 additional contiguous amino acid residues of this referenced  
 20 sequence. The additional contiguous amino acid residues is N-terminal or C- terminal to the integrins beta chain cysteine-rich domain.

- Alternatively, the additional contiguous amino acid residues is both N-terminal and C-terminal to the integrins beta chain cysteine-rich domain, wherein the total N- and C-terminal contiguous amino acid residues equal the specified number. The above  
 25 preferred polypeptide domain is characteristic of a signature specific to integrin proteins. Based on the sequence similarity, the translation product of this gene is expected to share at least some biological activities with integrin proteins, and specifically those containing

an integrins beta chain cysteine-rich domain. Such activities are known in the art, some of which are described elsewhere herein. The following publications were referenced above and are hereby incorporated herein by reference: [ 1] Davis C.G., New Biol. 2:410-419(1990); [ 2] Blomquist M.C., Hunt L.T., Barker W.C., Proc. Natl. Acad. Sci. U.S.A. 81:7363-7367(1984); [ 3] Barker W.C., Johnson G.C., Hunt L.T., George D.G., Protein Nucl. Acid Enz. 29:54-68(1986); [ 4] Doolittle R.F., Feng D.F., Johnson M.S., Nature 307:558-560(1984); [ 5] Appella E., Weber I.T., Blasi F., FEBS Lett. 231:1-4(1988); [ 6] Campbell I.D., Bork P., Curr. Opin. Struct. Biol. 3:385-392(1993); [ 7] Hynes R.O., Cell 48:549-554(1987); and [ 8] Albelda S.M., Buck C.A., FASEB J. 4:2868-2880(1990).

The polypeptide of the present invention has been putatively identified as a member of the integrin family and has been termed Ten Integrin Domains with EGF homology ("TIDE"). This identification has been made as a result of amino acid sequence homology to the human integrin beta-8 subunit (See Genbank Accession No. gi|184521).

Figures 4A-C shows the nucleotide (SEQ ID NO:12) and deduced amino acid sequence (SEQ ID NO:30) of TIDE. Predicted amino acids from about 1 to about 23 constitute the predicted signal peptide (amino acid residues from about 1 to about 23 in SEQ ID NO:30) and are represented by the underlined amino acid regions; amino acids from about 108 to about 136, from about 195 to about 223, from about 291 to about 319, from about 379 to about 407, and/or from about 465 to about 493 constitute the predicted EGF-like domain signature 1 and 2 domains (amino acids from about 108 to about 136, from about 195 to about 223, from about 291 to about 319, from about 379 to about 407, and/or from about 465 to about 493 in SEQ ID NO:30) and are represented by the double underlined amino acids; and amino acids from about 55 to about 89, from about 97 to about 129, from about 142 to about 175, from about 186 to about 216, from about 228 to about 261, from about 281 to about 314, from about 327 to about 359, from about 368 to



about 398, from about 417 to about 448, and/or from about 455 to about 487 constitute the predicted integrins beta chain cysteine-rich domains (amino acids from about 55 to about 89, from about 97 to about 129, from about 142 to about 175, from about 186 to about 216, from about 228 to about 261, from about 281 to about 314, from about 327 to about 359, from about 368 to about 398, from about 417 to about 448, and/or from about 455 to about 487 in SEQ ID NO:30) and are represented by the shaded amino acids.

Figure 5 shows the regions of similarity between the amino acid sequences of the Ten Integrin Domains with EGF homology (TIDE) protein (SEQ ID NO:30) and the human integrin beta-8 subunit (SEQ ID NO: 67).

Figure 6 shows an analysis of the Ten Integrin Domains with EGF homology (TIDE) amino acid sequence. Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic regions; flexible regions; antigenic index and surface probability are shown.

A polynucleotide encoding a polypeptide of the present invention is obtained from human osteoblasts, synovial hypoxia tissue, osteoblast and osteoclast, bone marrow stromal cells, umbilical vein, smooth muscle, placenta, and fetal lung. The polynucleotide of this invention was discovered in a human osteoblast II cDNA library. Its translation product has homology to the characteristic integrins beta chain cysteine-rich domains of integrin family members. The polynucleotide contains an open reading frame encoding the TIDE polypeptide of 494 amino acids. TIDE exhibits a high degree of homology at the amino acid level to the human integrin beta-8 subunit (as shown in Figure 5).

The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding the TIDE polypeptide having the amino acid sequence shown in Figures 4A-C (SEQ ID NO:30). The nucleotide sequence shown in Figures 4A-C (SEQ ID NO:12) was obtained by sequencing a cloned cDNA (HOHCH55), which was deposited on November 17 at the American Type Culture Collection, and given

Accession Number 203484. The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated DNA molecule having the nucleotide sequence of the deposited cDNA or the nucleotide sequence shown in SEQ ID NO:12 is intended DNA fragments at least about 15nt, and  
5 more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length which are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-1500 nt in length are also useful according to the present invention, as are fragments corresponding to most, if not all, of the nucleotide sequence of the deposited cDNA or as shown in SEQ ID NO:12. By  
10 a fragment at least 20 nt in length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of the deposited cDNA or the nucleotide sequence as shown in SEQ ID NO:12. In this context "about" includes the particularly recited size, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Representative examples of TIDE polynucleotide  
15 fragments of the invention include, for example, fragments that comprise, or alternatively, consist of, a sequence from about nucleotide 1 to about 50, from about 51 to about 100, from about 101 to about 150, from about 151 to about 200, from about 201 to about 250, from about 251 to about 300, from about 301 to about 350, from about 351 to about 400, from about 401 to about 450, from about 451 to about 500, from about 501  
20 to about 550, from about 551 to about 600, from about 601 to about 650, from about 651 to about 700, from about 701 to about 750, from about 751 to about 800, from about 801 to about 850, from about 851 to about 900, from about 901 to about 950, from about 951 to about 1000, from about 1001 to about 1050, from about 1051 to about 1100, from about 1101 to about 1150, from about 1151 to about 1200, from about 1201 to about  
25 1250, from about 1251 to about 1300, from about 1301 to about 1350, from about 1351 to about 1400, from about 1401 to about 1450, from about 1451 to about 1500, from about 1501 to about 1550, from about 1551 to about 1600, from about 1601 to about

1650, from about 1651 to about 1700, from about 1701 to about 1750, from about 1751 to about 1800, from about 1801 to about 1850, from about 1851 to about 1900, from about 1901 to about 1950, from about 1951 to about 2000, from about 2001 to about 2050, from about 2051 to about 2100, from about 2101 to about 2150, from about 2151  
5 to about 2200, from about 2201 to about 2250, from about 2251 to about 2300, from about 2301 to about 2350, from about 2351 to about 2400, from about 2401 to about 2450, from about 2451 to about 2499, from about 289 to about 1705, and/or from about 221 to about 1705 of SEQ ID NO:12, or the complementary strand thereto, or the cDNA contained in the deposited gene. In this context "about" includes the particularly recited  
10 ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini.

Preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding a member selected from the group: a polypeptide comprising or alternatively, consisting of, the mature TIDE protein (amino acid residues from about  
15 221 to about 1705 in Figures 4A-C (amino acids from about 221 to about 1705 in SEQ ID NO:30). Since the location of these domains have been predicted by computer analysis, one of ordinary skill would appreciate that the amino acid residues constituting these domains may vary slightly (e.g., by about 1 to 15 amino acid residues) depending on the criteria used to define each domain. In additional embodiments, the  
20 polynucleotides of the invention encode functional attributes of TIDE.

Preferred embodiments of the invention in this regard include fragments that comprise alpha-helix and alpha-helix forming regions ("alpha-regions"), beta-sheet and beta-sheet forming regions ("beta-regions"), turn and turn-forming regions ("turn-regions"), coil and coil-forming regions ("coil-regions"), hydrophilic regions,  
25 hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions and high antigenic index regions of TIDE. The data representing the structural or functional attributes of TIDE set forth in Figure 6 and/or

Table II, as described above, was generated using the various modules and algorithms of the DNA\*STAR set on default parameters. In a preferred embodiment, the data presented in columns VIII, IX, XIII, and XIV of Table II can be used to determine regions of TIDE which exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or XIV by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Certain preferred regions in these regards are set out in Figure 6, but may, as shown in Table II, be represented or identified by using tabular representations of the data presented in Figure 6. The DNA\*STAR computer algorithm used to generate Figure 6 (set on the original default parameters) was used to present the data in Figure 6 in a tabular format (See Table II). The tabular format of the data in Figure 6 is used to easily determine specific boundaries of a preferred region. The above-mentioned preferred regions set out in Figure 6 and in Table II include, but are not limited to, regions of the aforementioned types identified by analysis of the amino acid sequence set out in Figures 4A-C. As set out in Figure 6 and in Table II, such preferred regions include Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and Hopp-Woods hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schulz flexible regions, Jameson-Wolf regions of high antigenic index and Emini surface-forming regions. Even if deletion of one or more amino acids from the N-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, etc.) may still be retained. For example, the ability of shortened TIDE muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the

residues of the complete or mature polypeptide are removed from the N-terminus.

Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that an TIDE mutein  
 5 with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six TIDE amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the TIDE amino acid sequence shown  
 10 in Figures 4A-C, up to the leucine residue at position number 489 and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues n1-494 of Figures 4A-C, where n1 is an integer from 2 to 489 corresponding to the position of the amino acid residue in Figures 4A-C (which is identical to the sequence shown as SEQ ID NO:30). In another  
 15 embodiment, N-terminal deletions of the TIDE polypeptide can be described by the general formula n2-494, where n2 is a number from 2 to 489, corresponding to the position of amino acid identified in Figures 4A-C. N-terminal deletions of the TIDE polypeptide of the invention shown as SEQ ID NO:30 include polypeptides comprising the amino acid sequence of residues: N-terminal deletions of the TIDE polypeptide of the  
 20 invention shown as SEQ ID NO:30 include polypeptides comprising the amino acid sequence of residues: R-2 to P-494; P-3 to P-494; P-4 to P-494; G-5 to P-494; F-6 to P-494; R-7 to P-494; N-8 to P-494; F-9 to P-494; L-10 to P-494; L-11 to P-494; L-12 to P-494; A-13 to P-494; S-14 to P-494; S-15 to P-494; L-16 to P-494; L-17 to P-494; F-18 to P-494; A-19 to P-494; G-20 to P-494; L-21 to P-494; S-22 to P-494; A-23 to P-494; V-  
 25 24 to P-494; P-25 to P-494; Q-26 to P-494; S-27 to P-494; F-28 to P-494; S-29 to P-494; P-30 to P-494; S-31 to P-494; L-32 to P-494; R-33 to P-494; S-34 to P-494; W-35 to P-494; P-36 to P-494; G-37 to P-494; A-38 to P-494; A-39 to P-494; C-40 to P-494; R-41

to P-494; L-42 to P-494; S-43 to P-494; R-44 to P-494; A-45 to P-494; E-46 to P-494; S-47 to P-494; E-48 to P-494; R-49 to P-494; R-50 to P-494; C-51 to P-494; R-52 to P-494; A-53 to P-494; P-54 to P-494; G-55 to P-494; Q-56 to P-494; P-57 to P-494; P-58 to P-494; G-59 to P-494; A-60 to P-494; A-61 to P-494; L-62 to P-494; C-63 to P-494; H-64 to P-494; G-65 to P-494; R-66 to P-494; G-67 to P-494; R-68 to P-494; C-69 to P-494; D-70 to P-494; C-71 to P-494; G-72 to P-494; V-73 to P-494; C-74 to P-494; I-75 to P-494; C-76 to P-494; H-77 to P-494; V-78 to P-494; T-79 to P-494; E-80 to P-494; P-81 to P-494; G-82 to P-494; M-83 to P-494; F-84 to P-494; F-85 to P-494; G-86 to P-494; P-87 to P-494; L-88 to P-494; C-89 to P-494; E-90 to P-494; C-91 to P-494; H-92 to P-494; E-93 to P-494; W-94 to P-494; V-95 to P-494; C-96 to P-494; E-97 to P-494; T-98 to P-494; Y-99 to P-494; D-100 to P-494; G-101 to P-494; S-102 to P-494; T-103 to P-494; C-104 to P-494; A-105 to P-494; G-106 to P-494; H-107 to P-494; G-108 to P-494; K-109 to P-494; C-110 to P-494; D-111 to P-494; C-112 to P-494; G-113 to P-494; K-114 to P-494; C-115 to P-494; K-116 to P-494; C-117 to P-494; D-118 to P-494; Q-119 to P-494; G-120 to P-494; W-121 to P-494; Y-122 to P-494; G-123 to P-494; D-124 to P-494; A-125 to P-494; C-126 to P-494; Q-127 to P-494; Y-128 to P-494; P-129 to P-494; T-130 to P-494; N-131 to P-494; C-132 to P-494; D-133 to P-494; L-134 to P-494; T-135 to P-494; K-136 to P-494; K-137 to P-494; K-138 to P-494; S-139 to P-494; N-140 to P-494; Q-141 to P-494; M-142 to P-494; C-143 to P-494; K-144 to P-494; N-145 to P-494; S-146 to P-494; Q-147 to P-494; D-148 to P-494; I-149 to P-494; I-150 to P-494; C-151 to P-494; S-152 to P-494; N-153 to P-494; A-154 to P-494; G-155 to P-494; T-156 to P-494; C-157 to P-494; H-158 to P-494; C-159 to P-494; G-160 to P-494; R-161 to P-494; C-162 to P-494; K-163 to P-494; C-164 to P-494; D-165 to P-494; N-166 to P-494; S-167 to P-494; D-168 to P-494; G-169 to P-494; S-170 to P-494; G-171 to P-494; L-172 to P-494; V-173 to P-494; Y-174 to P-494; G-175 to P-494; K-176 to P-494; F-177 to P-494; C-178 to P-494; E-179 to P-494; C-180 to P-494; D-181 to P-494; D-182 to P-494; R-183 to P-494; E-184 to P-494; C-185 to P-494; I-186 to P-494; D-187 to P-494; D-188 to P-494;

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494; E-475 to P-494; C-476 to P-494; W-477 to P-494; D-478 to P-494; G-479 to P-494; W-480 to P-494; N-481 to P-494; G-482 to P-494; N-483 to P-494; A-484 to P-494; C-485 to P-494; E-486 to P-494; I-487 to P-494; W-488 to P-494; L-489 to P-494; of SEQ ID NO:30. Polypeptides encoded by these polynucleotides are also encompassed by the  
5 invention.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities may still be retained. For example the ability of the shortened TIDE mutein to induce and/or bind to antibodies which recognize  
10 the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that  
15 an TIDE mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six TIDE amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the TIDE  
20 polypeptide shown in Figures 4A-C, up to the phenylalanine residue at position number 6, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues 1-m1 of Figure 1, where m1 is an integer from 6 to 494 corresponding to the position of the amino acid residue in Figures 4A-C. Moreover, the invention provides polynucleotides encoding  
25 polypeptides comprising, or alternatively consisting of, the amino acid sequence of C-terminal deletions of the TIDE polypeptide of the invention shown as SEQ ID NO:30 include polypeptides comprising the amino acid sequence of residues: M-1 to Y-493; M-

l to E-492; M-1 to S-491; M-1 to G-490; M-1 to L-489; M-1 to W-488; M-1 to I-487; M-1 to E-486; M-1 to C-485; M-1 to A-484; M-1 to N-483; M-1 to G-482; M-1 to N-481; M-1 to W-480; M-1 to G-479; M-1 to D-478; M-1 to W-477; M-1 to C-476; M-1 to E-475; M-1 to C-474; M-1 to N-473; M-1 to G-472; M-1 to C-471; M-1 to S-470; M-1 to  
5 C-469; M-1 to I-468; M-1 to G-467; M-1 to N-466; M-1 to G-465; M-1 to T-464; M-1 to C-463; M-1 to I-462; M-1 to L-461; M-1 to G-460; M-1 to D-459; M-1 to H-458; M-1 to K-457; M-1 to D-456; M-1 to C-455; M-1 to D-454; M-1 to R-453; M-1 to D-452; M-1 to D-451; M-1 to C-450; M-1 to D-449; M-1 to C-448; M-1 to F-447; M-1 to E-446; M-1 to G-445; M-1 to S-444; M-1 to I-443; M-1 to Y-442; M-1 to W-441; M-1 to E-440; M-1 to E-439; M-1 to A-438; M-1 to S-437; M-1 to C-436; M-1 to I-435; M-1 to C-434; M-1 to K-433; M-1 to G-432; M-1 to C-431; M-1 to H-430; M-1 to C-429; M-1 to S-428; M-1 to G-427; M-1 to K-426; M-1 to G-425; M-1 to S-424; M-1 to C-423; M-1 to L-422; M-1 to I-421; M-1 to G-420; M-1 to D-419; M-1 to A-418; M-1 to S-417; M-1 to E-416; M-1 to C-415; M-1 to L-414; M-1 to N-413; M-1 to K-412; M-1 to S-411; M-1 to Q-  
15 410; M-1 to E-409; M-1 to E-408; M-1 to T-407; M-1 to M-406; M-1 to N-405; M-1 to C-404; M-1 to K-403; M-1 to R-402; M-1 to P-401; M-1 to H-400; M-1 to Q-399; M-1 to C-398; M-1 to L-397; M-1 to K-396; M-1 to G-395; M-1 to F-394; M-1 to W-393; M-1 to G-392; M-1 to R-391; M-1 to E-390; M-1 to C-389; M-1 to V-388; M-1 to C-387; M-1 to R-386; M-1 to G-385; M-1 to C-384; M-1 to S-383; M-1 to C-382; M-1 to T-381; M-1 to G-380; M-1 to H-379; M-1 to G-378; M-1 to G-377; M-1 to C-376; M-1 to V-375; M-1 to V-374; M-1 to G-373; M-1 to D-372; M-1 to L-371; M-1 to D-370; M-1 to E-369; M-1 to C-368; M-1 to R-367; M-1 to R-366; M-1 to D-365; M-1 to D-364; M-1 to C-363; M-1 to E-362; M-1 to C-361; M-1 to T-360; M-1 to K-359; M-1 to G-358; M-1 to Y-357; M-1 to V-356; M-1 to R-355; M-1 to R-354; M-1 to D-353; M-1 to G-352; M-1 to P-351; M-1 to P-350; M-1 to Y-349; M-1 to C-348; M-1 to T-347; M-1 to C-346; M-1 to K-345; M-1 to G-344; M-1 to C-343; M-1 to E-342; M-1 to C-341; M-1 to K-340; M-1 to G-339; M-1 to R-338; M-1 to G-337; M-1 to S-336; M-1 to C-335; M-1 to P-334; M-1

to L-333; M-1 to D-332; M-1 to S-331; M-1 to S-330; M-1 to G-329; M-1 to Q-328; M-1 to C-327; M-1 to K-326; M-1 to R-325; M-1 to I-324; M-1 to S-323; M-1 to E-322; M-1 to E-321; M-1 to A-320; M-1 to S-319; M-1 to L-318; M-1 to T-317; M-1 to C-316; M-1 to S-315; M-1 to Q-314; M-1 to P-313; M-1 to H-312; M-1 to E-311; M-1 to C-310; M-1 to K-309; M-1 to K-308; M-1 to G-307; M-1 to Y-306; M-1 to W-305; M-1 to G-304; M-1 to A-303; M-1 to K-302; M-1 to C-301; M-1 to D-300; M-1 to C-299; M-1 to R-298; M-1 to G-297; M-1 to C-296; M-1 to N-295; M-1 to C-294; M-1 to Q-293; M-1 to G-292; M-1 to H-291; M-1 to G-290; M-1 to S-289; M-1 to C-288; M-1 to F-287; M-1 to D-286; M-1 to D-285; M-1 to S-284; M-1 to Y-283; M-1 to R-282; M-1 to D-281; M-1 to Y-280; M-1 to V-279; M-1 to A-278; M-1 to R-277; M-1 to C-276; M-1 to D-275; M-1 to R-274; M-1 to E-273; M-1 to D-272; M-1 to C-271; M-1 to E-270; M-1 to C-269; M-1 to T-268; M-1 to D-267; M-1 to G-266; M-1 to H-265; M-1 to I-264; M-1 to D-263; M-1 to G-262; M-1 to W-261; M-1 to D-260; M-1 to G-259; M-1 to T-258; M-1 to P-257; M-1 to D-256; M-1 to V-255; M-1 to D-254; M-1 to H-253; M-1 to C-252; M-1 to T-251; M-1 to C-250; M-1 to E-249; M-1 to G-248; M-1 to C-247; M-1 to V-246; M-1 to C-245; M-1 to T-244; M-1 to G-243; M-1 to R-242; M-1 to N-241; M-1 to S-240; M-1 to C-239; M-1 to I-238; M-1 to K-237; M-1 to G-236; M-1 to D-235; M-1 to P-234; M-1 to S-233; M-1 to T-232; M-1 to C-231; M-1 to R-230; M-1 to R-229; M-1 to K-228; M-1 to S-227; M-1 to E-226; M-1 to W-225; M-1 to P-224; M-1 to T-223; M-1 to I-222; M-1 to D-221; M-1 to C-220; M-1 to Q-219; M-1 to F-218; M-1 to E-217; M-1 to C-216; M-1 to K-215; M-1 to D-214; M-1 to G-213; M-1 to H-212; M-1 to W-211; M-1 to G-210; M-1 to A-209; M-1 to K-208; M-1 to C-207; M-1 to Y-206; M-1 to C-205; M-1 to N-204; M-1 to G-203; M-1 to C-202; M-1 to Y-201; M-1 to C-200; M-1 to K-199; M-1 to G-198; M-1 to H-197; M-1 to G-196; M-1 to G-195; M-1 to C-194; M-1 to I-193; M-1 to E-192; M-1 to E-191; M-1 to T-190; M-1 to E-189; M-1 to D-188; M-1 to D-187; M-1 to I-186; M-1 to C-185; M-1 to E-184; M-1 to R-183; M-1 to D-182; M-1 to D-181; M-1 to C-180; M-1 to E-179; M-1 to C-178; M-1 to F-177; M-1 to K-176; M-1 to G-175; M-1 to

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 D-168; M-1 to S-167; M-1 to N-166; M-1 to D-165; M-1 to C-164; M-1 to K-163; M-1 to  
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 to T-156; M-1 to G-155; M-1 to A-154; M-1 to N-153; M-1 to S-152; M-1 to C-151; M-1  
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 to K-138; M-1 to K-137; M-1 to K-136; M-1 to T-135; M-1 to L-134; M-1 to D-133;  
 M-1 to C-132; M-1 to N-131; M-1 to T-130; M-1 to P-129; M-1 to Y-128; M-1 to Q-127;  
 M-1 to C-126; M-1 to A-125; M-1 to D-124; M-1 to G-123; M-1 to Y-122; M-1 to W-  
 10 121; M-1 to G-120; M-1 to Q-119; M-1 to D-118; M-1 to C-117; M-1 to K-116; M-1 to  
 C-115; M-1 to K-114; M-1 to G-113; M-1 to C-112; M-1 to D-111; M-1 to C-110; M-1 to  
 K-109; M-1 to G-108; M-1 to H-107; M-1 to G-106; M-1 to A-105; M-1 to C-104; M-1  
 to T-103; M-1 to S-102; M-1 to G-101; M-1 to D-100; M-1 to Y-99; M-1 to T-98; M-1 to  
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 15 M-1 to E-90; M-1 to C-89; M-1 to L-88; M-1 to P-87; M-1 to G-86; M-1 to F-85; M-1  
 to F-84; M-1 to M-83; M-1 to G-82; M-1 to P-81; M-1 to E-80; M-1 to T-79; M-1 to V-  
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 to C-71; M-1 to D-70; M-1 to C-69; M-1 to R-68; M-1 to G-67; M-1 to R-66; M-1  
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 20 59; M-1 to P-58; M-1 to P-57; M-1 to Q-56; M-1 to G-55; M-1 to P-54; M-1 to A-53; M-1  
 to R-52; M-1 to C-51; M-1 to R-50; M-1 to R-49; M-1 to E-48; M-1 to S-47; M-1 to E-  
 46; M-1 to A-45; M-1 to R-44; M-1 to S-43; M-1 to L-42; M-1 to R-41; M-1 to C-40; M-1  
 to A-39; M-1 to A-38; M-1 to G-37; M-1 to P-36; M-1 to W-35; M-1 to S-34; M-1 to  
 R-33; M-1 to L-32; M-1 to S-31; M-1 to P-30; M-1 to S-29; M-1 to F-28; M-1 to S-27;  
 25 M-1 to Q-26; M-1 to P-25; M-1 to V-24; M-1 to A-23; M-1 to S-22; M-1 to L-21; M-1 to  
 G-20; M-1 to A-19; M-1 to F-18; M-1 to L-17; M-1 to L-16; M-1 to S-15; M-1 to S-14;  
 M-1 to A-13; M-1 to L-12; M-1 to L-11; M-1 to L-10; M-1 to F-9; M-1 to N-8; M-1 to R-

7; M-1 to F-6; of SEQ ID NO:30. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In addition, the invention provides nucleic acid molecules having nucleotide sequences related to extensive portions of SEQ ID NO:12 which have been determined  
5 from the following related cDNA genes: HLHFV34R (SEQ ID NO:68), HSRDA85R (SEQ ID NO:69), HSRAZ62R (SEQ ID NO:70), HSRDA17R (SEQ ID NO:71), and HSLEC45R (SEQ ID NO:72).

Based on the sequence similarity to the human integrin beta-8 subunit, translation product of this gene is expected to share at least some biological activities with integrin  
10 proteins, and specifically the human integrin beta-8 subunit. Such activities are known in the art, some of which are described elsewhere herein.

Specifically, polynucleotides and polypeptides of the invention are also useful for modulating the differentiation of normal and malignant cells, modulating the proliferation and/or differentiation of cancer and neoplastic cells, and modulating the  
15 immune response. Polynucleotides and polypeptides of the invention may represent a diagnostic marker for hematopoietic and immune diseases and/or disorders. The full-length protein should be a secreted protein, based upon homology to the integrin family. Therefore, it is secreted into serum, urine, or feces and thus the levels is assayable from patient samples. Assuming specific expression levels are reflective of the presence of  
20 immune disorders, this protein would provide a convenient diagnostic for early detection. In addition, expression of this gene product may also be linked to the progression of immune diseases, and therefore may itself actually represent a therapeutic or therapeutic target for the treatment of cancer. Polynucleotides and polypeptides of the invention may play an important role in the pathogenesis of human cancers and cellular transformation,  
25 particularly those of the immune and hematopoietic systems. Polynucleotides and polypeptides of the invention may also be involved in the pathogenesis of developmental abnormalities based upon its potential effects on proliferation and differentiation of cells

and tissue cell types. Due to the potential proliferating and differentiating activity of said polynucleotides and polypeptides, the invention is useful as a therapeutic agent in inducing tissue regeneration, for treating inflammatory conditions (e.g., inflammatory bowel syndrome, diverticulitis, etc.). Moreover, the invention is useful in modulating the immune response to aberrant polypeptides, as may exist in rapidly proliferating cells and tissue cell types, particularly in adenocarcinoma cells, and other cancers.

Alternatively, the expression within cellular sources marked by proliferating cells indicates this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis, treatment, and/or prevention of developmental diseases and disorders, including cancer, and other proliferative conditions. Representative uses are described in the "Hyperproliferative Disorders" and "Regeneration" sections below and elsewhere herein. Briefly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation.

Dysregulation of apoptosis can result in inappropriate suppression of cell death, as occurs in the development of some cancers, or in failure to control the extent of cell death, as is believed to occur in acquired immunodeficiency and certain neurodegenerative disorders, such as spinal muscular atrophy (SMA).

Alternatively, this gene product is involved in the pattern of cellular proliferation that accompanies early embryogenesis. Thus, aberrant expression of this gene product in tissues - particularly adult tissues - may correlate with patterns of abnormal cellular proliferation, such as found in various cancers. Because of potential roles in proliferation and differentiation, this gene product may have applications in the adult for tissue regeneration and the treatment of cancers. It may also act as a morphogen to control cell and tissue type specification. Therefore, the polynucleotides and polypeptides of the present invention are useful in treating, detecting, and/or preventing said disorders and conditions, in addition to other types of degenerative conditions. Thus this protein may modulate apoptosis or tissue differentiation and is useful in the detection, treatment,

and/or prevention of degenerative or proliferative conditions and diseases. The protein is useful in modulating the immune response to aberrant polypeptides, as may exist in proliferating and cancerous cells and tissues. The protein can also be used to gain new insight into the regulation of cellular growth and proliferation. Furthermore, the protein  
5 may also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions, in addition to its use as a nutritional supplement. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

10 The translation product of this gene, sometimes referred to herein as TIDE (for Ten Integrin Domains with EGF homology), shares sequence homology with integrins, which are a superfamily of dimeric ab cell-surface glycoproteins that mediate the adhesive functions of many cell types, enabling cells to interact with one another and with the extracellular matrix (See Genomics 56, 169-178 (1999); all information and  
15 references contained within this publication are hereby incorporated herein by reference).

The gene encoding the disclosed cDNA is believed to reside on chromosome 13, at locus 13q33. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 13, generally, and particularly at locus 13q33.

20 This gene is expressed primarily in synovial hypoxia tissue, osteoblast and osteoclast, bone marrow stromal cells, and to a lesser extent in umbilical vein, smooth muscle, placenta, and fetal lung cDNA libraries. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and  
25 conditions which include, but are not limited to, disorders of bone and connective tissues, immune and hematopoietic diseases and/or disorders, vascular disorders, and other disorders involving aberrations in cell-surface interactions. Similarly, polypeptides and

antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the connective tissue and skeletal system, expression of this gene at significantly higher or lower levels is routinely detected in  
5 certain tissues or cell types (e.g. cartilage, bone, vascular, hypoxic tissue, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 Preferred polypeptides of the present invention comprise immunogenic epitopes shown in SEQ ID NO: 30 as residues: Met-1 to Phe-6, Arg-44 to Arg-52, His-64 to Cys-69, Tyr-99 to Gln-147, His-158 to Gly-169, Phe-177 to Asp-182, Cys-194 to Cys-202, Gly-213 to Phe-218, Pro-224 to Gly-236, Asp-254 to Trp-261, Asp-263 to Ala-303, Trp-305 to Cys-316, Lys-326 to Asp-332, Pro-334 to Cys-343, Pro-350 to Asp-370, Thr-407  
15 to Asn-413, Gly-425 to Cys-431, Asp-449 to Asp-459, Gly-472 to Asn-483.

Polynucleotides encoding said polypeptides are also provided.

The tissue distribution and homology to the human integrin beta-8 subunit indicates polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Representative uses are  
20 described in the "Immune Activity" and "infectious disease" sections below, in Example 11, 13, 14, 16, 18, 19, 20, and 27, and elsewhere herein.

Briefly, the expression indicates a role in regulating the proliferation; survival; differentiation; and/or activation of hematopoietic cell lineages, including blood stem cells. Involvement in the regulation of cytokine production, antigen presentation, or other  
25 processes indicates a usefulness for treatment of cancer (e.g. by boosting immune responses). Expression in cells of lymphoid origin, indicates the natural gene product is involved in immune functions. Therefore it would also be useful as an agent for



immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis, granulomatous Disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versus-host diseases, or autoimmunity disorders, such as autoimmune infertility, lense tissue injury, demyelination, systemic lupus erythematosus, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's Disease, and scleroderma. Moreover, the protein may represent a secreted factor that influences the differentiation or behavior of other blood cells, or that recruits hematopoietic cells to sites of injury. Thus, this gene product is thought to be useful in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Based upon the tissue distribution of this protein, antagonists directed against this protein is useful in blocking the activity of this protein. Accordingly, preferred are antibodies which specifically bind a portion of the translation product of this gene.

Also provided is a kit for detecting tumors in which expression of this protein occurs. Such a kit comprises in one embodiment an antibody specific for the translation product of this gene bound to a solid support. Also provided is a method of detecting these tumors in an individual which comprises a step of contacting an antibody specific for the translation product of this gene to a bodily fluid from the individual, preferably serum, and ascertaining whether antibody binds to an antigen found in the bodily fluid. Preferably the antibody is bound to a solid support and the bodily fluid is serum. The above embodiments, as well as other treatments and diagnostic tests (kits and methods), are more particularly described elsewhere herein.

Furthermore, the protein may also be used to determine biological activity, raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions, in addition to its use as a nutritional supplement. Protein,

as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:12 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2485 of SEQ ID NO:12, b is an integer of 15 to 2499, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:12, and where b is greater than or equal to a + 14.

### 15 FEATURES OF PROTEIN ENCODED BY GENE NO: 3

The translation product of this gene shares sequence homology with RAMP3 (receptor-activity-modifying proteins), which another group has recently published, which is thought to be important in the transport of the calcitonin-receptor-like receptor (CRLR) to the plasma membrane. RAMPs regulate the transport and ligand specificity of the calcitonin-receptor-like-receptor. There are two other related receptor-activity-modifying proteins, known as RAMP1 and RAMP2 (Nature 1998 May 28;393(6683):333-9). RAMP1 is thought to present the receptor at the cell surface as a mature glycoprotein and a Calcitonin-gene-related peptide (CGRP) receptor.

25 Alternatively, RAMP2-transported receptors are core-glycosylated and are adrenomedullin receptors. CGRP (a 37-amino-acid neuropeptide) and its receptors are widely distributed in the body, and it is the most potent endogenous vasodilatory peptide

discovered so far (Crit Rev Neurobiol 1997;11(2-3):167-239). Specific binding sites for adrenomedullin were present in every region of human brain (cerebral cortex, cerebellum, thalamus, hypothalamus, pons and medulla oblongata), suggesting that a novel neurotransmitter/neuromodulator role may exist for adrenomedullin in human  
5 brain (Peptides 1997;18(8):1125-9).

Figures 7A-B show the nucleotide (SEQ ID NO:13) and deduced amino acid sequence (SEQ ID NO:31) of the Intestine derived extracellular protein. Predicted amino acids from about 1 to about 27 constitute the predicted signal peptide (amino acid residues from about 1 to about 27 in SEQ ID NO:31) and are represented by the  
10 underlined amino acid regions; and amino acids from about 122 to about 138 constitute the predicted transmembrane domain (amino acid residues from about 122 to about 138 in SEQ ID NO:31) and are represented by the double-underlined amino acids.

Figure 8 shows the regions of similarity between the amino acid sequences of the Intestine derived extracellular protein SEQ ID NO:31, and the RAMP3 protein  
15 (gi|4587099) (SEQ ID NO: 75).

Figure 9 shows an analysis of the amino acid sequence of SEQ ID NO: 31.

Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic regions; flexible regions; antigenic index and surface probability are shown.

Northern analysis indicates that a 1.4kb transcript of this gene is primarily  
20 expressed in small intestine tissue, and to a lesser extent in colon and prostate tissue.

The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding the polypeptide having the amino acid sequence shown in Figure 1 (SEQ ID NO:31), which was determined by sequencing a cloned cDNA (HTLEW81). The nucleotide sequence shown in Figures 7A-B (SEQ ID NO:13) was  
25 obtained by sequencing a cloned cDNA (HTLEW81), which was deposited on Nov. 17, 1998 at the American Type Culture Collection, and given Accession Number 203484. The deposited gene is inserted in the pSport plasmid (Life Technologies, Rockville, MD)

using the Sall/NotI restriction endonuclease cleavage sites. The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated DNA molecule having the nucleotide sequence of the deposited cDNA or the nucleotide sequence shown in SEQ ID NO:13 is intended DNA fragments

5 at least about 15nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length which are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-1500 nt in length are also useful according to the present invention, as are fragments corresponding to most, if not all, of the nucleotide sequence of the deposited cDNA or as

10 shown in SEQ ID NO:13. By a fragment at least 20 nt in length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of the deposited cDNA or the nucleotide sequence as shown in SEQ ID NO:13. In this context "about" includes the particularly recited size, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Representative examples of

15 polynucleotide fragments of the invention include, for example, fragments that comprise, or alternatively, consist of, a sequence from about nucleotide 1 to about 50, from about 51 to about 100, from about 101 to about 150, from about 151 to about 200, from about 201 to about 250, from about 251 to about 300, from about 301 to about 350, from about 351 to about 400, from about 401 to about 450, from about 451 to about 500, and from

20 about 501 to about 550, and from about 551 to about 600, from about 601 to about 650, from about 651 to about 700, from about 701 to about 750, from about 751 to about 800, from about 801 to about 850, from about 851 to about 900, from about 901 to about 950, from about 951 to about 1000, from about 1001 to about 1050, from about 1051 to about 1100, from about 1101 to about 1150, from about 1151 to about 1200, from about 1201

25 to about 1250, from about 1251 to about 1300, from about 1301 to about 1339 of SEQ ID NO:13, or the complementary strand thereto, or the cDNA contained in the deposited gene. In this context "about" includes the particularly recited ranges, larger or smaller by

several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. In additional embodiments, the polynucleotides of the invention encode functional attributes of the corresponding protein.

Preferred embodiments of the invention in this regard include fragments that  
5 comprise alpha-helix and alpha-helix forming regions ("alpha-regions"), beta-sheet and beta-sheet forming regions ("beta-regions"), turn and turn-forming regions ("turn-regions"), coil and coil-forming regions ("coil-regions"), hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions and high antigenic index regions. The data representing  
10 the structural or functional attributes of the protein set forth in Figure 9 and/or Table III, as described above, was generated using the various modules and algorithms of the DNA\*STAR set on default parameters. In a preferred embodiment, the data presented in columns VIII, IX, XIII, and XIV of Table III can be used to determine regions of the protein which exhibit a high degree of potential for antigenicity. Regions of high  
15 antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or XIV by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Certain preferred regions in these regards are set out in Figure 9, but may, as  
20 shown in Table III, be represented or identified by using tabular representations of the data presented in Figure 9. The DNA\*STAR computer algorithm used to generate Figure 9 (set on the original default parameters) was used to present the data in Figure 9 in a tabular format (See Table III). The tabular format of the data in Figure 9 is used to easily determine specific boundaries of a preferred region. The above-mentioned preferred  
25 regions set out in Figure 9 and in Table III include, but are not limited to, regions of the aforementioned types identified by analysis of the amino acid sequence set out in Figures 7A-B. As set out in Figure 9 and in Table III, such preferred regions include Garnier-

Robson alpha-regions, beta-regions, turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and Hopp-Woods hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schulz flexible regions, Jameson-Wolf regions of high antigenic index and Emini

5 surface-forming regions. Even if deletion of one or more amino acids from the N-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, etc.) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the

10 polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of

15 deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence shown in

20 Figures 7A-B, up to the arginine residue at position number 143 and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues n1-148 of Figures 7A-B, where n1 is an integer from 2 to 143 corresponding to the position of the amino acid residue in Figures 7A-B (which is identical to the sequence shown as SEQ ID NO:31). N-terminal deletions

25 of the polypeptide of the invention shown as SEQ ID NO:31 include polypeptides comprising the amino acid sequence of residues: E-2 to L-148; T-3 to L-148; G-4 to L-148; A-5 to L-148; L-6 to L-148; R-7 to L-148; R-8 to L-148; P-9 to L-148; Q-10 to L-

148; L-11 to L-148; L-12 to L-148; P-13 to L-148; L-14 to L-148; L-15 to L-148; L-16 to L-148; L-17 to L-148; L-18 to L-148; C-19 to L-148; G-20 to L-148; G-21 to L-148; C-22 to L-148; P-23 to L-148; R-24 to L-148; A-25 to L-148; G-26 to L-148; G-27 to L-148; C-28 to L-148; N-29 to L-148; E-30 to L-148; T-31 to L-148; G-32 to L-148; M-33 to L-148; L-34 to L-148; E-35 to L-148; R-36 to L-148; L-37 to L-148; P-38 to L-148; L-39 to L-148; C-40 to L-148; G-41 to L-148; K-42 to L-148; A-43 to L-148; F-44 to L-148; A-45 to L-148; D-46 to L-148; M-47 to L-148; M-48 to L-148; G-49 to L-148; K-50 to L-148; V-51 to L-148; D-52 to L-148; V-53 to L-148; W-54 to L-148; K-55 to L-148; W-56 to L-148; C-57 to L-148; N-58 to L-148; L-59 to L-148; S-60 to L-148; E-61 to L-148; F-62 to L-148; I-63 to L-148; V-64 to L-148; Y-65 to L-148; Y-66 to L-148; E-67 to L-148; S-68 to L-148; F-69 to L-148; T-70 to L-148; N-71 to L-148; C-72 to L-148; T-73 to L-148; E-74 to L-148; M-75 to L-148; E-76 to L-148; A-77 to L-148; N-78 to L-148; V-79 to L-148; V-80 to L-148; G-81 to L-148; C-82 to L-148; Y-83 to L-148; W-84 to L-148; P-85 to L-148; N-86 to L-148; P-87 to L-148; L-88 to L-148; A-89 to L-148; Q-90 to L-148; G-91 to L-148; F-92 to L-148; I-93 to L-148; T-94 to L-148; G-95 to L-148; I-96 to L-148; H-97 to L-148; R-98 to L-148; Q-99 to L-148; F-100 to L-148; F-101 to L-148; S-102 to L-148; N-103 to L-148; C-104 to L-148; T-105 to L-148; V-106 to L-148; D-107 to L-148; R-108 to L-148; V-109 to L-148; H-110 to L-148; L-111 to L-148; E-112 to L-148; D-113 to L-148; P-114 to L-148; P-115 to L-148; D-116 to L-148; E-117 to L-148; V-118 to L-148; L-119 to L-148; I-120 to L-148; P-121 to L-148; L-122 to L-148; I-123 to L-148; V-124 to L-148; I-125 to L-148; P-126 to L-148; V-127 to L-148; V-128 to L-148; L-129 to L-148; T-130 to L-148; V-131 to L-148; A-132 to L-148; M-133 to L-148; A-134 to L-148; G-135 to L-148; L-136 to L-148; V-137 to L-148; V-138 to L-148; W-139 to L-148; R-140 to L-148; S-141 to L-148; K-142 to L-148; R-143 to L-148; of SEQ ID NO:31. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities (e.g., ability to illicit mitogenic activity, induce differentiation of normal or malignant cells, bind to EGF receptors, etc.)), may still be retained. For example the ability to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the polypeptide shown in Figures 7A-B, up to the arginine residue at position number 7, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues 1-m1 of Figures 7A-B, where m1 is an integer from 7 to 147 corresponding to the position of the amino acid residue in Figures 7A-B. Moreover, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of C-terminal deletions of the polypeptide of the invention shown as SEQ ID NO:31 include polypeptides comprising the amino acid sequence of residues: M-1 to L-147; M-1 to T-146; M-1 to D-145; M-1 to T-144; M-1 to R-143; M-1 to K-142; M-1 to S-141; M-1 to R-140; M-1 to W-139; M-1 to V-138; M-1 to V-137; M-1 to L-136; M-1 to G-135; M-1 to A-134; M-1 to M-133; M-1 to A-132; M-1 to V-131; M-1 to T-130; M-1 to L-129; M-1 to V-128; M-1 to V-127; M-1 to P-126; M-1 to I-125; M-1 to V-124; M-1 to I-123; M-1 to



L-122; M-1 to P-121; M-1 to I-120; M-1 to L-119; M-1 to V-118; M-1 to E-117; M-1 to  
 D-116; M-1 to P-115; M-1 to P-114; M-1 to D-113; M-1 to E-112; M-1 to L-111; M-1 to  
 H-110; M-1 to V-109; M-1 to R-108; M-1 to D-107; M-1 to V-106; M-1 to T-105; M-1 to  
 C-104; M-1 to N-103; M-1 to S-102; M-1 to F-101; M-1 to F-100; M-1 to Q-99; M-1 to  
 5 R-98; M-1 to H-97; M-1 to I-96; M-1 to G-95; M-1 to T-94; M-1 to I-93; M-1 to F-92;  
 M-1 to G-91; M-1 to Q-90; M-1 to A-89; M-1 to L-88; M-1 to P-87; M-1 to N-86; M-1 to  
 P-85; M-1 to W-84; M-1 to Y-83; M-1 to C-82; M-1 to G-81; M-1 to V-80; M-1 to V-79;  
 M-1 to N-78; M-1 to A-77; M-1 to E-76; M-1 to M-75; M-1 to E-74; M-1 to T-73; M-1 to  
 C-72; M-1 to N-71; M-1 to T-70; M-1 to F-69; M-1 to S-68; M-1 to E-67; M-1 to Y-66;  
 10 M-1 to Y-65; M-1 to V-64; M-1 to I-63; M-1 to F-62; M-1 to E-61; M-1 to S-60; M-1 to  
 L-59; M-1 to N-58; M-1 to C-57; M-1 to W-56; M-1 to K-55; M-1 to W-54; M-1 to V-  
 53; M-1 to D-52; M-1 to V-51; M-1 to K-50; M-1 to G-49; M-1 to M-48; M-1 to M-47;  
 M-1 to D-46; M-1 to A-45; M-1 to F-44; M-1 to A-43; M-1 to K-42; M-1 to G-41; M-1 to  
 C-40; M-1 to L-39; M-1 to P-38; M-1 to L-37; M-1 to R-36; M-1 to E-35; M-1 to L-34;  
 15 M-1 to M-33; M-1 to G-32; M-1 to T-31; M-1 to E-30; M-1 to N-29; M-1 to C-28; M-1  
 to G-27; M-1 to G-26; M-1 to A-25; M-1 to R-24; M-1 to P-23; M-1 to C-22; M-1 to G-  
 21; M-1 to G-20; M-1 to C-19; M-1 to L-18; M-1 to L-17; M-1 to L-16; M-1 to L-15; M-1  
 to L-14; M-1 to P-13; M-1 to L-12; M-1 to L-11; M-1 to Q-10; M-1 to P-9; M-1 to R-8;  
 M-1 to R-7; of SEQ ID NO:31. Polypeptides encoded by these polynucleotides are also  
 20 encompassed by the invention.

In addition, the invention provides nucleic acid molecules having nucleotide  
 sequences related to extensive portions of SEQ ID NO:31 which have been determined  
 from the following related cDNA genes: HLHCH17RA (SEQ ID NO:76), HTOAT51R  
 (SEQ ID NO:77), and/or HBNBO41R (SEQ ID NO:78).

25 The polypeptide of this gene has been determined to have a transmembrane  
 domain at about amino acid position 122 - 138 of the amino acid sequence referenced in  
 Table XIII for this gene. Moreover, a cytoplasmic tail encompassing amino acids 139 to

149 of this protein has also been determined. Based upon these characteristics, it is believed that the protein product of this gene shares structural features to type Ia membrane proteins.

Therefore, polynucleotides and polypeptides of the invention are useful as  
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, gastrointestinal and neurodegenerative diseases and disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a  
10 number of disorders of the above tissues or cells, particularly of the central nervous and gastrointestinal systems, expression of this gene at significantly higher or lower levels is routinely detected in certain tissues or cell types (e.g. brain, CNS, gastrointestinal, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual  
15 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred polypeptides of the present invention comprise immunogenic epitopes shown in SEQ ID NO: 31 as residues: Ala-5 to Gln-10, Pro-23 to Cys-28, Arg-140 to Asp-145. Polynucleotides encoding said polypeptides are also provided.

20 The tissue distribution and homology to RAMP3 suggest that the translation product of this gene is useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses,  
25 autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo.

Alternatively, the tissue distribution in small intestine and colon tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of disorders involving the small intestine. This may include diseases associated with digestion and food absorption, as well as hematopoietic disorders involving the Peyer's patches of the small intestine, or other hematopoietic cells and tissues within the body. Similarly, expression of this gene product in colon tissue indicates again involvement in digestion, processing, and elimination of food, as well as a potential role for this gene as a diagnostic marker or causative agent in the development of colon cancer, and cancer in general. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:13 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of  $a-b$ , where  $a$  is any integer between 1 to 1325 of SEQ ID NO:13,  $b$  is an integer of 15 to 1339, where both  $a$  and  $b$  correspond to the positions of nucleotide residues shown in SEQ ID NO:13, and where  $b$  is greater than or equal to  $a + 14$ .

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 4

The translation product of this gene shares sequence homology with a proteoglycan from *Gallus gallus*, and this proteoglycan is believed to participate in the

osteogenic processes of cartilage ossification (See Genbank Accession No. gi|222847). Based on the sequence similarity. The translation product of this gene is expected to share biological activities with the Gallus gallus proteoglycan polypeptide.

Figures 10A-B shows the nucleotide (SEQ ID NO:14) and deduced amino acid  
5 sequence (SEQ ID NO:32) of the retinal specific protein. Predicted amino acids from about 1 to about 21 constitute the predicted signal peptide (amino acid residues from about 1 to about 21 in SEQ ID NO:32) and are represented by the underlined amino acid regions.

Figure 11 shows the regions of similarity between the amino acid sequences of  
10 the retinal specific protein SEQ ID NO:32, and the Gallus gallus proteoglycan (SEQ ID NO:79).

Figure 12 shows an analysis of the amino acid sequence of SEQ ID NO: 32.

Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic regions; flexible regions; antigenic index and surface probability are shown.

15 Northern analysis indicates that this gene is expressed in adrenal cortex and adrenal medulla tissues. This gene is also expressed in retinal tissue.

The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding the polypeptide having the amino acid sequence shown in Figures 10A-B (SEQ ID NO:32), which was determined by sequencing a cloned cDNA  
20 (HARAO44). The nucleotide sequence shown in Figures 10A-B (SEQ ID NO:14) was obtained by sequencing a cloned cDNA (HARAO44), which was deposited on Nov. 17, 1998 at the American Type Culture Collection, and given Accession Number 203484. The deposited gene is inserted in the pSport plasmid (Life Technologies, Rockville, MD) using the Sall/NotI restriction endonuclease cleavage sites.

25 The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated DNA molecule having the nucleotide sequence of the deposited cDNA or the nucleotide sequence shown in SEQ ID

NO:14 is intended DNA fragments at least about 15nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length which are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-1500 nt in length are also useful according to the present invention, as are fragments corresponding to most, if not all, of the nucleotide sequence of the deposited cDNA or as shown in SEQ ID NO:14. By a fragment at least 20 nt in length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of the deposited cDNA or the nucleotide sequence as shown in SEQ ID NO:14. In this context "about" includes the particularly recited size, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini.

Representative examples of polynucleotide fragments of the invention include, for example, fragments that comprise, or alternatively, consist of, a sequence from about nucleotide 1 to about 50, from about 51 to about 100, from about 101 to about 150, from about 151 to about 200, from about 201 to about 250, from about 251 to about 300, from about 301 to about 350, from about 351 to about 400, from about 401 to about 450, from about 451 to about 500, and from about 501 to about 550, and from about 551 to about 600, from about 601 to about 650, from about 651 to about 700, from about 701 to about 750, from about 751 to about 800, from about 801 to about 850, from about 851 to about 900, from about 901 to about 950, from about 951 to about 1000, from about 1001 to about 1050, from about 1051 to about 1100, from about 1101 to about 1150, from about 1151 to about 1200, from about 1201 to about 1250, from about 1251 to about 1300, from about 1301 to about 1350, from about 1351 to about 1389, and from about 187 to about 1119 of SEQ ID NO:14, or the complementary strand thereto, or the cDNA contained in the deposited gene. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at

both termini. In additional embodiments, the polynucleotides of the invention encode functional attributes of the corresponding protein.

Preferred embodiments of the invention in this regard include fragments that comprise alpha-helix and alpha-helix forming regions ("alpha-regions"), beta-sheet and  
5 beta-sheet forming regions ("beta-regions"), turn and turn-forming regions ("turn-regions"), coil and coil-forming regions ("coil-regions"), hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions and high antigenic index regions. The data representing the structural or functional attributes of the protein set forth in Figure 12 and/or Table IV,  
10 as described above, was generated using the various modules and algorithms of the DNA\*STAR set on default parameters. In a preferred embodiment, the data presented in columns VIII, IX, XIII, and XIV of Table IV can be used to determine regions of the protein which exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or  
15 XIV by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Certain preferred regions in these regards are set out in Figure 12, but may, as shown in Table IV, be represented or identified by using tabular representations of the  
20 data presented in Figure 12. The DNA\*STAR computer algorithm used to generate Figure 12 (set on the original default parameters) was used to present the data in Figure 12 in a tabular format (See Table IV). The tabular format of the data in Figure 12 is used to easily determine specific boundaries of a preferred region. The above-mentioned preferred regions set out in Figure 12 and in Table IV include, but are not limited to,  
25 regions of the aforementioned types identified by analysis of the amino acid sequence set out in Figures 10A-B. As set out in Figure 12 and in Table IV, such preferred regions include Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions,

Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and Hopp-Woods hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schulz flexible regions, Jameson-Wolf regions of high antigenic index and Emini surface-forming regions. Even if deletion of one or more amino acids from the N-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, etc.) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence shown in Figures 10A-B, up to the proline residue at position number 327 and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues n1-332 of Figures 10A-B, where n1 is an integer from 2 to 327 corresponding to the position of the amino acid residue in Figures 10A-B (which is identical to the sequence shown as SEQ ID NO:32). N-terminal deletions of the polypeptide of the invention shown as SEQ ID NO:32 include polypeptides comprising the amino acid sequence of residues: R-2 to T-332; L-3 to T-332; L-4 to T-332; A-5 to T-332; F-6 to T-332; L-7 to T-332; S-8 to T-332; L-9 to T-332; L-10 to T-332; A-11 to T-332; L-12 to T-332; V-13 to T-332; L-14 to T-332; Q-15 to T-

332; E-16 to T-332; T-17 to T-332; G-18 to T-332; T-19 to T-332; A-20 to T-332; S-21 to T-332; L-22 to T-332; P-23 to T-332; R-24 to T-332; K-25 to T-332; E-26 to T-332; R-27 to T-332; K-28 to T-332; R-29 to T-332; R-30 to T-332; E-31 to T-332; E-32 to T-332; Q-33 to T-332; M-34 to T-332; P-35 to T-332; R-36 to T-332; E-37 to T-332; G-38 to T-332; D-39 to T-332; S-40 to T-332; F-41 to T-332; E-42 to T-332; V-43 to T-332; L-44 to T-332; P-45 to T-332; L-46 to T-332; R-47 to T-332; N-48 to T-332; D-49 to T-332; V-50 to T-332; L-51 to T-332; N-52 to T-332; P-53 to T-332; D-54 to T-332; N-55 to T-332; Y-56 to T-332; G-57 to T-332; E-58 to T-332; V-59 to T-332; I-60 to T-332; D-61 to T-332; L-62 to T-332; S-63 to T-332; N-64 to T-332; Y-65 to T-332; E-66 to T-332; E-67 to T-332; L-68 to T-332; T-69 to T-332; D-70 to T-332; Y-71 to T-332; G-72 to T-332; D-73 to T-332; Q-74 to T-332; L-75 to T-332; P-76 to T-332; E-77 to T-332; V-78 to T-332; K-79 to T-332; V-80 to T-332; T-81 to T-332; S-82 to T-332; L-83 to T-332; A-84 to T-332; P-85 to T-332; A-86 to T-332; T-87 to T-332; S-88 to T-332; I-89 to T-332; S-90 to T-332; P-91 to T-332; A-92 to T-332; K-93 to T-332; S-94 to T-332; T-95 to T-332; T-96 to T-332; A-97 to T-332; P-98 to T-332; G-99 to T-332; T-100 to T-332; P-101 to T-332; S-102 to T-332; S-103 to T-332; N-104 to T-332; P-105 to T-332; T-106 to T-332; M-107 to T-332; T-108 to T-332; R-109 to T-332; P-110 to T-332; T-111 to T-332; T-112 to T-332; A-113 to T-332; G-114 to T-332; L-115 to T-332; L-116 to T-332; L-117 to T-332; S-118 to T-332; S-119 to T-332; Q-120 to T-332; P-121 to T-332; N-122 to T-332; H-123 to T-332; G-124 to T-332; L-125 to T-332; P-126 to T-332; T-127 to T-332; C-128 to T-332; L-129 to T-332; V-130 to T-332; C-131 to T-332; V-132 to T-332; C-133 to T-332; L-134 to T-332; G-135 to T-332; S-136 to T-332; S-137 to T-332; V-138 to T-332; Y-139 to T-332; C-140 to T-332; D-141 to T-332; D-142 to T-332; I-143 to T-332; D-144 to T-332; L-145 to T-332; E-146 to T-332; D-147 to T-332; I-148 to T-332; P-149 to T-332; P-150 to T-332; L-151 to T-332; P-152 to T-332; R-153 to T-332; R-154 to T-332; T-155 to T-332; A-156 to T-332; Y-157 to T-332; L-158 to T-332; Y-159 to T-332; A-160 to T-332; R-161 to T-332; F-162 to T-332; N-163 to T-332;



R-164 to T-332; I-165 to T-332; S-166 to T-332; R-167 to T-332; I-168 to T-332; R-169  
 to T-332; A-170 to T-332; E-171 to T-332; D-172 to T-332; F-173 to T-332; K-174 to T-  
 332; G-175 to T-332; L-176 to T-332; T-177 to T-332; K-178 to T-332; L-179 to T-332;  
 K-180 to T-332; R-181 to T-332; I-182 to T-332; D-183 to T-332; L-184 to T-332; S-185  
 5 to T-332; N-186 to T-332; N-187 to T-332; L-188 to T-332; I-189 to T-332; S-190 to T-  
 332; S-191 to T-332; I-192 to T-332; D-193 to T-332; N-194 to T-332; D-195 to T-332;  
 A-196 to T-332; F-197 to T-332; R-198 to T-332; L-199 to T-332; L-200 to T-332; H-  
 201 to T-332; A-202 to T-332; L-203 to T-332; Q-204 to T-332; D-205 to T-332; L-206  
 to T-332; I-207 to T-332; L-208 to T-332; P-209 to T-332; E-210 to T-332; N-211 to T-  
 10 332; Q-212 to T-332; L-213 to T-332; E-214 to T-332; A-215 to T-332; L-216 to T-332;  
 P-217 to T-332; V-218 to T-332; L-219 to T-332; P-220 to T-332; S-221 to T-332; G-  
 222 to T-332; I-223 to T-332; E-224 to T-332; F-225 to T-332; L-226 to T-332; D-227 to  
 T-332; V-228 to T-332; R-229 to T-332; L-230 to T-332; N-231 to T-332; R-232 to T-  
 332; L-233 to T-332; Q-234 to T-332; S-235 to T-332; S-236 to T-332; G-237 to T-332;  
 15 I-238 to T-332; Q-239 to T-332; P-240 to T-332; A-241 to T-332; A-242 to T-332; F-  
 243 to T-332; R-244 to T-332; A-245 to T-332; M-246 to T-332; E-247 to T-332; K-248  
 to T-332; L-249 to T-332; Q-250 to T-332; F-251 to T-332; L-252 to T-332; Y-253 to T-  
 332; L-254 to T-332; S-255 to T-332; D-256 to T-332; N-257 to T-332; L-258 to T-332;  
 L-259 to T-332; D-260 to T-332; S-261 to T-332; I-262 to T-332; P-263 to T-332; G-264  
 20 to T-332; P-265 to T-332; L-266 to T-332; P-267 to T-332; P-268 to T-332; S-269 to T-  
 332; L-270 to T-332; R-271 to T-332; S-272 to T-332; V-273 to T-332; H-274 to T-332;  
 L-275 to T-332; Q-276 to T-332; N-277 to T-332; N-278 to T-332; L-279 to T-332; I-280  
 to T-332; E-281 to T-332; T-282 to T-332; M-283 to T-332; Q-284 to T-332; R-285 to T-  
 332; D-286 to T-332; V-287 to T-332; F-288 to T-332; C-289 to T-332; D-290 to T-332;  
 25 P-291 to T-332; E-292 to T-332; E-293 to T-332; H-294 to T-332; K-295 to T-332; H-  
 296 to T-332; T-297 to T-332; R-298 to T-332; R-299 to T-332; Q-300 to T-332; L-301  
 to T-332; E-302 to T-332; D-303 to T-332; I-304 to T-332; R-305 to T-332; L-306 to T-

332; D-307 to T-332; G-308 to T-332; N-309 to T-332; P-310 to T-332; I-311 to T-332;  
N-312 to T-332; L-313 to T-332; S-314 to T-332; L-315 to T-332; F-316 to T-332; P-317  
to T-332; S-318 to T-332; A-319 to T-332; Y-320 to T-332; F-321 to T-332; C-322 to T-  
332; L-323 to T-332; P-324 to T-332; R-325 to T-332; L-326 to T-332; P-327 to T-332;  
5 of SEQ ID NO:32. Polypeptides encoded by these polynucleotides are also encompassed  
by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the  
C-terminus of a protein results in modification or loss of one or more biological  
functions of the protein, other functional activities (e.g., biological activities (e.g., ability  
10 to illicit mitogenic activity, induce differentiation of normal or malignant cells, bind to  
EGF receptors, etc.)), may still be retained. For example the ability to induce and/or bind  
to antibodies which recognize the complete or mature forms of the polypeptide generally  
will be retained when less than the majority of the residues of the complete or mature  
polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking  
15 C-terminal residues of a complete polypeptide retains such immunologic activities can  
readily be determined by routine methods described herein and otherwise known in the  
art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid  
residues may retain some biological or immunogenic activities. In fact, peptides  
composed of as few as six amino acid residues may often evoke an immune response.

20 Accordingly, the present invention further provides polypeptides having one or  
more residues deleted from the carboxy terminus of the amino acid sequence of the  
polypeptide shown in Figures 10A-B, up to the glutamine residue at position number 7,  
and polynucleotides encoding such polypeptides. In particular, the present invention  
provides polypeptides comprising the amino acid sequence of residues 1-m1 of Figures  
25 10A-B, where m1 is an integer from 7 to 331 corresponding to the position of the amino  
acid residue in Figures 10A-B. Moreover, the invention provides polynucleotides  
encoding polypeptides comprising, or alternatively consisting of, the amino acid

sequence of C-terminal deletions of the polypeptide of the invention shown as SEQ ID NO:32 include polypeptides comprising the amino acid sequence of residues: M-1 to F-331; M-1 to R-330; M-1 to G-329; M-1 to I-328; M-1 to P-327; M-1 to L-326; M-1 to R-325; M-1 to P-324; M-1 to L-323; M-1 to C-322; M-1 to F-321; M-1 to Y-320; M-1 to A-319; M-1 to S-318; M-1 to P-317; M-1 to F-316; M-1 to L-315; M-1 to S-314; M-1 to L-313; M-1 to N-312; M-1 to I-311; M-1 to P-310; M-1 to N-309; M-1 to G-308; M-1 to D-307; M-1 to L-306; M-1 to R-305; M-1 to I-304; M-1 to D-303; M-1 to E-302; M-1 to L-301; M-1 to Q-300; M-1 to R-299; M-1 to R-298; M-1 to T-297; M-1 to H-296; M-1 to K-295; M-1 to H-294; M-1 to E-293; M-1 to E-292; M-1 to P-291; M-1 to D-290; M-1 to C-289; M-1 to F-288; M-1 to V-287; M-1 to D-286; M-1 to R-285; M-1 to Q-284; M-1 to M-283; M-1 to T-282; M-1 to E-281; M-1 to I-280; M-1 to L-279; M-1 to N-278; M-1 to N-277; M-1 to Q-276; M-1 to L-275; M-1 to H-274; M-1 to V-273; M-1 to S-272; M-1 to R-271; M-1 to L-270; M-1 to S-269; M-1 to P-268; M-1 to P-267; M-1 to L-266; M-1 to P-265; M-1 to G-264; M-1 to P-263; M-1 to I-262; M-1 to S-261; M-1 to D-260; M-1 to L-259; M-1 to L-258; M-1 to N-257; M-1 to D-256; M-1 to S-255; M-1 to L-254; M-1 to Y-253; M-1 to L-252; M-1 to F-251; M-1 to Q-250; M-1 to L-249; M-1 to K-248; M-1 to E-247; M-1 to M-246; M-1 to A-245; M-1 to R-244; M-1 to F-243; M-1 to A-242; M-1 to A-241; M-1 to P-240; M-1 to Q-239; M-1 to I-238; M-1 to G-237; M-1 to S-236; M-1 to S-235; M-1 to Q-234; M-1 to L-233; M-1 to R-232; M-1 to N-231; M-1 to L-230; M-1 to R-229; M-1 to V-228; M-1 to D-227; M-1 to L-226; M-1 to F-225; M-1 to E-224; M-1 to I-223; M-1 to G-222; M-1 to S-221; M-1 to P-220; M-1 to L-219; M-1 to V-218; M-1 to P-217; M-1 to L-216; M-1 to A-215; M-1 to E-214; M-1 to L-213; M-1 to Q-212; M-1 to N-211; M-1 to E-210; M-1 to P-209; M-1 to L-208; M-1 to I-207; M-1 to L-206; M-1 to D-205; M-1 to Q-204; M-1 to L-203; M-1 to A-202; M-1 to H-201; M-1 to L-200; M-1 to L-199; M-1 to R-198; M-1 to F-197; M-1 to A-196; M-1 to D-195; M-1 to N-194; M-1 to D-193; M-1 to I-192; M-1 to S-191; M-1 to S-190; M-1 to I-189; M-1 to L-188; M-1 to N-187; M-1 to N-186; M-1 to S-185; M-1 to L-184; M-1 to D-183; M-1 to I-

182; M-1 to R-181; M-1 to K-180; M-1 to L-179; M-1 to K-178; M-1 to T-177; M-1 to  
 L-176; M-1 to G-175; M-1 to K-174; M-1 to F-173; M-1 to D-172; M-1 to E-171; M-1  
 to A-170; M-1 to R-169; M-1 to I-168; M-1 to R-167; M-1 to S-166; M-1 to I-165; M-1  
 to R-164; M-1 to N-163; M-1 to F-162; M-1 to R-161; M-1 to A-160; M-1 to Y-159; M-1  
 5 to L-158; M-1 to Y-157; M-1 to A-156; M-1 to T-155; M-1 to R-154; M-1 to R-153; M-1  
 to P-152; M-1 to L-151; M-1 to P-150; M-1 to P-149; M-1 to I-148; M-1 to D-147; M-1  
 to E-146; M-1 to L-145; M-1 to D-144; M-1 to I-143; M-1 to D-142; M-1 to D-141; M-1  
 to C-140; M-1 to Y-139; M-1 to V-138; M-1 to S-137; M-1 to S-136; M-1 to G-135; M-1  
 to L-134; M-1 to C-133; M-1 to V-132; M-1 to C-131; M-1 to V-130; M-1 to L-129; M-1  
 10 to C-128; M-1 to T-127; M-1 to P-126; M-1 to L-125; M-1 to G-124; M-1 to H-123; M-1  
 to N-122; M-1 to P-121; M-1 to Q-120; M-1 to S-119; M-1 to S-118; M-1 to L-117; M-1  
 to L-116; M-1 to L-115; M-1 to G-114; M-1 to A-113; M-1 to T-112; M-1 to T-111; M-1  
 to P-110; M-1 to R-109; M-1 to T-108; M-1 to M-107; M-1 to T-106; M-1 to P-105; M-1  
 to N-104; M-1 to S-103; M-1 to S-102; M-1 to P-101; M-1 to T-100; M-1 to G-99; M-1  
 15 to P-98; M-1 to A-97; M-1 to T-96; M-1 to T-95; M-1 to S-94; M-1 to K-93; M-1 to A-  
 92; M-1 to P-91; M-1 to S-90; M-1 to I-89; M-1 to S-88; M-1 to T-87; M-1 to A-86; M-1  
 to P-85; M-1 to A-84; M-1 to L-83; M-1 to S-82; M-1 to T-81; M-1 to V-80; M-1 to K-  
 79; M-1 to V-78; M-1 to E-77; M-1 to P-76; M-1 to L-75; M-1 to Q-74; M-1 to D-73;  
 M-1 to G-72; M-1 to Y-71; M-1 to D-70; M-1 to T-69; M-1 to L-68; M-1 to E-67; M-1 to  
 20 E-66; M-1 to Y-65; M-1 to N-64; M-1 to S-63; M-1 to L-62; M-1 to D-61; M-1 to I-60;  
 M-1 to V-59; M-1 to E-58; M-1 to G-57; M-1 to Y-56; M-1 to N-55; M-1 to D-54; M-1  
 to P-53; M-1 to N-52; M-1 to L-51; M-1 to V-50; M-1 to D-49; M-1 to N-48; M-1 to R-  
 47; M-1 to L-46; M-1 to P-45; M-1 to L-44; M-1 to V-43; M-1 to E-42; M-1 to F-41; M-1  
 to S-40; M-1 to D-39; M-1 to G-38; M-1 to E-37; M-1 to R-36; M-1 to P-35; M-1 to M-  
 25 34; M-1 to Q-33; M-1 to E-32; M-1 to E-31; M-1 to R-30; M-1 to R-29; M-1 to K-28; M-  
 1 to R-27; M-1 to E-26; M-1 to K-25; M-1 to R-24; M-1 to P-23; M-1 to L-22; M-1 to S-  
 21; M-1 to A-20; M-1 to T-19; M-1 to G-18; M-1 to T-17; M-1 to E-16; M-1 to Q-15; M-

1 to L-14; M-1 to V-13; M-1 to L-12; M-1 to A-11; M-1 to L-10; M-1 to L-9; M-1 to S-8; M-1 to L-7; of SEQ ID NO:32. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In addition, the invention provides nucleic acid molecules having nucleotide  
5 sequences related to extensive portions of SEQ ID NO:14 which have been determined from the following related cDNA genes: HARAY79R (SEQ ID NO:80), HARAO44R (SEQ ID NO:81), HARAJ74R (SEQ ID NO:82), HARAO66R (SEQ ID NO:83), HARAN19R (SEQ ID NO:84), and HARAT78R (SEQ ID NO:85).

Therefore, polynucleotides and polypeptides of the invention are useful as  
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, retinal disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,  
15 particularly of the retina, expression of this gene at significantly higher or lower levels is routinely detected in certain tissues or cell types (e.g. retinal, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue  
20 or bodily fluid from an individual not having the disorder.

Preferred polypeptides of the present invention comprise immunogenic epitopes shown in SEQ ID NO: 32 as residues: Leu-22 to Asp-39, Asn-64 to Pro-76, Pro-98 to Thr-111, Pro-291 to Glu-302. Polynucleotides encoding said polypeptides are also provided.

25 The tissue distribution in retinal tissue, and the homology to a Gallus gallus proteoglycan involved in the ossification process indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of disorders of the

retina which involve the adhesion of tissues, or the binding of certain proteins to the cell surface. The translation products of this gene are useful for the treatment of retinal disorders such as retinal detachment in individuals suffering from myopia, or in the treatment of macular degeneration. Furthermore, this gene may serve as a tumor marker  
5 for retinoblastomas, or related tumors. More generally, the tissue distribution in retinal tissue indicates that The translation product of this gene is useful for the diagnosis, detection and/or treatment of eye disorders including blindness, color blindness, impaired vision, short and long sightedness, retinitis pigmentosa, retinitis proliferans, and retinoblastoma, retinochoroiditis, retinopathy and retinoschisis. Based upon the tissue  
10 distribution of this protein, antagonists directed against this protein is useful in blocking the activity of this protein. Accordingly, preferred are antibodies which specifically bind a portion of the translation product of this gene.

Also provided is a kit for detecting tumors in which expression of this protein occurs. Such a kit comprises in one embodiment an antibody specific for the translation  
15 product of this gene bound to a solid support. Also provided is a method of detecting these tumors in an individual which comprises a step of contacting an antibody specific for the translation product of this gene to a bodily fluid from the individual, preferably serum, and ascertaining whether antibody binds to an antigen found in the bodily fluid. Preferably the antibody is bound to a solid support and the bodily fluid is serum. The  
20 above embodiments, as well as other treatments and diagnostic tests (kits and methods), are more particularly described elsewhere herein. Furthermore, the protein may also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions, in addition to its use as a nutritional supplement. Protein, as well as, antibodies directed  
25 against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:14 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of  $a-b$ , where  $a$  is any integer between 1 to 1375 of SEQ ID NO:14,  $b$  is an integer of 15 to 1389, where both  $a$  and  $b$  correspond to the positions of nucleotide residues shown in SEQ ID NO:14, and where  $b$  is greater than or equal to  $a + 14$ .

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 5

The translation product of this gene shares sequence homology with the CD33 protein (See Genbank Accession No. gi|2913995). The expression pattern of CD33 within the hematopoietic system indicates a potential role in the regulation of myeloid cell differentiation. However, this expression is absent from hematopoietic stem cells. CD33 is expressed in clonogenic leukemia cells in about 90% of patients suffering from acute myeloid leukemia (AML). While about 60-70% of adults suffering from AML experience complete remission due to chemotherapy application, most of these patients will ultimately die of relapsed leukemia. It is believed that, like CD33, the CD33-like protein of the present invention is also expressed by clonogenic leukemia cells from the vast majority of patients with AML. Thus, there is a clear need to identify and isolate nucleic acid molecules encoding additional polypeptides having CD33-like protein activity. It is believed that cancerous tissue contains significantly greater amounts of CD33-like protein gene copy number and expresses significantly

enhanced levels of CD33-like protein and mRNA encoding the CD33-like protein when compared to a "standard" mammal, i.e.-a mammal of the same species not having the cancer or inflammatory disease. Thus, enhanced levels of the CD33-like protein will be detected in certain bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal  
5 fluid) from mammals when compared to sera from mammals of the same species not having the cancer or inflammatory disease.

Two related cDNA genes, HDPIB36 and HEOMH10, have been isolated. These cDNA genes appear to encode splice variants of this gene. Preferred polynucleotides comprise the following sequences:

10 CGACCCACGCGTCCGCCGCTTCGGCTTCCCCTTCTGCCAA  
GAGCCCTGAGCCACTCACAGCACGACCAGAGA (SEQ ID NO: 86),  
GTATGGAATGGGGTGGGAACCCCTGCCTCTCACTGGGGAGGGACCCTGGG  
GACAGCCTATGGGCTGAGCAGAGAGGGCTCTCAGGGACCCCTGCAGCACAA  
GAATCTCCCAACACGGTCTCTGTCCAGCCCTGACTCAGAAGCCTGATGTCTA  
15 CATCCCCGAGACCCTGGAGCCCGGGCAGCCGGTGACGGTCATCTGTGTGTTT  
AACTGGGCCTTTGAGGAATGTCCACCCCCTTCTTTCTCCTGGACGGGGGCTGC  
CCTCTCCTCCCAAGGAACCAAACCAACGACCTCCCACTTCTCAG (SEQ ID NO:  
87),  
ATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGGTA  
20 GGAAAGGGGACAGAGGAGCCAAGGCCTCTCAGTGCCGAATTGGGGGCCCAG  
GAGTCTGGAGGGTCCCCACGCAGGAGGGTCCCTGAGCCCTGAGCTGCTCATC  
GATICTGCCTCTTCCTTCCCT (SEQ ID NO: 88),  
GTGAGTGGGGGAAAGGGGACACCTGGGTCCCAGGAAGGGGACCCTGCTGAG  
TCCTGTCTCCTCCCCTCAG (SEQ ID NO: 89),  
25 CTGGCCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACACCAAACAGTCCTCG  
GACCCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAA  
AAGCAGTATCAGTTGCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCC



CAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCC  
AGGCGTCAGACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGA  
TTATGCAGAAGTCAAGTTCCAATGAGGGTCTCTTAGGCTTTAGGACTGGGAC  
TTCGGCTAGGGAGGAAGGTAGAGTAAGAGGTTGAAGATAACAGAGTGCAAA  
5 GTTTCCTTCTCTCCCTCTCTCTCTCTCTTTCTCTCTCTCTCTCTTTCTCTCTCT  
TTT (SEQ ID NO: 90), and/or  
AAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATCCCAGCACTT  
TGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTCTGGGAGTTCGAGACCAGCC  
TGGCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGG  
10 CATGGTGGCAGGCGCCTGTAATCCTACTACTTGGGAAGCTGAGGCAGGAGAA  
TCACTTGAACCTGGGAGACGGAGGTTGCAGTGAGCCAAGATCACACCATTTGC  
ACGCCAGCTTGGGCAACAAAGCGAGACTCCATCTCAAAAAAAAAAATCCTCC  
AAATGGGTTGGGTGTCTGTAATCCCAGCACTTTGGGAGGCTAAGGTGGGTGG  
ATTGCTTGAGCCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAACCCC  
15 ATCTCTACAAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAG  
TCCCAGCTGTCAGACATTTAAACCAGAGCAACTCCCATCTGGAATGGGAGCT  
GAATAAAATGAGGCTGAGACCTACTGGGCTGCCATTCTCAGACAGTGGAGGC  
CATTCTAAGTCACAGGATGAGACAGGAGGTCCGTACAAGATACAGGTCATA  
AAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCAACCAAATCCCACC  
20 AAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCGTCCTCACTGCTACACTC  
CTGACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACC  
CGATATGTCCCAAAGGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAA  
TAAGCAAGAAATAACCATAAAAGTGGGCAACCAGCAGCTCTAGGCGCTGCT  
CTTGTCTATGGAGTAGCCATTCTTTTGTTCCTTTACTTTCTTAATAAACTTGCT  
25 TTCACCTTAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:91). Also preferred  
are the polypeptides encoded by these polynucleotides.

Figures 13A-C shows the nucleotide (SEQ ID NO:15) and deduced amino acid sequence (SEQ ID NO:33) of the CD33-like protein. Predicted amino acids from about 1 to about 16 constitute the predicted signal peptide (amino acid residues from about 1 to about 16 in SEQ ID NO:33) and are represented by the underlined amino acid regions; and amino acids from about 496 to about 512 constitute the predicted transmembrane domain (amino acid residues from about 496 to about 512 in SEQ ID NO:33) and are represented by the double-underlined amino acid regions.

Figure 14 shows the regions of similarity between the amino acid sequences of the CD33-like protein SEQ ID NO:33, and the CD33L1 protein (gi|88178) (SEQ ID NO: 92).

Figure 15 shows an analysis of the amino acid sequence of SEQ ID NO:33.

Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic regions; flexible regions; antigenic index and surface probability are shown.

Northern analysis indicates that this gene is expressed highest in spleen tissue and peripheral blood leukocytes, and to a lesser extent in ovary and lung tissue.

The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding the polypeptide having the amino acid sequence shown in Figures 13A-C (SEQ ID NO:33), which was determined by sequencing a cloned cDNA (HDPCL05). The nucleotide sequence shown in Figures 13A-C (SEQ ID NO:15) was obtained by sequencing a cloned cDNA (HDPCL05), which was deposited on Nov. 17, 1998 at the American Type Culture Collection, and given Accession Number 203484. The deposited gene is inserted in the pSport plasmid (Life Technologies, Rockville, MD) using the SalI/NotI restriction endonuclease cleavage sites.

The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated DNA molecule having the nucleotide sequence of the deposited cDNA or the nucleotide sequence shown in SEQ ID NO:15 is intended DNA fragments at least about 15nt, and more preferably at least about

20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length which are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-1500 nt in length are also useful according to the present invention, as are fragments corresponding to most, if not all, of the nucleotide sequence of the deposited cDNA or as shown in SEQ ID NO:15. By a fragment at least 20 nt in length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of the deposited cDNA or the nucleotide sequence as shown in SEQ ID NO:15. In this context "about" includes the particularly recited size, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Representative examples of polynucleotide fragments of the invention include, for example, fragments that comprise, or alternatively, consist of, a sequence from about nucleotide 1 to about 50, from about 51 to about 100, from about 101 to about 150, from about 151 to about 200, from about 201 to about 250, from about 251 to about 300, from about 301 to about 350, from about 351 to about 400, from about 401 to about 450, from about 451 to about 500, from about 501 to about 550, from about 551 to about 600, from about 601 to about 650, from about 651 to about 700, from about 701 to about 750, from about 751 to about 800, from about 801 to about 850, from about 851 to about 900, from about 901 to about 950, from about 951 to about 1000, from about 1001 to about 1050, from about 1051 to about 1100, from about 1101 to about 1150, from about 1151 to about 1200, from about 1201 to about 1250, from about 1251 to about 1300, from about 1301 to about 1350, from about 1351 to about 1400, from about 1401 to about 1450, from about 1451 to about 1500, from about 1501 to about 1550, from about 1551 to about 1600, from about 1601 to about 1650, from about 1651 to about 1700, from about 1701 to about 1750, from about 1751 to about 1800, from about 1801 to about 1850, from about 1851 to about 1900, from about 1901 to about 1950, from about 1951 to about 2000, from about 2001 to about 2050, from about 2051 to about 2100, from about 2101 to about 2150, from about 2151 to about 2200, from about 2201 to about 2250,

from about 2251 to about 2295, from about 307 to about 1977, and from about 106 to about 1977, of SEQ ID NO:15, or the complementary strand thereto, or the cDNA contained in the deposited gene. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. In additional embodiments, the polynucleotides of the invention encode functional attributes of the corresponding protein.

Preferred embodiments of the invention in this regard include fragments that comprise alpha-helix and alpha-helix forming regions ("alpha-regions"), beta-sheet and beta-sheet forming regions ("beta-regions"), turn and turn-forming regions ("turn-regions"), coil and coil-forming regions ("coil-regions"), hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions and high antigenic index regions. The data representing the structural or functional attributes of the protein set forth in Figure 15 and/or Table V, as described above, was generated using the various modules and algorithms of the DNA\*STAR set on default parameters. In a preferred embodiment, the data presented in columns VIII, IX, XIII, and XIV of Table V can be used to determine regions of the protein which exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or XIV by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Certain preferred regions in these regards are set out in Figure 15, but may, as shown in Table V, be represented or identified by using tabular representations of the data presented in Figure 15. The DNA\*STAR computer algorithm used to generate Figure 15 (set on the original default parameters) was used to present the data in Figure 15 in a tabular format (See Table V). The tabular format of the data in Figure 15 is used to easily determine specific boundaries of a preferred region. The above-mentioned

preferred regions set out in Figure 15 and in Table V include, but are not limited to, regions of the aforementioned types identified by analysis of the amino acid sequence set out in Figures 13A-C. As set out in Figure 15 and in Table V, such preferred regions include Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions, 5 Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and Hopp-Woods hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schulz flexible regions, Jameson-Wolf regions of high antigenic index and Emini surface-forming regions. Even if deletion of one or more amino acids from the N-terminus of a protein results in modification or loss of one or more biological 10 functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, etc.) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus. Whether a particular 15 polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often 20 evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence shown in Figures 13A-C, up to the alanine residue at position number 634 and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides 25 comprising the amino acid sequence of residues n1-639 of Figures 13A-C, where n1 is an integer from 2 to 634 corresponding to the position of the amino acid residue in Figures 13A-C (which is identical to the sequence shown as SEQ ID NO:33). N-terminal

deletions of the polypeptide of the invention shown as SEQ ID NO:33 include polypeptides comprising the amino acid sequence of residues: L-2 to Q-639; L-3 to Q-639; P-4 to Q-639; L-5 to Q-639; L-6 to Q-639; L-7 to Q-639; S-8 to Q-639; S-9 to Q-639; L-10 to Q-639; L-11 to Q-639; G-12 to Q-639; G-13 to Q-639; S-14 to Q-639; Q-15 to Q-639; A-16 to Q-639; M-17 to Q-639; D-18 to Q-639; G-19 to Q-639; R-20 to Q-639; F-21 to Q-639; W-22 to Q-639; I-23 to Q-639; R-24 to Q-639; V-25 to Q-639; Q-26 to Q-639; E-27 to Q-639; S-28 to Q-639; V-29 to Q-639; M-30 to Q-639; V-31 to Q-639; P-32 to Q-639; E-33 to Q-639; A-34 to Q-639; C-35 to Q-639; D-36 to Q-639; I-37 to Q-639; S-38 to Q-639; V-39 to Q-639; P-40 to Q-639; C-41 to Q-639; S-42 to Q-639; F-43 to Q-639; S-44 to Q-639; Y-45 to Q-639; P-46 to Q-639; R-47 to Q-639; Q-48 to Q-639; D-49 to Q-639; W-50 to Q-639; T-51 to Q-639; G-52 to Q-639; S-53 to Q-639; T-54 to Q-639; P-55 to Q-639; A-56 to Q-639; Y-57 to Q-639; G-58 to Q-639; Y-59 to Q-639; W-60 to Q-639; F-61 to Q-639; K-62 to Q-639; A-63 to Q-639; V-64 to Q-639; T-65 to Q-639; E-66 to Q-639; T-67 to Q-639; T-68 to Q-639; K-69 to Q-639; G-70 to Q-639; A-71 to Q-639; P-72 to Q-639; V-73 to Q-639; A-74 to Q-639; T-75 to Q-639; N-76 to Q-639; H-77 to Q-639; Q-78 to Q-639; S-79 to Q-639; R-80 to Q-639; E-81 to Q-639; V-82 to Q-639; E-83 to Q-639; M-84 to Q-639; S-85 to Q-639; T-86 to Q-639; R-87 to Q-639; G-88 to Q-639; R-89 to Q-639; F-90 to Q-639; Q-91 to Q-639; L-92 to Q-639; T-93 to Q-639; G-94 to Q-639; D-95 to Q-639; P-96 to Q-639; A-97 to Q-639; K-98 to Q-639; G-99 to Q-639; N-100 to Q-639; C-101 to Q-639; S-102 to Q-639; L-103 to Q-639; V-104 to Q-639; I-105 to Q-639; R-106 to Q-639; D-107 to Q-639; A-108 to Q-639; Q-109 to Q-639; M-110 to Q-639; Q-111 to Q-639; D-112 to Q-639; E-113 to Q-639; S-114 to Q-639; Q-115 to Q-639; Y-116 to Q-639; F-117 to Q-639; F-118 to Q-639; R-119 to Q-639; V-120 to Q-639; E-121 to Q-639; R-122 to Q-639; G-123 to Q-639; S-124 to Q-639; Y-125 to Q-639; V-126 to Q-639; R-127 to Q-639; Y-128 to Q-639; N-129 to Q-639; F-130 to Q-639; M-131 to Q-639; N-132 to Q-639; D-133 to Q-639; G-134 to Q-639; F-135 to Q-639; F-136 to Q-639; L-137 to Q-639; K-138 to Q-639; V-139 to Q-639; T-140 to Q-639;

V-141 to Q-639; L-142 to Q-639; S-143to Q-639; F-144 to Q-639; T-145 to Q-639; P-146 to Q-639; R-147to Q-639; P-148 to Q-639; Q-149 to Q-639; D-150 to Q-639;H-151 to Q-639; N-152 to Q-639; T-153 to Q-639; D-154 toQ-639; L-155 to Q-639; T-156 to Q-639; C-157 to Q-639; H-158to Q-639; V-159 to Q-639; D-160 to Q-639; F-161 to Q-639; S-162to Q-639; R-163 to Q-639; K-164 to Q-639; G-165 to Q-639;V-166 to Q-639; S-167 to Q-639; A-168 to Q-639; Q-169 toQ-639; R-170 to Q-639; T-171 to Q-639; V-172 to Q-639; R-173to Q-639; L-174 to Q-639; R-175 to Q-639; V-176 to Q-639;A-177 to Q-639; Y-178 to Q-639; A-179 to Q-639; P-180 toQ-639; R-181 to Q-639; D-182 to Q-639; L-183 to Q-639; V-184to Q-639; I-185 to Q-639; S-186 to Q-639; I-187 to Q-639; S-188to Q-639; R-189 to Q-639; D-190 to Q-639; N-191 to Q-639;T-192 to Q-639; P-193 to Q-639; A-194 to Q-639; L-195 to Q-639;E-196 to Q-639; P-197 to Q-639; Q-198 to Q-639; P-199 to Q-639;Q-200 to Q-639; G-201 to Q-639; N-202 to Q-639; V-203 toQ-639; P-204 to Q-639; Y-205 to Q-639; L-206 to Q-639; E-207 toQ-639; A-208 to Q-639; Q-209 to Q-639; K-210 to Q-639; G-211to Q-639; Q-212 to Q-639; F-213 to Q-639; L-214 to Q-639; R-215to Q-639; L-216 to Q-639; L-217 to Q-639; C-218 to Q-639; A-219to Q-639; A-220 to Q-639; D-221 to Q-639; S-222 to Q-639;Q-223 to Q-639; P-224 to Q-639; P-225 to Q-639; A-226 to Q-639;T-227 to Q-639; L-228 to Q-639; S-229 to Q-639; W-230 toQ-639; V-231 to Q-639; L-232 to Q-639; Q-233 to Q-639; N-234to Q-639; R-235 to Q-639; V-236 to Q-639; L-237 to Q-639; S-238to Q-639; S-239 to Q-639; S-240 to Q-639; H-241 to Q-639; P-242to Q-639; W-243 to Q-639; G-244 to Q-639; P-245 to Q-639;R-246 to Q-639; P-247 to Q-639; L-248 to Q-639; G-249 toQ-639; L-250 to Q-639; E-251 to Q-639; L-252 to Q-639; P-253 toQ-639; G-254 to Q-639; V-255 to Q-639; K-256 to Q-639; A-257to Q-639; G-258 to Q-639; D-259 to Q-639; S-260 to Q-639;G-261 to Q-639; R-262 to Q-639; Y-263 to Q-639; T-264 toQ-639; C-265 to Q-639; R-266 to Q-639; A-267 to Q-639; E-268to Q-639; N-269 to Q-639; R-270 to Q-639; L-271 to Q-639;G-272 to Q-639; S-273 to Q-639; Q-274 to Q-639; Q-275 toQ-639; R-276 to Q-639; A-277 to Q-639; L-278 to Q-639; D-279to Q-639; L-280 to Q-639; S-

281 to Q-639; V-282 to Q-639; Q-283to Q-639; Y-284 to Q-639; P-285 to Q-639; P-286 to Q-639; E-287to Q-639; N-288 to Q-639; L-289 to Q-639; R-290 to Q-639;V-291 to Q-639; M-292 to Q-639; V-293 to Q-639; S-294 toQ-639; Q-295 to Q-639; A-296 to Q-639; N-297 to Q-639; R-298to Q-639; T-299 to Q-639; V-300 to Q-639; L-301 to Q-639;

5 E-302to Q-639; N-303 to Q-639; L-304 to Q-639; G-305 to Q-639;N-306 to Q-639; G-307 to Q-639; T-308 to Q-639; S-309 toQ-639; L-310 to Q-639; P-311 to Q-639; V-312 to Q-639; L-313 toQ-639; E-314 to Q-639; G-315 to Q-639; Q-316 to Q-639; S-317to Q-639; L-318 to Q-639; C-319 to Q-639; L-320 to Q-639; V-321to Q-639; C-322 to Q-639; V-323 to Q-639; T-324 to Q-639;H-325 to Q-639; S-326 to Q-639; S-327 to Q-639; P-

10 328 to Q-639;P-329 to Q-639; A-330 to Q-639; R-331 to Q-639; L-332 to Q-639;S-333 to Q-639; W-334 to Q-639; T-335 to Q-639; Q-336 toQ-639; R-337 to Q-639; G-338 to Q-639; Q-339 to Q-639; V-340to Q-639; L-341 to Q-639; S-342 to Q-639; P-343 to Q-639; S-344to Q-639; Q-345 to Q-639; P-346 to Q-639; S-347 to Q-639; D-348to Q-639; P-349 to Q-639; G-350 to Q-639; V-351 to Q-639;L-352 to Q-639; E-353 to Q-639; L-

15 354 to Q-639; P-355 to Q-639;R-356 to Q-639; V-357 to Q-639; Q-358 to Q-639; V-359 toQ-639; E-360 to Q-639; H-361 to Q-639; E-362 to Q-639; G-363to Q-639; E-364 to Q-639; F-365 to Q-639; T-366 to Q-639; C-367to Q-639; H-368 to Q-639; A-369 to Q-639; R-370 to Q-639;H-371 to Q-639; P-372 to Q-639; L-373 to Q-639; G-374 toQ-639; S-

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Q-639; A-631 toQ-639; D-632 to Q-639; Y-633 to Q-639; A-634 to Q-639; of SEQID  
15 NO:33. Polypeptides encoded by these polynucleotides are also encompassed by the  
invention.

Also as mentioned above, even if deletion of one or more amino acids from the  
C-terminus of a protein results in modification or loss of one or more biological  
functions of the protein, other functional activities (e.g., biological activities (e.g., ability  
20 to illicit mitogenic activity, induce differentiation of normal or malignant cells, bind to  
EGF receptors, etc.)), may still be retained. For example the ability to induce and/or bind  
to antibodies which recognize the complete or mature forms of the polypeptide generally  
will be retained when less than the majority of the residues of the complete or mature  
polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking  
25 C-terminal residues of a complete polypeptide retains such immunologic activities can  
readily be determined by routine methods described herein and otherwise known in the  
art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid

residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the polypeptide shown in Figures 13A-C, up to the leucine residue at position number 7, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues 1-m1 of Figures 13A-C, where m1 is an integer from 7 to 638 corresponding to the position of the amino acid residue in Figures 13A-C. Moreover, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of C-terminal deletions of the polypeptide of the invention shown as SEQ ID NO:33 include polypeptides comprising the amino acid sequence of residues: M-1 to F-638; M-1 to K-637; M-1 to V-636; M-1 to E-635; M-1 to A-634; M-1 to Y-633; M-1 to D-632; M-1 to A-631; M-1 to Q-630; M-1 to T-629; M-1 to G-628; M-1 to K-627; M-1 to P-626; M-1 to M-625; M-1 to R-624; M-1 to A-623; M-1 to E-622; M-1 to P-621; M-1 to R-620; M-1 to P-619; M-1 to R-618; M-1 to V-617; M-1 to G-616; M-1 to P-615; M-1 to F-614; M-1 to N-613; M-1 to L-612; M-1 to T-611; M-1 to A-610; M-1 to Y-609; M-1 to H-608; M-1 to L-607; M-1 to E-606; M-1 to E-605; M-1 to Q-604; M-1 to S-603; M-1 to E-602; M-1 to Q-601; M-1 to S-600; M-1 to E-599; M-1 to P-598; M-1 to A-597; M-1 to Q-596; M-1 to T-595; M-1 to S-594; M-1 to S-593; M-1 to K-592; M-1 to P-591; M-1 to E-590; M-1 to P-589; M-1 to F-588; M-1 to S-587; M-1 to P-586; M-1 to L-585; M-1 to Q-584; M-1 to Y-583; M-1 to Q-582; M-1 to K-581; M-1 to K-580; M-1 to Q-579; M-1 to N-578; M-1 to K-577; M-1 to K-576; M-1 to S-575; M-1 to E-574; M-1 to P-573; M-1 to S-572; M-1 to P-571; M-1 to A-570; M-1 to G-569; M-1 to P-568; M-1 to P-567; M-1 to L-566; M-1 to P-565; M-1 to T-564; M-1 to R-563; M-1 to P-562; M-1 to S-561; M-1 to N-560; M-1 to P-559; M-1 to T-558; M-1 to A-557; M-1 to K-556; M-1 to Q-555; M-1 to N-554; M-1 to R-553; M-1 to K-552; M-1 to Q-551; M-1 to A-550; M-1 to L-549;

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 M-1 to A-74; M-1 to V-73; M-1 to P-72; M-1 to A-71; M-1 to G-70; M-1 to K-69; M-1 to  
 T-68; M-1 to T-67; M-1 to E-66; M-1 to T-65; M-1 to V-64; M-1 to A-63; M-1 to K-62;

M-1 to F-61; M-1 to W-60; M-1 to Y-59; M-1 to G-58; M-1 to Y-57; M-1 to A-56; M-1 to P-55; M-1 to T-54; M-1 to S-53; M-1 to G-52; M-1 to T-51; M-1 to W-50; M-1 to D-49; M-1 to Q-48; M-1 to R-47; M-1 to P-46; M-1 to Y-45; M-1 to S-44; M-1 to F-43; M-1 to S-42; M-1 to C-41; M-1 to P-40; M-1 to V-39; M-1 to S-38; M-1 to I-37; M-1 to D-36; M-1 to C-35; M-1 to A-34; M-1 to E-33; M-1 to P-32; M-1 to V-31; M-1 to M-30; M-1 to V-29; M-1 to S-28; M-1 to E-27; M-1 to Q-26; M-1 to V-25; M-1 to R-24; M-1 to I-23; M-1 to W-22; M-1 to F-21; M-1 to R-20; M-1 to G-19; M-1 to D-18; M-1 to M-17; M-1 to A-16; M-1 to Q-15; M-1 to S-14; M-1 to G-13; M-1 to G-12; M-1 to L-11; M-1 to L-10; M-1 to S-9; M-1 to S-8; M-1 to L-7; of SEQ ID NO:33. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In addition, the invention provides nucleic acid molecules having nucleotide sequences related to extensive portions of SEQ ID NO:15 which have been determined from the following related cDNA genes: HTOFA26R (SEQ ID NO:93), HWAEM43R (SEQ ID NO:94), HDPMQ69R (SEQ ID NO:95), HDPGA09RA (SEQ ID NO:96), HEOMH10R (SEQ ID NO:97), and HFKCT73F (SEQ ID NO:98).

The polypeptide of this gene has been determined to have a transmembrane domain at about amino acid position 496 – 512 of the amino acid sequence referenced in Table XIII for this gene. Moreover, a cytoplasmic tail encompassing amino acids 513 to 639 of this protein has also been determined. Based upon these characteristics, it is believed that the protein product of this gene shares structural features to type Ia membrane proteins.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of the following diseases and conditions which include, but are not limited to, disorders of the immune system, in particular the immunodiagnosis of acute leukemias. Similarly, polypeptides and antibodies directed to these polypeptides are useful to provide immunological probes for differential

identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels is detected in certain tissues or cell types (e.g., immune, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue from an individual not having the disorder.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 33 as residues: Pro-46 to Gly-52, Asn-76 to Val-82, Ser-85 to Phe-90, Gly-94 to Asn-100, Gln-111 to Tyr-116, Pro-146 to Leu-155, Ser-188 to Asn-202, Ser-240 to Arg-246, Gly-258 to Tyr-263, Ala-267 to Arg-276, Ser-326 to Arg-331, Ser-333 to Gln-339, Pro-343 to Asp-348, Glu-426 to Asp-432, Pro-517 to His-533, Ala-550 to Pro-565, Gly-569 to Gln-582, Pro-589 to Glu-606, Gly-616 to Ala-623, Met-625 to Ala-631.

CD33 monoclonal antibodies (MoAB) are important in the immunodiagnosis of AML. CD33 MoABs have been used in preliminary therapeutic trials for purging bone marrow of AML patients, either before transplantation or for diseases resistant to chemotherapy. To prevent AML patients in remission from suffering relapse, or due to the lack of an appropriate allogenic bone marrow donor, a method is necessary for purging leukemia cells from the autografts of patients with advanced AML. By the invention, this method is provided by which bone marrow from an AML patient is obtained by, for example, percutaneous aspirations from the posterior iliac crest, isolating bone marrow mononuclear by Ficoll-hypaque density gradient centrifugation, and incubating with an anti-CD33-like protein MoAB, for example, 3-5 times for 15-30 min. at 4-6 degrees C, followed by incubation with rabbit complement at about 37 degrees C for 30 minutes. The patient is then subject to myeloablative chemotherapy, followed by reinfusion of the treated autologous bone marrow according to standard techniques. By the invention, clonogenic tumor cells are depleted from the bone marrow



while sparing hematopoietic cells necessary for engraftment. In a further embodiment, the invention provides an in vivo method for selectively killing or inhibiting growth of tumor cells expressing CD33-like protein antigen of the present invention. The method involves administering to the patient an effective amount of an antagonist to

5 inhibit the CD33-like protein receptor signaling pathway. By the invention, administering such antagonist of the CD33-like protein to a patient may also be useful for treating inflammatory diseases including arthritis and colitis. Antagonists for use in the present invention include polyclonal and monoclonal antibodies raised against the CD33-like protein or a fragment thereof, antisense molecules which control gene

10 expression through antisense DNA or RNA or through triple-helix formation, proteins or other compounds which bind the CD33-like protein domains, or soluble forms of the CD33-like protein, such as protein fragments including the extracellular region from the full length receptor, which antagonize CD33-like protein mediated signaling by competing with the cell surface CD33-like protein for binding to CD33 receptor ligands.

15

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:15 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the

20 scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2281 of SEQ ID NO:15, b is an integer of 15 to 2295, where both a and b correspond to the positions of nucleotide residues shown in

25 SEQ ID NO:15, and where b is greater than or equal to a + 14.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 6**

This invention relates to newly identified polynucleotides, polypeptides encoded  
5 by such polynucleotides, the use of such polynucleotides and polypeptides, as well as the  
production of such polynucleotides and polypeptides. The polypeptide of the present  
invention has been putatively identified as a CD33 homolog derived from a human  
primary dendritic cells cDNA library. More particularly, the polypeptide of the present  
invention has been putatively identified as a human siglec homolog, sometimes hereafter  
10 referred to as "CD33-like 3" and/or "siglec 7". The invention also relates to inhibiting  
the action of such polypeptides.

The siglecs (sialic acid binding Ig-like lectins) are type 1 membrane proteins that  
constitute a distinct subset of the Ig superfamily, characterised by their sequence  
similarities and abilities to bind sialic acids in glycoproteins and glycolipid (Crocker,  
15 P.R., et al., *Glycobiology*:8 (1998)). Members of the Ig Superfamily of proteins are  
defined as molecules that share domains of sequence similarity with the variable or  
constant domains of antibodies.

Many Ig superfamily proteins consist of multiple tandem Ig-like domains  
connected to other domains, such as Fn-III repeat domains (Vaughn, D.E., and P.J.  
20 Bjorkman, *Neuron*, 16:261-73 (1996)). At the primary structural level, traditional Ig-like  
domains can be identified by the presence of two cysteine residues separated by  
approximately 55-75 amino acid residues, and an "invariant" tryptophan residue located  
10-15 residues C-terminal to the first of the two conserved cysteine residues. The two  
conserved cysteine residues are thought to be involved in disulfide bonding to form the  
25 folded Ig structures (Vaughn, D.E., (1996)).

Ig-like domains further share a common folding pattern, that of a sandwich or  
fold structure of two  $\beta$ -sheets consisting of antiparallel  $\beta$ -strands containing 5-10 amino

acids (Huang, Z., et al., Biopolymers, 43:367-82 (1997)). Ig-like domains are divided, based upon sequence and structural similarities, into four classifications known as C1, C2, I and V-like domains.

The functional determinants of the Ig-like domains are presented on the faces of b-sheets or the loop regions of the Ig-fold. Accordingly, protein-protein interactions can occur either between the faces of the b-sheets, or the loop regions of the Ig-fold (Huang, Z., (1998)). These Ig-like domains are involved in mediating a diversity of biological functions such as intermolecular binding and protein-protein homophilic or heterophilic interactions.

Thus, Ig-like domains play an integral role in facilitating the activities of proteins of the Ig superfamily. In mammals, the group currently comprises sialoadhesin/siglec-1, CD22/siglec-2, CD33/siglec-3, myelin associated glycoprotein (MAG/siglec-4), siglecs-5, -6 and -7 (Crocker, P.R., et al., EMBO J., 13:4490-503 (1994); Sgroi, D., et al., J Biol. Chem., 268:7011-18 (1993); Freeman, D.S., et al., Blood, 85:2005-12 (1995); Kelm, S., et al., Curr Biol., 4:965-72 (1994); Cornish, A.L., et al., Blood, 92:2123-132 (1998); Patel, N., et al., J Biol. Chem, 274:22729-738 (1999); Nicol, G., et al., J Biol. Chem, In Press (1999)). Siglec-7 has also recently been characterised independently as the NK receptor p75/AIRM1 (Falco, M., et al., J. Exp. Med., 190:793-802 (1999)). In addition, the gene encoding another siglec-like sequence, OBBP-like protein has been reported but there is no information on its binding activity (Yousef, G.M., et al., Biochem. Biophys. Res. Commun., In Press (1999)).

Each of these proteins has an extracellular region made up of a membrane distal V-set domain followed by varying numbers of C2 set domains which range from 16 in sialoadhesin to 1 in CD33. In the cases of sialoadhesin, CD22, MAG and CD33, the sialic acid binding site has been mapped to the V-set domain and for sialoadhesin it has been further characterised at the molecular level by X-ray crystallography (Nath, D.,

et al., *J Biol. Chem.*, 270:26184-91 (1995); van der Merwe, P.A., et al., *J. Biol. Chem.*, 271:9273-80 (1996); Tang, S., et al., *J. Cell Biol.*, 138:1355-66 (1997); Taylor, V.C., et al., *J. Biol. Chem.*, 274:11505-12 (1999); May, A.P., et al., *Molecular Cell*, 1:719-28 (1998)).

- 5            Apart from MAG and SMP that are found exclusively in the nervous system, all siglecs characterised to date are expressed on discrete subsets of hemopoietic cells and can provide useful lineage-restricted markers. Thus, CD22 is present only on mature B cells, sialoadhesin is on macrophage subsets, CD33 is a marker of early committed myeloid progenitor cells, siglec-5 is expressed by monocytes and mature neutrophils, siglec-6 is on B cells and siglec-7 is expressed by NK cells and monocytes (Dorken, B., et al., *J. Immunology*, 136:4470-79 (1986); Crocker, P.R., et al., *J. Exp. Med.*, 164:1862-75 (1986); Peiper, S.C., et al., In *Leukocyte Typing IV*. Oxford University Press, Oxford. 814-16 (1989); Cornish, A.L., et al., *Blood*, 92:2123-132 (1998); Patel, N., et al., *J Biol. Chem*, 274:22729-738 (1999); Nicol, G., et al., *J Biol. Chem*, In Press (1999)). These
- 10            expression patterns indicate discrete functions amongst hemopoietic cell subsets, but apart from CD22, a well-characterised negative regulator of B cell activation (reviewed in Cyster, J.G. and C.C. Goodnow, *Immunity*, 6:509-17 (1997)), the biological functions of siglecs expressed in the hemopoietic system are unknown. Proposed functions include cell-cell interactions through recognition of sialylated glycoconjugates on other cells.
- 15            However, a number of studies have also shown that cell-cell adhesion mediated by siglecs can be modulated by cis-interactions with sialic acids present in the host plasma membrane. This is particularly striking for CD22, CD33 and siglec-5, whose binding activities can be greatly increased if host cells are pretreated with sialidase to remove the cis-competing sialic acids (Freeman, D.S., et al., *Blood*, 85:2005-12 (1995); Cornish, A.L., et al., *Blood*, 92:2123-132 (1998); Sgroi, D., et al., *P.N.A.S.*, 92:4026-30 (1995)).
- 20            A.L., et al., *Blood*, 92:2123-132 (1998); Sgroi, D., et al., *P.N.A.S.*, 92:4026-30 (1995)).
- 25            A.L., et al., *Blood*, 92:2123-132 (1998); Sgroi, D., et al., *P.N.A.S.*, 92:4026-30 (1995)).

Besides potential roles in cellular interactions, there is growing evidence that, similar to CD22, the more recently characterised siglecs are involved in signalling

functions. The cytoplasmic tails of CD33 and siglecs-5, -6 and -7 have two well-conserved tyrosine-based motifs that are similar to well-characterised signaling motifs in other leukocyte receptors (Gergely, J., et al., *Immun. Lett.*, 68:3-15 (1999)). Where studied, both tyrosine residues can be phosphorylated by src-like kinase(s) and, in the case of the membrane proximal tyrosine, this leads to subsequent recruitment of the tyrosine phosphatases, SHP-1 and SHP-2 (Falco, M., et al., *J. Exp. Med.*, 190:793-802 (1999); Taylor, V.C., et al., *J. Biol. Chem.*, 274:11505-12 (1999)).

Thus there exists a clear need for identifying and exploiting novel members of the siglec family of immunoglobulin proteins. Although structurally related, such proteins may possess diverse and multifaceted functions in a variety of cell and tissue types. The inventive purified siglec proteins are research tools useful for the identification, characterization and purification of cell signaling molecules. Furthermore, the identification of new siglecs permits the development of a range of derivatives, agonists and antagonists at the nucleic acid and protein levels which in turn have applications in the treatment and diagnosis of a range of conditions such as cancer, inflammation, neurological disorders and immunological disorders, amongst many other conditions. The polypeptide of the present invention has been putatively identified as a member of the siglec family and has been termed CD33-like 3. This identification has been made as a result of amino acid sequence homology to the human cd3311 (See Genbank Accession No. gi|2913995).

Figures 16A-B show the nucleotide (SEQ ID NO:16) and deduced amino acid sequence (SEQ ID NO:34) of CD33-like 3. Predicted amino acids from about 1 to about 18 constitute the predicted signal peptide (amino acid residues from about 1 to about 18 in SEQ ID NO:34) and are represented by the underlined amino acid regions; and amino acids from about 360 to about 376 constitute the predicted transmembrane domain (amino acids from about 360 to about 376 in SEQ ID NO:34) and are represented by the double underlined amino acids.

Figure 17 shows the regions of similarity between the amino acid sequences of the CD33-like 3 protein (SEQ ID NO:34) and the human CD33L1 protein (SEQ ID NO:99).

Figure 18 shows an analysis of the CD33-like 3 amino acid sequence. Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic regions; flexible regions; antigenic index and surface probability are shown.

A polynucleotide encoding a polypeptide of the present invention is obtained from human NK cells, T-cells, primary dendritic cells, placenta, spleen, primary breast cancer, gall bladder, apoptotic t-cells, macrophage, and chronic lymphocytic leukemia spleen. The polynucleotide of this invention was discovered in a human primary dendritic cell cDNA library.

As shown in Figures 16A-B, CD33-like 3 has a transmembrane domain (the transmembrane domains comprise amino acids from about 360 to about 376 of SEQ ID NO:34; which correspond to amino acids from about 360 to about 376 of Figures 16A-B ). The polynucleotide contains an open reading frame encoding the CD33-like 3 polypeptide of 467 amino acids. CD33-like 3 exhibits a high degree of homology at the amino acid level to the human CD33L1 (as shown in Figure 18).

The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding the CD33-like 3 polypeptide having the amino acid sequence shown in Figures 16A-B (SEQ ID NO:34). The nucleotide sequence shown in Figures 16A-B (SEQ ID NO:16) was obtained by sequencing a cloned cDNA (HDPUW68), which was deposited on November 17 at the American Type Culture Collection, and given Accession Number 203484.

The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated DNA molecule having the nucleotide sequence of the deposited cDNA or the nucleotide sequence shown in SEQ ID NO:16 is intended DNA fragments at least about 15nt, and more preferably at least about

20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length which are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-1500 nt in length are also useful according to the present invention, as are fragments corresponding to most, if not all, of the nucleotide sequence of the deposited cDNA or as shown in SEQ ID NO:16. By a fragment at least 20 nt in length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of the deposited cDNA or the nucleotide sequence as shown in SEQ ID NO:16. In this context "about" includes the particularly recited size, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Representative examples of CD33-like 3 polynucleotide fragments of the invention include, for example, fragments that comprise, or alternatively, consist of, a sequence from about nucleotide 1 to about 50, from about 51 to about 100, from about 101 to about 150, from about 151 to about 200, from about 201 to about 250, from about 251 to about 300, from about 301 to about 350, from about 351 to about 400, from about 401 to about 450, from about 451 to about 500, from about 501 to about 550, from about 551 to about 600, from about 601 to about 650, from about 651 to about 700, from about 701 to about 750, from about 751 to about 800, from about 801 to about 850, from about 851 to about 900, from about 901 to about 950, from about 951 to about 1000, from about 1001 to about 1050, from about 1051 to about 1100, from about 1101 to about 1150, from about 1151 to about 1200, from about 1201 to about 1250, from about 1251 to about 1300, from about 1301 to about 1350, from about 1351 to about 1400, from about 1401 to about 1450, from about 1451 to about 1500, from about 1501 to about 1550, from about 1551 to about 1600, from about 1601 to about 1650, from about 1651 to about 1700, from about 1701 to about 1748 of SEQ ID NO:16, or the complementary strand thereto, or the cDNA contained in the deposited gene. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini.

Preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding a member selected from the group: a polypeptide comprising or alternatively, consisting of, the transmembrane domain (amino acid residues from about 360 to about 376 in Figures 16A-B (amino acids from about 360 to about 376 in SEQ ID NO:34). Since the location of these domains have been predicted by computer analysis, one of ordinary skill would appreciate that the amino acid residues constituting these domains may vary slightly (e.g., by about 1 to 15 amino acid residues) depending on the criteria used to define each domain.

In additional embodiments, the polynucleotides of the invention encode functional attributes of CD33-like 3.

Preferred embodiments of the invention in this regard include fragments that comprise alpha-helix and alpha-helix forming regions ("alpha-regions"), beta-sheet and beta-sheet forming regions ("beta-regions"), turn and turn-forming regions ("turn-regions"), coil and coil-forming regions ("coil-regions"), hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions and high antigenic index regions of CD33-like 3. The data representing the structural or functional attributes of CD33-like 3 set forth in Figure 18 and/or Table VI, as described above, was generated using the various modules and algorithms of the DNA\*STAR set on default parameters. In a preferred embodiment, the data presented in columns VIII, IX, XIII, and XIV of Table VI can be used to determine regions of CD33-like 3 which exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or XIV by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Certain preferred regions in these regards are set out in Figure 18, but may, as shown in Table VI, be represented or identified by using tabular representations of the



data presented in Figure 18 . The DNA\*STAR computer algorithm used to generate Figure 18 (set on the original default parameters) was used to present the data in Figure 18 in a tabular format (See Table VI). The tabular format of the data in Figure 18 is used to easily determine specific boundaries of a preferred region. The above-mentioned

5 preferred regions set out in Figure 18 and in Table VI include, but are not limited to, regions of the aforementioned types identified by analysis of the amino acid sequence set out in Figures 16A-B. As set out in Figure 18 and in Table VI, such preferred regions include Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic

10 regions and Hopp-Woods hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schulz flexible regions, Jameson-Wolf regions of high antigenic index and Emini surface-forming regions. Even if deletion of one or more amino acids from the N-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to

15 multimerize, modulate cellular interaction, or signalling pathways, etc.) may still be retained. For example, the ability of shortened CD33-like 3 muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus. Whether a particular polypeptide

20 lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that an CD33-like 3 mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six CD33-like 3 amino acid residues

25 may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the CD33-like 3 amino acid sequence

shown in Figures 16A-B , up to the glutamic acid residue at position number 462 and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues n1-467 of Figures 16A-B , where n1 is an integer from 2 to 462 corresponding to the position of the amino acid residue in Figures 16A-B (which is identical to the sequence shown as SEQ ID NO:34). In another embodiment, N-terminal deletions of the CD33-like 3 polypeptide can be described by the general formula n2-467, where n2 is a number from 2 to 462, corresponding to the position of amino acid identified in Figures 16A-B . N-terminal deletions of the CD33-like 3 polypeptide of the invention shown as SEQ ID NO:34 include polypeptides comprising the amino acid sequence of residues: N-terminal deletions of the CD33-like 3 polypeptide of the invention shown as SEQ ID NO:34 include polypeptides comprising the amino acid sequence of residues: L-2 to K-467; L-3 to K-467; L-4 to K-467; L-5 to K-467; L-6 to K-467; L-7 to K-467; P-8 to K-467; L-9 to K-467; L-10 to K-467; W-11 to K-467; G-12 to K-467; R-13 to K-467; E-14 to K-467; R-15 to K-467; V-16 to K-467; E-17 to K-467; G-18 to K-467; Q-19 to K-467; K-20 to K-467; S-21 to K-467; N-22 to K-467; R-23 to K-467; K-24 to K-467; D-25 to K-467; Y-26 to K-467; S-27 to K-467; L-28 to K-467; T-29 to K-467; M-30 to K-467; Q-31 to K-467; S-32 to K-467; S-33 to K-467; V-34 to K-467; T-35 to K-467; V-36 to K-467; Q-37 to K-467; E-38 to K-467; G-39 to K-467; M-40 to K-467; C-41 to K-467; V-42 to K-467; H-43 to K-467; V-44 to K-467; R-45 to K-467; C-46 to K-467; S-47 to K-467; F-48 to K-467; S-49 to K-467; Y-50 to K-467; P-51 to K-467; V-52 to K-467; D-53 to K-467; S-54 to K-467; Q-55 to K-467; T-56 to K-467; D-57 to K-467; S-58 to K-467; D-59 to K-467; P-60 to K-467; V-61 to K-467; H-62 to K-467; G-63 to K-467; Y-64 to K-467; W-65 to K-467; F-66 to K-467; R-67 to K-467; A-68 to K-467; G-69 to K-467; N-70 to K-467; D-71 to K-467; I-72 to K-467; S-73 to K-467; W-74 to K-467; K-75 to K-467; A-76 to K-467; P-77 to K-467; V-78 to K-467; A-79 to K-467; T-80 to K-467; N-81 to K-467; N-82 to K-467; P-83 to K-467; A-84 to K-467; W-85 to K-467; A-86 to K-

467; V-87 to K-467; Q-88 to K-467; E-89 to K-467; E-90 to K-467; T-91 to K-467; R-92 to K-467; D-93 to K-467; R-94 to K-467; F-95 to K-467; H-96 to K-467; L-97 to K-467; L-98 to K-467; G-99 to K-467; D-100 to K-467; P-101 to K-467; Q-102 to K-467; T-103 to K-467; K-104 to K-467; N-105 to K-467; C-106 to K-467; T-107 to K-467; L-108 to  
5 K-467; S-109 to K-467; I-110 to K-467; R-111 to K-467; D-112 to K-467; A-113 to K-467; R-114 to K-467; M-115 to K-467; S-116 to K-467; D-117 to K-467; A-118 to K-467; G-119 to K-467; R-120 to K-467; Y-121 to K-467; F-122 to K-467; F-123 to K-467; R-124 to K-467; M-125 to K-467; E-126 to K-467; K-127 to K-467; G-128 to K-467; N-129 to K-467; I-130 to K-467; K-131 to K-467; W-132 to K-467; N-133 to K-467; Y-  
10 134 to K-467; K-135 to K-467; Y-136 to K-467; D-137 to K-467; Q-138 to K-467; L-139 to K-467; S-140 to K-467; V-141 to K-467; N-142 to K-467; V-143 to K-467; T-144 to K-467; A-145 to K-467; L-146 to K-467; T-147 to K-467; H-148 to K-467; R-149 to K-467; P-150 to K-467; N-151 to K-467; I-152 to K-467; L-153 to K-467; I-154 to K-467; P-155 to K-467; G-156 to K-467; T-157 to K-467; L-158 to K-467; E-159 to K-467; S-  
15 160 to K-467; G-161 to K-467; C-162 to K-467; F-163 to K-467; Q-164 to K-467; N-165 to K-467; L-166 to K-467; T-167 to K-467; C-168 to K-467; S-169 to K-467; V-170 to K-467; P-171 to K-467; W-172 to K-467; A-173 to K-467; C-174 to K-467; E-175 to K-467; Q-176 to K-467; G-177 to K-467; T-178 to K-467; P-179 to K-467; P-180 to K-467; M-181 to K-467; I-182 to K-467; S-183 to K-467; W-184 to K-467; M-185 to K-  
20 467; G-186 to K-467; T-187 to K-467; S-188 to K-467; V-189 to K-467; S-190 to K-467; P-191 to K-467; L-192 to K-467; H-193 to K-467; P-194 to K-467; S-195 to K-467; T-196 to K-467; T-197 to K-467; R-198 to K-467; S-199 to K-467; S-200 to K-467; V-201 to K-467; L-202 to K-467; T-203 to K-467; L-204 to K-467; I-205 to K-467; P-206 to K-467; Q-207 to K-467; P-208 to K-467; Q-209 to K-467; H-210 to K-467; H-211 to  
25 K-467; G-212 to K-467; T-213 to K-467; S-214 to K-467; L-215 to K-467; T-216 to K-467; C-217 to K-467; Q-218 to K-467; V-219 to K-467; T-220 to K-467; L-221 to K-467; P-222 to K-467; G-223 to K-467; A-224 to K-467; G-225 to K-467; V-226 to K-

467; T-227 to K-467; T-228 to K-467; N-229 to K-467; R-230 to K-467; T-231 to K-467;  
 I-232 to K-467; Q-233 to K-467; L-234 to K-467; N-235 to K-467; V-236 to K-467; S-  
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 5 to K-467; F-248 to K-467; Q-249 to K-467; G-250 to K-467; E-251 to K-467; G-252 to  
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 467; S-263 to K-467; L-264 to K-467; S-265 to K-467; V-266 to K-467; L-267 to K-467;  
 E-268 to K-467; G-269 to K-467; Q-270 to K-467; S-271 to K-467; L-272 to K-467; R-  
 10 273 to K-467; L-274 to K-467; V-275 to K-467; C-276 to K-467; A-277 to K-467; V-  
 278 to K-467; D-279 to K-467; S-280 to K-467; N-281 to K-467; P-282 to K-467; P-283  
 to K-467; A-284 to K-467; R-285 to K-467; L-286 to K-467; S-287 to K-467; W-288 to  
 K-467; T-289 to K-467; W-290 to K-467; R-291 to K-467; S-292 to K-467; L-293 to K-  
 467; T-294 to K-467; L-295 to K-467; Y-296 to K-467; P-297 to K-467; S-298 to K-467;  
 15 Q-299 to K-467; P-300 to K-467; S-301 to K-467; N-302 to K-467; P-303 to K-467; L-  
 304 to K-467; V-305 to K-467; L-306 to K-467; E-307 to K-467; L-308 to K-467; Q-309  
 to K-467; V-310 to K-467; H-311 to K-467; L-312 to K-467; G-313 to K-467; D-314 to  
 K-467; E-315 to K-467; G-316 to K-467; E-317 to K-467; F-318 to K-467; T-319 to K-  
 467; C-320 to K-467; R-321 to K-467; A-322 to K-467; Q-323 to K-467; N-324 to K-  
 20 467; S-325 to K-467; L-326 to K-467; G-327 to K-467; S-328 to K-467; Q-329 to K-467;  
 H-330 to K-467; V-331 to K-467; S-332 to K-467; L-333 to K-467; N-334 to K-467; L-  
 335 to K-467; S-336 to K-467; L-337 to K-467; Q-338 to K-467; Q-339 to K-467; E-340  
 to K-467; Y-341 to K-467; T-342 to K-467; G-343 to K-467; K-344 to K-467; M-345 to  
 K-467; R-346 to K-467; P-347 to K-467; V-348 to K-467; S-349 to K-467; G-350 to K-  
 25 467; V-351 to K-467; L-352 to K-467; L-353 to K-467; G-354 to K-467; A-355 to K-  
 467; V-356 to K-467; G-357 to K-467; G-358 to K-467; A-359 to K-467; G-360 to K-  
 467; A-361 to K-467; T-362 to K-467; A-363 to K-467; L-364 to K-467; V-365 to K-

467; F-366 to K-467; L-367 to K-467; S-368 to K-467; F-369 to K-467; C-370 to K-467; V-371 to K-467; I-372 to K-467; F-373 to K-467; I-374 to K-467; V-375 to K-467; V-376 to K-467; R-377 to K-467; S-378 to K-467; C-379 to K-467; R-380 to K-467; K-381 to K-467; K-382 to K-467; S-383 to K-467; A-384 to K-467; R-385 to K-467; P-386 to K-467; A-387 to K-467; A-388 to K-467; D-389 to K-467; V-390 to K-467; G-391 to K-467; D-392 to K-467; I-393 to K-467; G-394 to K-467; M-395 to K-467; K-396 to K-467; D-397 to K-467; A-398 to K-467; N-399 to K-467; T-400 to K-467; I-401 to K-467; R-402 to K-467; G-403 to K-467; S-404 to K-467; A-405 to K-467; S-406 to K-467; Q-407 to K-467; G-408 to K-467; N-409 to K-467; L-410 to K-467; T-411 to K-467; E-412 to K-467; S-413 to K-467; W-414 to K-467; A-415 to K-467; D-416 to K-467; D-417 to K-467; N-418 to K-467; P-419 to K-467; R-420 to K-467; H-421 to K-467; H-422 to K-467; G-423 to K-467; L-424 to K-467; A-425 to K-467; A-426 to K-467; H-427 to K-467; S-428 to K-467; S-429 to K-467; G-430 to K-467; E-431 to K-467; E-432 to K-467; R-433 to K-467; E-434 to K-467; I-435 to K-467; Q-436 to K-467; Y-437 to K-467; A-438 to K-467; P-439 to K-467; L-440 to K-467; S-441 to K-467; F-442 to K-467; H-443 to K-467; K-444 to K-467; G-445 to K-467; E-446 to K-467; P-447 to K-467; Q-448 to K-467; D-449 to K-467; L-450 to K-467; S-451 to K-467; G-452 to K-467; Q-453 to K-467; E-454 to K-467; A-455 to K-467; T-456 to K-467; N-457 to K-467; N-458 to K-467; E-459 to K-467; Y-460 to K-467; S-461 to K-467; E-462 to K-467; of SEQ ID NO:34. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities may still be retained. For example the ability of the shortened CD33-like 3 mutein to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature polypeptide are

removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a CD33-like 3 mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six CD33-like 3 amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the CD33-like 3 polypeptide shown in Figures 16A-B, up to the leucine residue at position number 6, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues 1-m1 of Figure 1, where m1 is an integer from 6 to 467 corresponding to the position of the amino acid residue in Figures 16A-B.

Moreover, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of C-terminal deletions of the CD33-like 3 polypeptide of the invention shown as SEQ ID NO:34 include polypeptides comprising the amino acid sequence of residues: M-1 to P-466; M-1 to I-465; M-1 to K-464; M-1 to I-463; M-1 to E-462; M-1 to S-461; M-1 to Y-460; M-1 to E-459; M-1 to N-458; M-1 to N-457; M-1 to T-456; M-1 to A-455; M-1 to E-454; M-1 to Q-453; M-1 to G-452; M-1 to S-451; M-1 to L-450; M-1 to D-449; M-1 to Q-448; M-1 to P-447; M-1 to E-446; M-1 to G-445; M-1 to K-444; M-1 to H-443; M-1 to F-442; M-1 to S-441; M-1 to L-440; M-1 to P-439; M-1 to A-438; M-1 to Y-437; M-1 to Q-436; M-1 to I-435; M-1 to E-434; M-1 to R-433; M-1 to E-432; M-1 to E-431; M-1 to G-430; M-1 to S-429; M-1 to S-428; M-1 to H-427; M-1 to A-426; M-1 to A-425; M-1 to L-424; M-1 to G-423; M-1 to H-422; M-1 to H-421; M-1 to R-420; M-1 to P-419; M-1 to N-418; M-1 to D-417; M-1 to D-416; M-1 to A-415; M-1 to W-414; M-1 to S-413; M-1 to E-412; M-1 to T-411; M-1

to L-410; M-1 to N-409; M-1 to G-408; M-1 to Q-407; M-1 to S-406; M-1 to A-405; M-1 to S-404; M-1 to G-403; M-1 to R-402; M-1 to I-401; M-1 to T-400; M-1 to N-399; M-1 to A-398; M-1 to D-397; M-1 to K-396; M-1 to M-395; M-1 to G-394; M-1 to I-393; M-1 to D-392; M-1 to G-391; M-1 to V-390; M-1 to D-389; M-1 to A-388; M-1 to A-387; M-1 to P-386; M-1 to R-385; M-1 to A-384; M-1 to S-383; M-1 to K-382; M-1 to K-381; M-1 to R-380; M-1 to C-379; M-1 to S-378; M-1 to R-377; M-1 to V-376; M-1 to V-375; M-1 to I-374; M-1 to F-373; M-1 to I-372; M-1 to V-371; M-1 to C-370; M-1 to F-369; M-1 to S-368; M-1 to L-367; M-1 to F-366; M-1 to V-365; M-1 to L-364; M-1 to A-363; M-1 to T-362; M-1 to A-361; M-1 to G-360; M-1 to A-359; M-1 to G-358; M-1 to G-357; M-1 to V-356; M-1 to A-355; M-1 to G-354; M-1 to L-353; M-1 to L-352; M-1 to V-351; M-1 to G-350; M-1 to S-349; M-1 to V-348; M-1 to P-347; M-1 to R-346; M-1 to M-345; M-1 to K-344; M-1 to G-343; M-1 to T-342; M-1 to Y-341; M-1 to E-340; M-1 to Q-339; M-1 to Q-338; M-1 to L-337; M-1 to S-336; M-1 to L-335; M-1 to N-334; M-1 to L-333; M-1 to S-332; M-1 to V-331; M-1 to H-330; M-1 to Q-329; M-1 to S-328; M-1 to G-327; M-1 to L-326; M-1 to S-325; M-1 to N-324; M-1 to Q-323; M-1 to A-322; M-1 to R-321; M-1 to C-320; M-1 to T-319; M-1 to F-318; M-1 to E-317; M-1 to G-316; M-1 to E-315; M-1 to D-314; M-1 to G-313; M-1 to L-312; M-1 to H-311; M-1 to V-310; M-1 to Q-309; M-1 to L-308; M-1 to E-307; M-1 to L-306; M-1 to V-305; M-1 to L-304; M-1 to P-303; M-1 to N-302; M-1 to S-301; M-1 to P-300; M-1 to Q-299; M-1 to S-298; M-1 to P-297; M-1 to Y-296; M-1 to L-295; M-1 to T-294; M-1 to L-293; M-1 to S-292; M-1 to R-291; M-1 to W-290; M-1 to T-289; M-1 to W-288; M-1 to S-287; M-1 to L-286; M-1 to R-285; M-1 to A-284; M-1 to P-283; M-1 to P-282; M-1 to N-281; M-1 to S-280; M-1 to D-279; M-1 to V-278; M-1 to A-277; M-1 to C-276; M-1 to V-275; M-1 to L-274; M-1 to R-273; M-1 to L-272; M-1 to S-271; M-1 to Q-270; M-1 to G-269; M-1 to E-268; M-1 to L-267; M-1 to V-266; M-1 to S-265; M-1 to L-264; M-1 to S-263; M-1 to S-262; M-1 to S-261; M-1 to N-260; M-1 to G-259; M-1 to L-258; M-1 to A-257; M-1 to T-256; M-1 to S-255; M-1 to A-254; M-1 to T-253; M-1 to G-252; M-1 to E-251; M-1 to

G-250; M-1 to Q-249; M-1 to F-248; M-1 to V-247; M-1 to T-246; M-1 to V-245; M-1 to T-244; M-1 to L-243; M-1 to N-242; M-1 to Q-241; M-1 to P-240; M-1 to P-239; M-1 to Y-238; M-1 to S-237; M-1 to V-236; M-1 to N-235; M-1 to L-234; M-1 to Q-233; M-1 to I-232; M-1 to T-231; M-1 to R-230; M-1 to N-229; M-1 to T-228; M-1 to T-227; M-1 to V-226; M-1 to G-225; M-1 to A-224; M-1 to G-223; M-1 to P-222; M-1 to L-221; M-1 to T-220; M-1 to V-219; M-1 to Q-218; M-1 to C-217; M-1 to T-216; M-1 to L-215; M-1 to S-214; M-1 to T-213; M-1 to G-212; M-1 to H-211; M-1 to H-210; M-1 to Q-209; M-1 to P-208; M-1 to Q-207; M-1 to P-206; M-1 to I-205; M-1 to L-204; M-1 to T-203; M-1 to L-202; M-1 to V-201; M-1 to S-200; M-1 to S-199; M-1 to R-198; M-1 to T-197; M-1 to T-196; M-1 to S-195; M-1 to P-194; M-1 to H-193; M-1 to L-192; M-1 to P-191; M-1 to S-190; M-1 to V-189; M-1 to S-188; M-1 to T-187; M-1 to G-186; M-1 to M-185; M-1 to W-184; M-1 to S-183; M-1 to I-182; M-1 to M-181; M-1 to P-180; M-1 to P-179; M-1 to T-178; M-1 to G-177; M-1 to Q-176; M-1 to E-175; M-1 to C-174; M-1 to A-173; M-1 to W-172; M-1 to P-171; M-1 to V-170; M-1 to S-169; M-1 to C-168; M-1 to T-167; M-1 to L-166; M-1 to N-165; M-1 to Q-164; M-1 to F-163; M-1 to C-162; M-1 to G-161; M-1 to S-160; M-1 to E-159; M-1 to L-158; M-1 to T-157; M-1 to G-156; M-1 to P-155; M-1 to I-154; M-1 to L-153; M-1 to I-152; M-1 to N-151; M-1 to P-150; M-1 to R-149; M-1 to H-148; M-1 to T-147; M-1 to L-146; M-1 to A-145; M-1 to T-144; M-1 to V-143; M-1 to N-142; M-1 to V-141; M-1 to S-140; M-1 to L-139; M-1 to Q-138; M-1 to D-137; M-1 to Y-136; M-1 to K-135; M-1 to Y-134; M-1 to N-133; M-1 to W-132; M-1 to K-131; M-1 to I-130; M-1 to N-129; M-1 to G-128; M-1 to K-127; M-1 to E-126; M-1 to M-125; M-1 to R-124; M-1 to F-123; M-1 to F-122; M-1 to Y-121; M-1 to R-120; M-1 to G-119; M-1 to A-118; M-1 to D-117; M-1 to S-116; M-1 to M-115; M-1 to R-114; M-1 to A-113; M-1 to D-112; M-1 to R-111; M-1 to I-110; M-1 to S-109; M-1 to L-108; M-1 to T-107; M-1 to C-106; M-1 to N-105; M-1 to K-104; M-1 to T-103; M-1 to Q-102; M-1 to P-101; M-1 to D-100; M-1 to G-99; M-1 to L-98; M-1 to L-97; M-1 to H-96; M-1 to F-95; M-1 to R-94; M-1 to D-93; M-1 to R-92; M-1 to T-91; M-1 to E-90; M-1 to E-



89; M-1 to Q-88; M-1 to V-87; M-1 to A-86; M-1 to W-85; M-1 to A-84; M-1 to P-83; M-1 to N-82; M-1 to N-81; M-1 to T-80; M-1 to A-79; M-1 to V-78; M-1 to P-77; M-1 to A-76; M-1 to K-75; M-1 to W-74; M-1 to S-73; M-1 to I-72; M-1 to D-71; M-1 to N-70; M-1 to G-69; M-1 to A-68; M-1 to R-67; M-1 to F-66; M-1 to W-65; M-1 to Y-64; M-1 to G-63; M-1 to H-62; M-1 to V-61; M-1 to P-60; M-1 to D-59; M-1 to S-58; M-1 to D-57; M-1 to T-56; M-1 to Q-55; M-1 to S-54; M-1 to D-53; M-1 to V-52; M-1 to P-51; M-1 to Y-50; M-1 to S-49; M-1 to F-48; M-1 to S-47; M-1 to C-46; M-1 to R-45; M-1 to V-44; M-1 to H-43; M-1 to V-42; M-1 to C-41; M-1 to M-40; M-1 to G-39; M-1 to E-38; M-1 to Q-37; M-1 to V-36; M-1 to T-35; M-1 to V-34; M-1 to S-33; M-1 to S-32; M-1 to Q-31; M-1 to M-30; M-1 to T-29; M-1 to L-28; M-1 to S-27; M-1 to Y-26; M-1 to D-25; M-1 to K-24; M-1 to R-23; M-1 to N-22; M-1 to S-21; M-1 to K-20; M-1 to Q-19; M-1 to G-18; M-1 to E-17; M-1 to V-16; M-1 to R-15; M-1 to E-14; M-1 to R-13; M-1 to G-12; M-1 to W-11; M-1 to L-10; M-1 to L-9; M-1 to P-8; M-1 to L-7; M-1 to L-6; of SEQ ID NO:34. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In addition, the invention provides nucleic acid molecules having nucleotide sequences related to extensive portions of SEQ ID NO:16 which have been determined from the following related cDNA genes: HGBAY02R (SEQ ID NO:100) and HLYBY62R (SEQ ID NO:101).

Based on the sequence similarity to the human CD33L1, translation product of this gene is expected to share at least some biological activities with CD33 proteins, and specifically myeloid modulatory proteins and/or siglec proteins. Such activities are known in the art, some of which are described elsewhere herein.

Specifically, polynucleotides and polypeptides of the invention are also useful for modulating the differentiation of normal and malignant cells, modulating the proliferation and/or differentiation of cancer and neoplastic cells, and modulating the immune response. Polynucleotides and polypeptides of the invention may represent a

diagnostic marker for hematopoietic and immune diseases and/or disorders. The full-length protein should be a secreted protein, based upon homology to the CD33 family. Therefore, it is secreted into serum, urine, or feces and thus the levels is assayable from patient samples. Assuming specific expression levels are reflective of the presence of  
5 immune disorders, this protein would provide a convenient diagnostic for early detection. In addition, expression of this gene product may also be linked to the progression of immune diseases, and therefore may itself actually represent a therapeutic or therapeutic target for the treatment of cancer.

Polynucleotides and polypeptides of the invention may play an important role in  
10 the pathogenesis of human cancers and cellular transformation, particularly those of the immune and hematopoietic systems. Polynucleotides and polypeptides of the invention may also be involved in the pathogenesis of developmental abnormalities based upon its potential effects on proliferation and differentiation of cells and tissue cell types. Due to the potential proliferating and differentiating activity of said polynucleotides and  
15 polypeptides, the invention is useful as a therapeutic agent in inducing tissue regeneration, for treating inflammatory conditions (e.g., inflammatory bowel syndrome, diverticulitis, etc.). Moreover, the invention is useful in modulating the immune response to aberrant polypeptides, as may exist in rapidly proliferating cells and tissue cell types, particularly in adenocarcinoma cells, and other cancers.

20 This gene is expressed predominantly on NK cells, and to a lesser extent on T-cells. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of the following diseases and conditions which include, but are not limited to, immune disorders and cancer, as well as the immunodiagnosis of acute  
25 leukemias. Similarly, polypeptides and antibodies directed to these polypeptides are useful to provide immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the

immune system, and breast tissue, expression of this gene at significantly higher or lower levels is detected in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue from an individual not having the disorder.

Preferred polypeptides of the present invention comprise immunogenic epitopes shown in SEQ ID NO: 34 as residues: Gly-12 to Tyr-26, Val-52 to Asp-59, Gln-88 to Asp-93, Arg-124 to Asn-129, His-193 to Arg-198, Gln-207 to Thr-213, Gln-338 to Arg-346, Ser-378 to Ala-384, Ser-413 to Arg-420, Ser-428 to Glu-434, His-443 to Ser-451, Glu-454 to Ser-461. Polynucleotides encoding said polypeptides are also provided.

The tissue distribution in NK cells, in combination with the homology to siglec family of proteins indicates the protein product of this gene is useful for the diagnosis and treatment of a variety of immune system disorders. NK cells are bone-marrow derived granular lymphocytes that play an important role in natural immunity to infectious diseases and have the capacity to kill certain virally-infected cells and tumor cells that have down-regulated MHC Class-I antigen expression. The killing and proinflammatory activities of NK cells are regulated through a variety of cell surface receptors that can mediate either activity or inhibitory signals. The best understood receptors are those that recognize MHC Class I molecules at the cell surface and deliver a negative signal, thereby protecting normal host cells from cytotoxicity. These receptors can belong either to the C-type lectin superfamily or the Ig superfamily, although in humans the majority are members of the Ig superfamily known as killer cell Ig-like receptors (KIRs). Representative uses are described in the "Immune Activity" and "infectious disease" sections below, in Example 11, 13, 14, 16, 18, 19, 20, and 27, and elsewhere herein. Briefly, the expression indicates a role in regulating the proliferation; survival; differentiation; and/or activation of hematopoietic cell lineages, including blood

stem cells. Involvement in the regulation of cytokine production, antigen presentation, or other processes indicates a usefulness for treatment of cancer (e.g. by boosting immune responses). Expression in cells of lymphoid origin, indicates the natural gene product is involved in immune functions. Therefore it would also be useful as an agent

5 for immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis, granulomatous Disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versus-host diseases, or autoimmunity disorders, such

10 as autoimmune infertility, lense tissue injury, demyelination, systemic lupus erythematosus, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's Disease, and scleroderma. Moreover, the protein may represent a secreted factor that influences the differentiation or behavior of other blood cells, or that recruits hematopoietic cells to sites of injury. Thus, this gene product is thought to be useful in the expansion of

15 stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Based upon the tissue distribution of this protein, antagonists directed against this protein is useful in blocking the activity of this protein. Accordingly, preferred are antibodies which specifically bind a portion of the translation product of this gene.

20 Also provided is a kit for detecting tumors in which expression of this protein occurs. Such a kit comprises in one embodiment an antibody specific for the translation product of this gene bound to a solid support. Also provided is a method of detecting these tumors in an individual which comprises a step of contacting an antibody specific for the translation product of this gene to a bodily fluid from the individual, preferably

25 serum, and ascertaining whether antibody binds to an antigen found in the bodily fluid. Preferably the antibody is bound to a solid support and the bodily fluid is serum. The above embodiments, as well as other treatments and diagnostic tests (kits and methods),

are more particularly described elsewhere herein. Furthermore, the protein may also be used to determine biological activity, raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions, in addition to its use as a nutritional supplement. Protein, as well as, antibodies directed  
5 against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:16 and may have been publicly available prior to conception of the present  
10 invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-  
b, where a is any integer between 1 to 1734 of SEQ ID NO:16, b is an integer of 15 to  
15 1748, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:16, and where b is greater than or equal to a + 14.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 7

20

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the use of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides. The polypeptide of the present invention has been putatively identified as a human integrin alpha 11 homolog derived  
25 from a human osteoblast II cDNA library. More particularly, the polypeptide of the present invention has been putatively identified as a human integrin alpha 11-subunit homolog, sometimes hereafter referred to as "integrin alpha 11", "integrin alpha 11-

subunit", "a11", "A11-subunit", and/or "Integrin a11-subunit". The invention also relates to inhibiting the action of such polypeptides.

The integrins are a large family of cell adhesion molecules consisting of noncovalently associated ab heterodimers.

5       We have cloned and sequenced a novel human integrin a -subunit cDNA, designated a11. The a11 cDNA encodes a protein with a 22 amino acid signal peptide, a large 1120 residue extracellular domain that contains an I-domain of 207 residues and is linked by a transmembrane domain to a short cytoplasmic domain of 24 amino acids. The deduced a11 protein shows the typical structural features of integrin a-subunits and is  
10       similar to a distinct group of a-subunits from collagen-binding integrins. However, it differs from most integrin a-chains by an incompletely preserved cytoplasmic GFFKR motif.

      The human ITGA11 gene was located to bands q22.3-23 on chromosome 15, and its transcripts were found predominantly in bone, cartilage as well as in cardiac and  
15       skeletal muscle. Expression of the 5.5 kilobase a11 mRNA was also detectable in ovary and small intestine.

      All vertebrate cells express members of the integrin family of cell adhesion molecules, which mediate cellular adhesion to other cells and extracellular substratum, cell migration and participate in important physiologic processes from signal transduction to cell  
20       proliferation and differentiation {Hynes, 92; Springer, 92 }.

      Integrins are structurally homologous heterodimeric type-I membrane glycoproteins formed by the noncovalent association of one of eight b -subunits with one of the 17 different a-subunits described to date, resulting in at least 22 different ab complexes. Their binding specificities for cellular and extracellular ligands are  
25       determined by both subunits and are dynamically regulated in a cell-type-specific mode by the cellular environment as well as by the developmental and activation state of the cell {Diamond and Springer, 94}. In integrin a -subunits, the aminoterminal region of the

large extracellular domain consists of a seven-fold repeated structure which is predicted to fold into a  $\beta$ -propeller domain {Corbi et al., 1987; Springer, 1997}. The three or four C-terminal repeats contain putative divalent cation binding motifs that are thought to be important for ligand binding and subunit association {Diamond and Springer, 94}. The

5 a1, a2, a10, aD, aE, aL, aM and aX-subunits contain an approximately 200 amino acid I-domain inserted between the second and third repeat that is not present in other  $\alpha$ -chains {Larson et al., 1989}. Several isolated I-domains have been shown to independently bind the ligands of the parent integrin heterodimer {Kamata and Takada, 1994; Randi and Hogg, 1994}. The a3, a5-8, aIIb and aV-subunits are proteolytically processed at a

10 conserved site into disulphide-linked heavy and light chains, while the a4-subunit is cleaved at a more aminoterminal site into two fragments that remain noncovalently associated {Hemler et al., 90}. Additional  $\alpha$ -subunit variants are generated by alternative splicing of primary transcripts {Ziober et al., 93; Delwel et al., 95; Leung et al., 98}.

The extracellular domains of  $\alpha$ -integrin subunits are connected by a single

15 spanning transmembrane domain to short, diverse cytoplasmic domains whose only conserved feature is a membrane-proximal KXGFF(K/R)R motif {Sastry and Horwitz, 1993}. The cytoplasmic domains have been implicated in the cell-type-specific modulation of integrin affinity states {Williams et al., 1994}.

The polypeptide of the present invention has been putatively identified as a

20 member of the integrin family and has been termed integrin  $\alpha$ 11 subunit ("a11"). This identification has been made as a result of amino acid sequence homology to the human integrin  $\alpha$ 1 subunit (See Genbank Accession No. gi|346210).

Figures 19A-F show the nucleotide (SEQ ID NO:17) and deduced amino acid sequence (SEQ ID NO:35) of a11. Predicted amino acids from about 1 to about 22

25 constitute the predicted signal peptide (amino acid residues from about 1 to about 22 in SEQ ID NO:35) and are represented by the underlined amino acid regions; amino acids from about 666 to about 682, and/or amino acids from about 1145 to about 1161

constitute the predicted transmembrane domains (amino acids from about 666 to about 682, and/or amino acids from about 1145 to about 1161 in SEQ ID NO:35) and are represented by the double underlined amino acids; and amino acids from about 64 to about 96 constitute the predicted immunoglobulin and major histocompatibility complex protein domain (amino acids from about 64 to about 96 in SEQ ID NO:35) and are represented by the bold amino acids.

Figure 20 shows the regions of similarity between the amino acid sequences of the integrin alpha 11 subunit (a11) protein (SEQ ID NO:35) and the human integrin alpha 1 subunit (SEQ ID NO: 103).

Figure 21 shows an analysis of the integrin alpha 11 subunit (a11) amino acid sequence. Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic regions; flexible regions; antigenic index and surface probability are shown.

A polynucleotide encoding a polypeptide of the present invention is obtained from human ovary, small intestine, fetal heart, fetal brain, large intestine, osteoblasts, human trabecular bone cells, mesangial cells, adipocytes, osteosarcoma, chondrosarcoma, breast cancer cells, and bone marrow tissues and cells. The polynucleotide of this invention was discovered in a human osteoblast II cDNA library. Its translation product has homology to the characteristic immunoglobulin and major histocompatibility complex protein domain of integrin family members. As shown in Figures 19A-F, a11 has transmembrane domains (the transmembrane domains comprise amino acids 666 – 682 and/or 1145 - 1161 of SEQ ID NO:35; which correspond to amino acids 666 – 682 and/or 1145 - 1161 of Figures 19A-F) with strong conservation between other members of the integrin family. The polynucleotide contains an open reading frame encoding the a11 polypeptide of 1189 amino acids. The present invention exhibits a high degree of homology at the amino acid level to the human integrin alpha 1 subunit (as shown in Figure 20).

Preferred polypeptides of the invention comprise the following amino acid



sequence: TNGYQKTGDVYKCPVIHGNCTKLNLRVTLSNV (SEQ ID NO:102).

Polynucleotides encoding these polypeptides are also provided.

The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding the all polypeptide having the amino acid sequence shown in  
5 Figures 19A-F (SEQ ID NO:35). The nucleotide sequence shown in Figures 19A-F (SEQ ID NO:35) was obtained by sequencing a cloned cDNA (HOHBY69), which was deposited on November 17 at the American Type Culture Collection, and given Accession Number 203484.

The present invention is further directed to fragments of the isolated nucleic acid  
10 molecules described herein. By a fragment of an isolated DNA molecule having the nucleotide sequence of the deposited cDNA or the nucleotide sequence shown in SEQ ID NO:17 is intended DNA fragments at least about 15nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length which are useful as diagnostic probes and primers as discussed herein. Of  
15 course, larger fragments 50-1500 nt in length are also useful according to the present invention, as are fragments corresponding to most, if not all, of the nucleotide sequence of the deposited cDNA or as shown in SEQ ID NO:17. By a fragment at least 20 nt in length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of the deposited cDNA or the nucleotide sequence as  
20 shown in SEQ ID NO:17. In this context "about" includes the particularly recited size, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Representative examples of all polynucleotide fragments of the invention include, for example, fragments that comprise, or alternatively, consist of, a sequence from about nucleotide 1 to about 50, from about 51 to about 100, from about 101 to  
25 about 150, from about 151 to about 200, from about 201 to about 250, from about 251 to about 300, from about 301 to about 350, from about 351 to about 400, from about 401 to about 450, from about 451 to about 500, from about 501 to about 550, from about 551 to

about 600, from about 601 to about 650, from about 651 to about 700, from about 701 to about 750, from about 751 to about 800, from about 801 to about 850, from about 851 to about 900, from about 901 to about 950, from about 951 to about 1000, from about 1001 to about 1050, from about 1051 to about 1100, from about 1101 to about 1150, from  
5 about 1151 to about 1200, from about 1201 to about 1250, from about 1251 to about 1300, from about 1301 to about 1350, from about 1351 to about 1400, from about 1401 to about 1450, from about 1451 to about 1500, from about 1501 to about 1550, from about 1551 to about 1600, from about 1601 to about 1650, from about 1651 to about 1700, from about 1701 to about 1750, from about 1751 to about 1800, from about 1801  
10 to about 1850, from about 1851 to about 1900, from about 1901 to about 1950, from about 1951 to about 2000, from about 2001 to about 2050, from about 2051 to about 2100, from about 2101 to about 2150, from about 2151 to about 2200, from about 2201 to about 2250, from about 2251 to about 2300, from about 2301 to about 2350, from about 2351 to about 2400, from about 2401 to about 2450, from about 2451 to about  
15 2500, from about 2501 to about 2550, from about 2551 to about 2600, from about 2601 to about 2650, from about 2651 to about 2700, from about 2701 to about 2750, from about 2751 to about 2800, from about 2801 to about 2850, from about 2851 to about 2900, from about 2901 to about 2950, from about 2951 to about 3000, from about 3001 to about 3050, from about 3051 to about 3100, from about 3101 to about 3150, from  
20 about 3151 to about 3200, from about 3201 to about 3250, from about 3251 to about 3300, from about 3301 to about 3350, from about 3351 to about 3400, from about 3401 to about 3450, from about 3451 to about 3500, from about 3501 to about 3550, from about 3551 to about 3600, from about 3601 to about 3650, from about 3651 to about 3700, from about 3701 to about 3750, from about 3751 to about 3800, from about 3801  
25 to about 3850, from about 3851 to about 3900, from about 3901 to about 3950, from about 3951 to about 4000, from about 4001 to about 4050, from about 4051 to about 4100, from about 4101 to about 4150, from about 4151 to about 4200, from about 4201

to about 4250, from about 4251 to about 4300, from about 4301 to about 4350, from about 4351 to about 4400, from about 4401 to about 4450, from about 4451 to about 4500, from about 4501 to about 4550, from about 4551 to about 4600, from about 4601 to about 4650, from about 4651 to about 4700, from about 4701 to about 4750, from about 4751 to about 4800, from about 4801 to about 4850, from about 4851 to about 4900, from about 4901 to about 4950, from about 4951 to about 4995, from about, from about 1 to about 236, from about 144 to about 188, from about 231 to about 276 of SEQ ID NO:17, or the complementary strand thereto, or the cDNA contained in the deposited gene. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini.

Preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding a member selected from the group: a polypeptide comprising or alternatively, consisting of, any one of the transmembrane domains (amino acid residues from about 666 to about 682 and/or 1145 to about 1161 in Figures 19A-F (amino acids from about 666 to about 682 and/or 1145 to about 1161 in SEQ ID NO:35), in addition to the immunoglobulin and major histocompatibility complex protein domain (amino acid residues from about 64 to about 96 in Figures 19A-F (amino acids from about 64 to about 96 in SEQ ID NO:35). Since the location of these domains have been predicted by computer analysis, one of ordinary skill would appreciate that the amino acid residues constituting these domains may vary slightly (e.g., by about 1 to 15 amino acid residues) depending on the criteria used to define each domain. In additional embodiments, the polynucleotides of the invention encode functional attributes of all.

Preferred embodiments of the invention in this regard include fragments that comprise alpha-helix and alpha-helix forming regions ("alpha-regions"), beta-sheet and beta-sheet forming regions ("beta-regions"), turn and turn-forming regions ("turn-regions"), coil and coil-forming regions ("coil-regions"), hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible

regions, surface-forming regions and high antigenic index regions of the present invention.

The data representing the structural or functional attributes of all set forth in Figure 21 and/or Table VII, as described above, was generated using the various modules and algorithms of the DNA\*STAR set on default parameters. In a preferred embodiment, the data presented in columns VIII, IX, XIII, and XIV of Table VII can be used to determine regions of all which exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or XIV by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Certain preferred regions in these regards are set out in Figure 21, but may, as shown in Table VII, be represented or identified by using tabular representations of the data presented in Figure 21. The DNA\*STAR computer algorithm used to generate Figure 21 (set on the original default parameters) was used to present the data in Figure 21 in a tabular format (See Table VII). The tabular format of the data in Figure 21 is used to easily determine specific boundaries of a preferred region. The above-mentioned preferred regions set out in Figure 21 and in Table VII include, but are not limited to, regions of the aforementioned types identified by analysis of the amino acid sequence set out in Figures 19A-F. As set out in Figure 21 and in Table VII, such preferred regions include Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and Hopp-Woods hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schulz flexible regions, Jameson-Wolf regions of high antigenic index and Emini surface-forming regions. Even if deletion of one or more amino acids from the N-terminus of a protein results in modification of loss of one or more biological

functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, etc.) may still be retained. For example, the ability of shortened a11 muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that an a11 mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six a11 amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the a11 amino acid sequence shown in Figures 19A-F, up to the threonine residue at position number 1184 and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues n1-1189 of Figures 19A-F, where n1 is an integer from 2 to 1184 corresponding to the position of the amino acid residue in Figures 19A-F (which is identical to the sequence shown as SEQ ID NO:35). In another embodiment, N-terminal deletions of the a11 polypeptide can be described by the general formula n2-1189, where n2 is a number from 2 to 1184, corresponding to the position of amino acid identified in Figure 19. N-terminal deletions of the a11 polypeptide of the invention shown as SEQ ID NO:35 include polypeptides comprising the amino acid sequence of residues: N-terminal deletions of the a11 polypeptide of the invention shown as SEQ ID NO:35 include polypeptides comprising the amino acid sequence of residues: D-2 to E-1189; L-3 to E-1189; P-4 to E-1189; R-5 to E-1189; G-6 to E-1189; L-7 to E-1189; V-8 to E-1189; V-9 to E-1189; A-10 to E-1189; W-11 to E-1189; A-12 to E-1189; L-13 to E-1189; S-14 to E-1189; L-15 to E-1189; W-16 to E-1189; P-17 to E-1189; G-18

to E-1189; F-19 to E-1189; T-20 to E-1189; D-21 to E-1189; T-22 to E-1189; F-23 to E-1189; N-24 to E-1189; M-25 to E-1189; D-26 to E-1189; T-27 to E-1189; R-28 to E-1189; K-29 to E-1189; P-30 to E-1189; R-31 to E-1189; V-32 to E-1189; I-33 to E-1189; P-34 to E-1189; G-35 to E-1189; S-36 to E-1189; R-37 to E-1189; T-38 to E-1189;  
5 A-39 to E-1189; F-40 to E-1189; F-41 to E-1189; G-42 to E-1189; Y-43 to E-1189; T-44 to E-1189; V-45 to E-1189; Q-46 to E-1189; Q-47 to E-1189; H-48 to E-1189; D-49 to E-1189; I-50 to E-1189; S-51 to E-1189; G-52 to E-1189; N-53 to E-1189; K-54 to E-1189; W-55 to E-1189; L-56 to E-1189; V-57 to E-1189; V-58 to E-1189; G-59 to E-1189; A-60 to E-1189; P-61 to E-1189; L-62 to E-1189; E-63 to E-1189; T-64 to E-1189; N-65 to  
10 E-1189; G-66 to E-1189; Y-67 to E-1189; Q-68 to E-1189; K-69 to E-1189; T-70 to E-1189; G-71 to E-1189; D-72 to E-1189; V-73 to E-1189; Y-74 to E-1189; K-75 to E-1189; C-76 to E-1189; P-77 to E-1189; V-78 to E-1189; I-79 to E-1189; H-80 to E-1189; G-81 to E-1189; N-82 to E-1189; C-83 to E-1189; T-84 to E-1189; K-85 to E-1189; L-86 to E-1189; N-87 to E-1189; L-88 to E-1189; G-89 to E-1189; R-90 to E-1189; V-91 to E-1189;  
15 1189; T-92 to E-1189; L-93 to E-1189; S-94 to E-1189; N-95 to E-1189; V-96 to E-1189; S-97 to E-1189; E-98 to E-1189; R-99 to E-1189; K-100 to E-1189; D-101 to E-1189; N-102 to E-1189; M-103 to E-1189; R-104 to E-1189; L-105 to E-1189; G-106 to E-1189; L-107 to E-1189; S-108 to E-1189; L-109 to E-1189; A-110 to E-1189; T-111 to E-1189; N-112 to E-1189; P-113 to E-1189; K-114 to E-1189; D-115 to E-1189; N-116 to E-1189;  
20 S-117 to E-1189; F-118 to E-1189; L-119 to E-1189; A-120 to E-1189; C-121 to E-1189; S-122 to E-1189; P-123 to E-1189; L-124 to E-1189; W-125 to E-1189; S-126 to E-1189; H-127 to E-1189; E-128 to E-1189; C-129 to E-1189; G-130 to E-1189; S-131 to E-1189; S-132 to E-1189; Y-133 to E-1189; Y-134 to E-1189; T-135 to E-1189; T-136 to E-1189; G-137 to E-1189; M-138 to E-1189; C-139 to E-1189; S-140 to E-1189; R-141 to E-1189;  
25 1189; V-142 to E-1189; N-143 to E-1189; S-144 to E-1189; N-145 to E-1189; F-146 to E-1189; R-147 to E-1189; F-148 to E-1189; S-149 to E-1189; K-150 to E-1189; T-151 to E-1189; V-152 to E-1189; A-153 to E-1189; P-154 to E-1189; A-155 to E-1189; L-156 to

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 to E-1189; S-373 toE-1189; H-374 to E-1189; V-375 to E-1189; V-376 to E-1189; E-  
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 20 382 to E-1189; G-383 to E-1189; A-384 toE-1189; V-385 to E-1189; G-386 to E-1189;  
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Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more biological

functions of the protein, other functional activities (e.g., biological activities (e.g., ability to illicit mitogenic activity, induce differentiation of normal or malignant cells, ability to multimerize, etc.) may still be retained. For example the ability of the shortened a11 mutein to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that an a11 mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six a11 amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the a11 polypeptide shown in Figures 19A-F, up to the glycine residue at position number 6, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues 1-m1 of Figures 19A-F, where m1 is an integer from 6 to 1189 corresponding to the position of the amino acid residue in Figures 19A-F. Moreover, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of C-terminal deletions of the a11 polypeptide of the invention shown as SEQ ID NO:35 include polypeptides comprising the amino acid sequence of residues: M-1 to L-1188; M-1 to V-1187; M-1 to K-1186; M-1 to P-1185; M-1 to T-1184; M-1 to P-1183; M-1 to D-1182; M-1 to L-1181; M-1 to G-1180; M-1 to P-1179; M-1 to E-1178; M-1 to R-1177; M-1 to R-1176; M-1 to R-1175; M-1 to R-1174; M-1 to A-1173; M-1 to S-1172; M-1 to R-1171; M-1 to F-1170; M-1 to F-1169; M-1 to G-1168; M-1 to L-1167; M-1 to K-1166; M-1 to W-1165; M-1 to L-1164; M-1 to A-1163; M-1 to L-1162; M-1 to V-

1161; M-1 to L-1160; M-1 to L-1159; M-1 to A-1158; M-1 to L-1157; M-1 to L-1156;  
 M-1 to L-1155; M-1 to L-1154; M-1 to G-1153; M-1 to G-1152; M-1 to L-1151; M-1 to  
 T-1150; M-1 to S-1149; M-1 to G-1148; M-1 to V-1147; M-1 to I-1146; M-1 to I-1145;  
 M-1 to W-1144; M-1 to I-1143; M-1 to P-1142; M-1 to V-1141; M-1 to Q-1140; M-1  
 5 to W-1139; M-1 to D-1138; M-1 to E-1137; M-1 to Q-1136; M-1 to K-1135; M-1 to S-  
 1134; M-1 to I-1133; M-1 to E-1132; M-1 to F-1131; M-1 to V-1130; M-1 to I-1129; M-  
 1 to Q-1128; M-1 to R-1127; M-1 to S-1126; M-1 to P-1125; M-1 to D-1124; M-1 to E-  
 1123; M-1 to E-1122; M-1 to R-1121; M-1 to F-1120; M-1 to I-1119; M-1 to F-1118; M-  
 1 to P-1117; M-1 to S-1116; M-1 to H-1115; M-1 to F-1114; M-1 to Q-1113; M-1 to R-  
 10 1112; M-1 to Q-1111; M-1 to L-1110; M-1 to A-1109; M-1 to A-1108; M-1 to N-1107;  
 M-1 to V-1106; M-1 to M-1105; M-1 to I-1104; M-1 to K-1103; M-1 to M-1102; M-1 to  
 S-1101; M-1 to K-1100; M-1 to Y-1099; M-1 to K-1098; M-1 to L-1097; M-1 to A-1096;  
 M-1 to K-1095; M-1 to L-1094; M-1 to S-1093; M-1 to R-1092; M-1 to L-1091; M-1 to  
 W-1090; M-1 to L-1089; M-1 to N-1088; M-1 to G-1087; M-1 to L-1086; M-1 to L-  
 15 1085; M-1 to H-1084; M-1 to F-1083; M-1 to N-1082; M-1 to I-1081; M-1 to E-1080;  
 M-1 to Q-1079; M-1 to N-1078; M-1 to P-1077; M-1 to V-1076; M-1 to L-1075; M-1 to  
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5 M-1 to E-508; M-1 to N-507; M-1 to F-506; M-1 to Y-505; M-1 to M-504; M-1 to P-503; M-1 to A-502; M-1 to G-501; M-1 to V-500; M-1 to L-499; M-1 to L-498; M-1 to V-497; M-1 to D-496; M-1 to T-495; M-1 to V-494; M-1 to G-493; M-1 to D-492; M-1 to G-491; M-1 to D-490; M-1 to I-489; M-1 to D-488; M-1 to V-487; M-1 to S-486; M-1 to T-485; M-1 to I-484; M-1 to E-483; M-1 to S-482; M-1 to G-481; M-1 to F-480; M-1 to Y-

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 D-271; M-1 to T-270; M-1 to I-269; M-1 to V-268; M-1 to I-267; M-1 to M-266; M-1 to  
 V-265; M-1 to K-264; M-1 to K-263; M-1 to A-262; M-1 to G-261; M-1 to K-260; M-1  
 20 to R-259; M-1 to G-258; M-1 to G-257; M-1 to K-256; M-1 to Q-255; M-1 to F-254; M-  
 1 to A-253; M-1 to E-252; M-1 to S-251; M-1 to R-250; M-1 to A-249; M-1 to F-248; M-  
 1 to E-247; M-1 to I-246; M-1 to G-245; M-1 to F-244; M-1 to A-243; M-1 to T-242; M-  
 1 to R-241; M-1 to T-240; M-1 to E-239; M-1 to T-238; M-1 to G-237; M-1 to G-236;  
 M-1 to R-235; M-1 to Q-234; M-1 to E-233; M-1 to I-232; M-1 to H-231; M-1 to S-230;  
 25 M-1 to A-229; M-1 to A-228; M-1 to E-227; M-1 to V-226; M-1 to V-225; M-1 to D-  
 224; M-1 to K-223; M-1 to V-222; M-1 to S-221; M-1 to R-220; M-1 to Y-219; M-1 to  
 D-218; M-1 to N-217; M-1 to L-216; M-1 to H-215; M-1 to F-214; M-1 to E-213; M-1 to

H-212; M-1 to V-211; M-1 to V-210; M-1 to D-209; M-1 to E-208; M-1 to G-207; M-1  
 to Y-206; M-1 to Q-205; M-1 to V-204; M-1 to V-203; M-1 to G-202; M-1 to V-201; M-  
 1 to Q-200; M-1 to I-199; M-1 to Q-198; M-1 to G-197; M-1 to P-196; M-1 to G-195; M-  
 1 to I-194; M-1 to Y-193; M-1 to F-192; M-1 to K-191; M-1 to K-190; M-1 to L-189; M-  
 5 1 to I-188; M-1 to N-187; M-1 to I-186; M-1 to L-185; M-1 to F-184; M-1 to H-183; M-  
 1 to Q-182; M-1 to V-181; M-1 to E-180; M-1 to V-179; M-1 to W-178; M-1 to P-177;  
 M-1 to Y-176; M-1 to I-175; M-1 to S-174; M-1 to N-173; M-1 to S-172; M-1 to G-171;  
 M-1 to D-170; M-1 to L-169; M-1 to V-168; M-1 to I-167; M-1 to V-166; M-1 to I-165;  
 M-1 to D-164; M-1 to M-163; M-1 to Y-162; M-1 to T-161; M-1 to Q-160; M-1 to C-  
 10 159; M-1 to R-158; M-1 to Q-157; M-1 to L-156; M-1 to A-155; M-1 to P-154; M-1 to  
 A-153; M-1 to V-152; M-1 to T-151; M-1 to K-150; M-1 to S-149; M-1 to F-148; M-1 to  
 R-147; M-1 to F-146; M-1 to N-145; M-1 to S-144; M-1 to N-143; M-1 to V-142; M-1 to  
 R-141; M-1 to S-140; M-1 to C-139; M-1 to M-138; M-1 to G-137; M-1 to T-136; M-1 to  
 T-135; M-1 to Y-134; M-1 to Y-133; M-1 to S-132; M-1 to S-131; M-1 to G-130; M-1 to  
 15 C-129; M-1 to E-128; M-1 to H-127; M-1 to S-126; M-1 to W-125; M-1 to L-124; M-1 to  
 P-123; M-1 to S-122; M-1 to C-121; M-1 to A-120; M-1 to L-119; M-1 to F-118; M-1 to  
 S-117; M-1 to N-116; M-1 to D-115; M-1 to K-114; M-1 to P-113; M-1 to N-112; M-1 to  
 T-111; M-1 to A-110; M-1 to L-109; M-1 to S-108; M-1 to L-107; M-1 to G-106; M-1 to  
 L-105; M-1 to R-104; M-1 to M-103; M-1 to N-102; M-1 to D-101; M-1 to K-100; M-1  
 20 to R-99; M-1 to E-98; M-1 to S-97; M-1 to V-96; M-1 to N-95; M-1 to S-94; M-1 to L-  
 93; M-1 to T-92; M-1 to V-91; M-1 to R-90; M-1 to G-89; M-1 to L-88; M-1 to N-87;  
 M-1 to L-86; M-1 to K-85; M-1 to T-84; M-1 to C-83; M-1 to N-82; M-1 to G-81; M-1 to  
 H-80; M-1 to I-79; M-1 to V-78; M-1 to P-77; M-1 to C-76; M-1 to K-75; M-1 to Y-74;  
 M-1 to V-73; M-1 to D-72; M-1 to G-71; M-1 to T-70; M-1 to K-69; M-1 to Q-68; M-1  
 25 to Y-67; M-1 to G-66; M-1 to N-65; M-1 to T-64; M-1 to E-63; M-1 to L-62; M-1 to P-  
 61; M-1 to A-60; M-1 to G-59; M-1 to V-58; M-1 to V-57; M-1 to L-56; M-1 to W-55;  
 M-1 to K-54; M-1 to N-53; M-1 to G-52; M-1 to S-51; M-1 to I-50; M-1 to D-49; M-1 to

H-48; M-1 to Q-47; M-1 to Q-46; M-1 to V-45; M-1 to T-44; M-1 to Y-43; M-1 to G-42; M-1 to F-41; M-1 to F-40; M-1 to A-39; M-1 to T-38; M-1 to R-37; M-1 to S-36; M-1 to G-35; M-1 to P-34; M-1 to I-33; M-1 to V-32; M-1 to R-31; M-1 to P-30; M-1 to K-29; M-1 to R-28; M-1 to T-27; M-1 to D-26; M-1 to M-25; M-1 to N-24; M-1 to F-23; M-1 to T-22; M-1 to D-21; M-1 to T-20; M-1 to F-19; M-1 to G-18; M-1 to P-17; M-1 to W-16; M-1 to L-15; M-1 to S-14; M-1 to L-13; M-1 to A-12; M-1 to W-11; M-1 to A-10; M-1 to V-9; M-1 to V-8; M-1 to L-7; M-1 to G-6; of SEQ ID NO:35. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In addition, the invention provides nucleic acid molecules having nucleotide sequences related to extensive portions of SEQ ID NO:17 which have been determined from the following related cDNA genes: HEEAB54R (SEQ ID NO:104), HRDAF83R (SEQ ID NO:105), HOUBC62R (SEQ ID NO:106), HCDBI19R (SEQ ID NO:107), HOHCU94R (SEQ ID NO:108), HOACC13R (SEQ ID NO:109), HCDAP21R (SEQ ID NO:110), HNHHA34R (SEQ ID NO:111), HOHEA75R (SEQ ID NO:112) and HNGEL59R (SEQ ID NO:113).

Based on the sequence similarity to the human integrin alpha 1 subunit, translation product of this gene is expected to share at least some biological activities with integrin proteins, and specifically the integrin alpha 1 protein. Such activities are known in the art, some of which are described elsewhere herein.

Specifically, polynucleotides and polypeptides of the invention are also useful for modulating the differentiation of normal and malignant cells, modulating the proliferation and/or differentiation of cancer and neoplastic cells, and modulating the immune response. Polynucleotides and polypeptides of the invention may represent a diagnostic marker for hematopoietic and immune diseases and/or disorders. The full-length protein should be a secreted protein, based upon homology to the integrin family. Therefore, it is secreted into serum, urine, or feces and thus the levels is assayable from patient samples. Assuming specific expression levels are reflective of the presence of

immune disorders, this protein would provide a convenient diagnostic for early detection. In addition, expression of this gene product may also be linked to the progression of immune diseases, and therefore may itself actually represent a therapeutic or therapeutic target for the treatment of cancer.

5 Polynucleotides and polypeptides of the invention may play an important role in the pathogenesis of human cancers and cellular transformation, particularly those of the immune and hematopoietic systems. Polynucleotides and polypeptides of the invention may also be involved in the pathogenesis of developmental abnormalities based upon its potential effects on proliferation and differentiation of cells and tissue cell types. Due to  
10 the potential proliferating and differentiating activity of said polynucleotides and polypeptides, the invention is useful as a therapeutic agent in inducing tissue regeneration, for treating inflammatory conditions (e.g., inflammatory bowel syndrome, diverticulitis, etc.). Moreover, the invention is useful in modulating the immune response to aberrant polypeptides, as may exist in rapidly proliferating cells and tissue  
15 cell types, particularly in adenocarcinoma cells, and other cancers.

Alternatively, the expression within cellular sources marked by proliferating cells indicates this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis, treatment, and/or prevention of developmental diseases and disorders, including cancer, and other proliferative conditions. Representative uses are  
20 described in the "Hyperproliferative Disorders" and "Regeneration" sections below and elsewhere herein. Briefly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation.

Dysregulation of apoptosis can result in inappropriate suppression of cell death, as occurs in the development of some cancers, or in failure to control the extent of cell  
25 death, as is believed to occur in acquired immunodeficiency and certain neurodegenerative disorders, such as spinal muscular atrophy (SMA).



Alternatively, this gene product is involved in the pattern of cellular proliferation that accompanies early embryogenesis. Thus, aberrant expression of this gene product in tissues - particularly adult tissues - may correlate with patterns of abnormal cellular proliferation, such as found in various cancers. Because of potential roles in proliferation and differentiation, this gene product may have applications in the adult for tissue regeneration and the treatment of cancers. It may also act as a morphogen to control cell and tissue type specification. Therefore, the polynucleotides and polypeptides of the present invention are useful in treating, detecting, and/or preventing said disorders and conditions, in addition to other types of degenerative conditions. Thus

10 this protein may modulate apoptosis or tissue differentiation and is useful in the detection, treatment, and/or prevention of degenerative or proliferative conditions and diseases. The protein is useful in modulating the immune response to aberrant polypeptides, as may exist in proliferating and cancerous cells and tissues. The protein can also be used to gain new insight into the regulation of cellular growth and

15 proliferation. Furthermore, the protein may also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions, in addition to its use as a nutritional supplement. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

20 This gene is expressed almost exclusively in osteoblasts, human trabecular bone cells, mesangial cells, adipocytes, and to a lesser extent in osteosarcoma, chondrosarcoma, breast cancer cells, and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

25 biological sample and for diagnosis of the following diseases and conditions which include, but are not limited to, disorders of the skeletal system, connective tissues, and immune and hematopoietic diseases and/or disorders. Similarly, polypeptides and

antibodies directed to these polypeptides are useful to provide immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the connective tissue and skeletal system, expression of this gene at significantly higher or lower levels is detected in certain

5 tissues or cell types (e.g. immune, hematopoietic, skeletal, bone, cartilage, developmental, reproductive, secretory, and cancerous and wounded tissues) or bodily fluids or cell types (e.g., lymph, serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue from an

10 individual not having the disorder.

Preferred polypeptides of the present invention comprise immunogenic epitopes shown in SEQ ID NO: 35 as residues: Phe-23 to Arg-31, Leu-62 to Asp-72, Val-96 to Asp-101, Thr-111 to Asn-116, Glu-128 to Thr-135, Val-142 to Ser-149, Asn-217 to Val-222, Glu-233 to Arg-241, Gly-272 to Leu-280, Gln-286 to Thr-293, Tyr-303 to Ile-308,

15 Gly-354 to Thr-360, Glu-408 to Lys-419, Glu-508 to Lys-514, Arg-521 to Val-526, Gly-529 to Phe-542, Asp-551 to Tyr-557, Thr-587 to Thr-593, His-656 to Asp-665, Met-697 to Arg-705, Asp-709 to Thr-716, Glu-755 to Gly-760, Asn-779 to His-786, Leu-810 to Asp-816, Leu-844 to Ala-851, Gln-871 to Gly-877, Glu-884 to Gln-889, Ser-931 to Asn-943, Ser-974 to Ile-982, Gly-1039 to Gln-1058, Arg-1121 to Arg-1127, Ser-1134 to Trp-

20 1139, Ser-1172 to Pro-1183. Polynucleotides encoding said polypeptides are also provided.

The tissue distribution in osteoblasts and homology to integrin alpha subunit 10 indicates that the protein products of this gene are useful for the treatment of disorders and conditions affecting the skeletal system, in particular osteoporosis as well as

25 disorders afflicting connective tissues (e.g. arthritis, trauma, tendonitis, chondromalacia and inflammation), such as in the diagnosis and treatment of various autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis as well

as dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias (ie. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid). polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of

5 hematopoietic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. Such a use is consistent with the observed homology to integrin family members, in conjunction with       The tissue distribution in bone marrow cells. Integrins play pivotal roles in cell migration, inflammation, proliferation,

10 and cellular infiltration. Thus, the present invention is expected to share at least some of these activities. Representative uses are described in the "Immune Activity" and "infectious disease" sections below, in Example 11, 13, 14, 16, 18, 19, 20, and 27, and elsewhere herein. Briefly, the uses include bone marrow cell ex-vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of

15 neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Based upon the tissue distribution of this

20 protein, antagonists directed against this protein is useful in blocking the activity of this protein. Accordingly, preferred are antibodies which specifically bind a portion of the translation product of this gene.

Also provided is a kit for detecting tumors in which expression of this protein occurs. Such a kit comprises in one embodiment an antibody specific for the translation

25 product of this gene bound to a solid support. Also provided is a method of detecting these tumors in an individual which comprises a step of contacting an antibody specific for the translation product of this gene to a bodily fluid from the individual, preferably

serum, and ascertaining whether antibody binds to an antigen found in the bodily fluid. Preferably the antibody is bound to a solid support and the bodily fluid is serum. The above embodiments, as well as other treatments and diagnostic tests (kits and methods), are more particularly described elsewhere herein. Furthermore, the protein may also be  
5 used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions, in addition to its use as a nutritional supplement. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are  
10 publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:17 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or  
15 more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4981 of SEQ ID NO:17, b is an integer of 15 to 4995, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:17, and where b is greater than or equal to a + 14.

20

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 8**

The present invention relates to three novel peptidoglycan recognition binding proteins expressed by keratinocytes, wound-healing tissues and chondrosarcoma tissue.  
25 More specifically, isolated nucleic acid molecules are provided encoding a human peptidoglycan recognition protein-related protein, sometimes referred to herein as "human tag7" or "tag7" or "htag7". Further provided are vectors, host cells and

recombinant methods for producing the same. The invention also relates to both the inhibition and enhancement of activities of the tag7 protein, polypeptides and diagnostic methods for detecting tag7 gene expression.

Peptidoglycan, as well as Lipopolysaccharide (LPS), is a surface component of many bacteria which illicit a wide range of physiological and immune responses in humans. Specifically, peptidoglycan has been shown to manifest itself clinically by reproducing most of the symptoms of bacterial infection, including fever, acute-phase response, inflammation, septic shock, leukocytosis, sleepiness, malaise, abcess formation, and arthritis (see Dziarski et al., JBC, 273 (15): 8680 (1998)). Furthermore, the type of peptidoglycan (i.e.- the specific stereoisomers or analogs of muramyl dipeptide, N-acetylglucosaminyl-beta(1-4)-N-acetylmuramyl tetrapeptides, etc.), were shown to elicit a broad range of activities, including exhibiting greater pyrogenicity, inducing acute joint inflammation, stimulating macrophages, and causing hemorrhagic necrosis at a primed site (See Kotani et al., Fed Proc, 45(11): 2534 (1986)). It has been demonstrated in humans that a lipopolysaccharide binding protein exists that was discovered as a trace plasma protein (See Schumann et al., Science, 249(4975):1429 (1990)). It is thought that one of the modes of action by which this lipopolysaccharide binding protein functions is by forming high-affinity complexes with lipopolysaccharide, that then bind to macrophages and monocytes, inducing the secretion of tumor necrosis factor. Dziarski and Gupta (See Dziarski et al., JBC, 269(3): 2100 (1994)) demonstrated that a 70kDa receptor protein present on the surface of mouse lymphocytes served to bind heparin, heparinoids, bacterial lipoteichoic acids, peptidoglycan, and lipopolysaccharides. Recently, Dziarski et al. demonstrated that the CD14, a glycosylphosphatidylinositol-linked protein present on the surface of macrophage and polymorphonuclear leukocytes, bound peptidoglycan and lipopolysaccharide.

Furthermore, the binding affinity of CD14 for lipopolysaccharide was significantly increased in the presence of a LPS-binding protein present in plasma. It is

thought that the LPS-binding protein functions as a transfer molecule, whereby it binds LPS and presents it to the CD14 receptor (See Dziarski et al., JBC, 273(15): 8680 (1998)). Yoshida et al. isolated a peptidoglycan binding protein from the hemolymph of the Silkworm, *Bombyx mori*, using column chromatography. This protein was found to have a very specific affinity for peptidoglycan (See Yoshida et al., JBC, 271(23): 13854 (1996)).

Additionally, Kang et al. recently cloned a peptidoglycan binding protein from the moth *Trichoplusia ni*. The peptidoglycan binding protein was shown to bind strongly to insoluble peptidoglycan (See Kang et al., PNAS, 95(17): 10078 (1998)). In this study the peptidoglycan binding protein was upregulated by a bacterial infection in *T. ni*. The insect immune system is regarded as a model for innate immunity. Thus, Kang et al were able to gene both mouse and human homologs of the *T. ni* peptidoglycan binding protein. All of these peptidoglycan binding proteins shared regions of homology, as well as four conserved cysteine residues which may function in the tertiary structure of the protein, possibly in helping to form binding domains. Given that peptidoglycan is an integral component of bacterial cell walls, and that it induces many physiological responses from cytokine secretion to inflammation and macrophage activation, it appears as if this family of proteins is a ubiquitous group involved in the binding and recognition of peptidoglycan, the presentation of antigens (e.g., cell wall components, etc.), and the activation of the immune system, such as the secretion of cytokines, such as TNF. TNF is noted for its pro-inflammatory actions which result in tissue injury, such as induction of procoagulant activity on vascular endothelial cells (Poher, J.S. et al., J. Immunol. 136:1680 (1986)), increased adherence of neutrophils and lymphocytes (Poher, J.S. et al., J. Immunol. 138:3319 (1987)), and stimulation of the release of platelet activating factor from macrophages, neutrophils and vascular endothelial cells (Camussi, G. et al., J. Exp. Med. 166:1390 (1987)).

Recent evidence implicates TNF in the pathogenesis of many infections (Cerami, A. et al., Immunol. Today 9:28 (1988)), immune disorders, neoplastic pathology, e.g., in cachexia accompanying some malignancies (Oliff, A. et al., Cell 50:555 (1987)), and in autoimmune pathologies and graft-versus host pathology (Piguet, P.-F. et al., J. Exp. Med. 166:1280 (1987)). The association of TNF with cancer and infectious pathologies is often related to the host's catabolic state. A major problem in cancer patients is weight loss, usually associated with anorexia. The extensive wasting which results is known as "cachexia" (Kern, K. A. et al. J. Parent. Enter. Nutr. 12:286-298 (1988)). Cachexia includes progressive weight loss, anorexia, and persistent erosion of body mass in response to a malignant growth. The cachectic state is thus associated with significant morbidity and is responsible for the majority of cancer mortality.

A number of studies have suggested that TNF is an important mediator of the cachexia in cancer, infectious pathology, and in other catabolic states. TNF is thought to play a central role in the pathophysiological consequences of Gram-negative sepsis and endotoxic shock (Michie, H.R. et al., Br. J. Surg. 76:670-671 (1989); Debets, J. M. H. et al., Second Vienna Shock Forum, p.463-466 (1989); Simpson, S. Q. et al., Crit. Care Clin. 5:27-47 (1989)), including fever, malaise, anorexia, and cachexia. Endotoxin is a potent monocyte/macrophage activator which stimulates production and secretion of TNF (Kornbluth, S.K. et al., J. Immunol. 137:2585-2591 (1986)) and other cytokines. Because TNF could mimic many biological effects of endotoxin, it was concluded to be a central mediator responsible for the clinical manifestations of endotoxin-related illness. TNF and other monocyte-derived cytokines mediate the metabolic and neurohormonal responses to endotoxin (Michie, H.R. et al., N. Eng. J. Med. 318:1481-1486 (1988)). Endotoxin administration to human volunteers produces acute illness with flu-like symptoms including fever, tachycardia, increased metabolic rate and stress hormone release (Revhaug, A. et al., Arch. Surg. 123:162-170 (1988)). Elevated levels of circulating TNF have also been found in patients suffering from Gram-negative sepsis

(Waage, A. et al., *Lancet* 1:355-357 (1987); Hammerle, A.F. et al., *Second Vienna Shock Forum* p. 715-718 (1989); Debets, J. M. H. et al., *Crit. Care Med.* 17:489-497 (1989); Calandra, T. et al., *J. Infec. Dis.* 161:982-987 (1990)). Passive immunotherapy directed at neutralizing TNF may have a beneficial effect in Gram-negative sepsis and  
5 endotoxemia, based on the increased TNF production and elevated TNF levels in these pathology states, as discussed above.

Antibodies to a "modulator" material which was characterized as cachectin (later found to be identical to TNF) were disclosed by Cerami et al. (EPO Patent Publication 0,212,489, March 4, 1987). Such antibodies were said to be useful in diagnostic  
10 immunoassays and in therapy of shock in bacterial infections. Rubin et al. (EPO Patent Publication 0,218,868, April 22, 1987) disclosed monoclonal antibodies to human TNF, the hybridomas secreting such antibodies, methods of producing such antibodies, and the use of such antibodies in immunoassay of TNF. Yone et al. (EPO Patent Publication 0,288,088, October 26, 1988) disclosed anti-TNF antibodies, including mAbs, and their  
15 utility in immunoassay diagnosis of pathologies, in particular Kawasaki's pathology and bacterial infection. The body fluids of patients with Kawasaki's pathology (infantile acute febrile mucocutaneous lymph node syndrome; Kawasaki, T., *Allergy* 16:178 (1967); Kawasaki, T., *Shonica (Pediatrics)* 26:935 (1985)) were said to contain elevated TNF levels which were related to progress of the pathology (Yone et al., *supra*).

20 Accordingly, there is a need to provide molecules that are involved in pathological conditions. Such novel proteins could be useful in augmenting the immune system in such areas as immune recognition, antigen presentation, and immune system activation. Antibodies or antagonists directed against these proteins is useful in reducing or eliminating disorders associated with TNF and TNF-like cytokines, such as endotoxic  
25 shock and auto-immune disorders, for example.

The polypeptide of the present invention has been putatively identified as a member of the novel peptidoglycan recognition binding protein family and has been



termed human tag7. This identification has been made as a result of amino acid sequence homology to the mouse tag7 (See Genbank Accession No. emb|CAA60133).

Figure 34 shows the nucleotide (SEQ ID NO:18) and deduced amino acid sequence (SEQ ID NO:36) of htag7. Predicted amino acids from about 1 to about 21 constitute the predicted signal peptide (amino acid residues from about 1 to about 21 in SEQ ID NO:36) and are represented by the underlined amino acid regions; and amino acids from about 34 to about 117 constitute the predicted PGRP-like domain (amino acids from about 34 to about 117 in SEQ ID NO:36) and are represented by the double underlined amino acids.

Figure 35 shows the regions of similarity between the amino acid sequences of the htag7 protein (SEQ ID NO:36) and the mouse tag7 protein (SEQ ID NO:114).

Figure 36 shows an analysis of the htag7 amino acid sequence. Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic regions; flexible regions; antigenic index and surface probability are shown.

A polynucleotide encoding a polypeptide of the present invention is obtained from human chondrosarcoma cells, bone marrow, and neutrophils. The polynucleotide of this invention was discovered in a human chondrosarcoma cDNA library.

As shown in Figure 34, htag7 has a PGRP domain (the PGRP domain comprise amino acids from about 34 to about 117 of SEQ ID NO:36; which correspond to amino acids from about 34 to about 117 of Figure 34). The polynucleotide contains an open reading frame encoding the htag7 polypeptide of 198 amino acids. htag7 exhibits a high degree of homology at the amino acid level to the mouse tag7 (as shown in Figure 35). The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding the htag7 polypeptide having the amino acid sequence shown in Figure 34 (SEQ ID NO:36). The nucleotide sequence shown in Figure 34 (SEQ ID NO:18) was obtained by sequencing a cloned cDNA (HCDDP40), which was deposited

on November 17 at the American Type Culture Collection, and given Accession Number 203484.

The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated DNA molecule having the

5 nucleotide sequence of the deposited cDNA or the nucleotide sequence shown in SEQ ID NO:18 is intended DNA fragments at least about 15nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length which are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-1500 nt in length are also useful according to the present

10 invention, as are fragments corresponding to most, if not all, of the nucleotide sequence of the deposited cDNA or as shown in SEQ ID NO:18. By a fragment at least 20 nt in length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of the deposited cDNA or the nucleotide sequence as shown in SEQ ID NO:18. In this context "about" includes the particularly recited size,

15 larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Representative examples of htag7 polynucleotide fragments of the invention include, for example, fragments that comprise, or alternatively, consist of, a sequence from about nucleotide 1 to about 50, from about 51 to about 100, from about 101 to about 150, from about 151 to about 200, from about 201 to about 250, from about 251 to

20 about 300, from about 301 to about 350, from about 351 to about 400, from about 401 to about 450, from about 451 to about 500, from about 501 to about 550, from about 551 to about 600, from about 601 to about 650, from about 651 to about 700, from about 701 to about 726, and from about 130 to about 379 of SEQ ID NO:18, or the complementary strand thereto, or the cDNA contained in the deposited gene. In this context "about"

25 includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini.

Preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding a member selected from the group: a polypeptide comprising or alternatively, consisting of, the PGRP-like domain (amino acid residues from about 34 to about 117 in Figure 34 (amino acids from about 34 to about 117 in SEQ ID NO:36).

- 5 Since the location of these domains have been predicted by computer analysis, one of ordinary skill would appreciate that the amino acid residues constituting these domains may vary slightly (e.g., by about 1 to 15 amino acid residues) depending on the criteria used to define each domain. As indicated, nucleic acid molecules of the present invention which encode a htag7 polypeptide may include, but are not limited to those encoding the
- 10 amino acid sequence of the PGRP-like domain of the polypeptide, by itself; and the coding sequence for the PGRP-like domain of the polypeptide and additional sequences, such as a pre-, or pro or prepro- protein sequence. In additional embodiments, the polynucleotides of the invention encode functional attributes of htag7.

- Preferred embodiments of the invention in this regard include fragments that
- 15 comprise alpha-helix and alpha-helix forming regions ("alpha-regions"), beta-sheet and beta-sheet forming regions ("beta-regions"), turn and turn-forming regions ("turn-regions"), coil and coil-forming regions ("coil-regions"), hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions and high antigenic index regions of htag7. The data
- 20 representing the structural or functional attributes of htag7 set forth in Figure 36 and/or Table XII, as described above, was generated using the various modules and algorithms of the DNA\*STAR set on default parameters. In a preferred embodiment, the data presented in columns VIII, IX, XIII, and XIV of Table XII can be used to determine regions of htag7 which exhibit a high degree of potential for antigenicity. Regions of
- 25 high antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or XIV by choosing values which represent regions of the polypeptide which are

likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Certain preferred regions in these regards are set out in Figure 36, but may, as shown in Table XII, be represented or identified by using tabular representations of the data presented in Figure 36. The DNA\*STAR computer algorithm used to generate Figure 36 (set on the original default parameters) was used to present the data in Figure 36 in a tabular format (See Table XII). The tabular format of the data in Figure 36 is used to easily determine specific boundaries of a preferred region. The above-mentioned preferred regions set out in Figure 36 and in Table XII include, but are not limited to, regions of the aforementioned types identified by analysis of the amino acid sequence set out in Figure 34. As set out in Figure 36 and in Table XII, such preferred regions include Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and Hopp-Woods hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schulz flexible regions, Jameson-Wolf regions of high antigenic index and Emini surface-forming regions. Even if deletion of one or more amino acids from the N-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, modulate cellular interaction, or signalling pathways, etc.) may still be retained. For example, the ability of shortened htag7 muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that an htag7 mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact,

peptides composed of as few as six htag7 amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the htag7 amino acid sequence shown in Figure 34, up to the proline residue at position number 191 and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues n1-196 of Figure 34, where n1 is an integer from 2 to 191 corresponding to the position of the amino acid residue in Figure 34 (which is identical to the sequence shown as SEQ ID NO:36). In another embodiment, N-terminal deletions of the htag7 polypeptide can be described by the general formula n2-196, where n2 is a number from 2 to 191, corresponding to the position of amino acid identified in Figure 34. N-terminal deletions of the htag7 polypeptide of the invention shown as SEQ ID NO:36 include polypeptides comprising the amino acid sequence of residues: N-terminal deletions of the htag7 polypeptide of the invention shown as SEQ ID NO:36 include polypeptides comprising the amino acid sequence of residues: S-2 to P-196; R-3 to P-196; R-4 to P-196; S-5 to P-196; M-6 to P-196; L-7 to P-196; L-8 to P-196; A-9 to P-196; W-10 to P-196; A-11 to P-196; L-12 to P-196; P-13 to P-196; S-14 to P-196; L-15 to P-196; L-16 to P-196; R-17 to P-196; L-18 to P-196; G-19 to P-196; A-20 to P-196; A-21 to P-196; Q-22 to P-196; E-23 to P-196; T-24 to P-196; E-25 to P-196; D-26 to P-196; P-27 to P-196; A-28 to P-196; C-29 to P-196; C-30 to P-196; S-31 to P-196; P-32 to P-196; I-33 to P-196; V-34 to P-196; P-35 to P-196; R-36 to P-196; N-37 to P-196; E-38 to P-196; W-39 to P-196; K-40 to P-196; A-41 to P-196; L-42 to P-196; A-43 to P-196; S-44 to P-196; E-45 to P-196; C-46 to P-196; A-47 to P-196; Q-48 to P-196; H-49 to P-196; L-50 to P-196; S-51 to P-196; L-52 to P-196; P-53 to P-196; L-54 to P-196; R-55 to P-196; Y-56 to P-196; V-57 to P-196; V-58 to P-196; V-59 to P-196; S-60 to P-196; H-61 to P-196; T-62 to P-196; A-63 to P-196; G-64 to P-196; S-65 to P-196; S-66 to P-196; C-67 to P-196; N-68 to P-196; T-69 to P-196; P-70 to P-196; A-71

to P-196; S-72 to P-196; C-73 to P-196; Q-74 to P-196; Q-75 to P-196; Q-76 to P-196; A-77 to P-196; R-78 to P-196; N-79 to P-196; V-80 to P-196; Q-81 to P-196; H-82 to P-196; Y-83 to P-196; H-84 to P-196; M-85 to P-196; K-86 to P-196; T-87 to P-196; L-88 to P-196; G-89 to P-196; W-90 to P-196; C-91 to P-196; D-92 to P-196; V-93 to P-196; 5 G-94 to P-196; Y-95 to P-196; N-96 to P-196; F-97 to P-196; L-98 to P-196; I-99 to P-196; G-100 to P-196; E-101 to P-196; D-102 to P-196; G-103 to P-196; L-104 to P-196; V-105 to P-196; Y-106 to P-196; E-107 to P-196; G-108 to P-196; R-109 to P-196; G-110 to P-196; W-111 to P-196; N-112 to P-196; F-113 to P-196; T-114 to P-196; G-115 to P-196; A-116 to P-196; H-117 to P-196; S-118 to P-196; G-119 to P-196; H-120 to P-196; 10 L-121 to P-196; W-122 to P-196; N-123 to P-196; P-124 to P-196; M-125 to P-196; S-126 to P-196; I-127 to P-196; G-128 to P-196; I-129 to P-196; S-130 to P-196; F-131 to P-196; M-132 to P-196; G-133 to P-196; N-134 to P-196; Y-135 to P-196; M-136 to P-196; D-137 to P-196; R-138 to P-196; V-139 to P-196; P-140 to P-196; T-141 to P-196; P-142 to P-196; Q-143 to P-196; A-144 to P-196; I-145 to P-196; R-146 to P-196; 15 A-147 to P-196; A-148 to P-196; Q-149 to P-196; G-150 to P-196; L-151 to P-196; L-152 to P-196; A-153 to P-196; C-154 to P-196; G-155 to P-196; V-156 to P-196; A-157 to P-196; Q-158 to P-196; G-159 to P-196; A-160 to P-196; L-161 to P-196; R-162 to P-196; S-163 to P-196; N-164 to P-196; Y-165 to P-196; V-166 to P-196; L-167 to P-196; K-168 to P-196; G-169 to P-196; H-170 to P-196; R-171 to P-196; D-172 to P-196; V-20 173 to P-196; Q-174 to P-196; R-175 to P-196; T-176 to P-196; L-177 to P-196; S-178 to P-196; P-179 to P-196; G-180 to P-196; N-181 to P-196; Q-182 to P-196; L-183 to P-196; Y-184 to P-196; H-185 to P-196; L-186 to P-196; I-187 to P-196; Q-188 to P-196; N-189 to P-196; W-190 to P-196; P-191 to P-196; of SEQ ID NO:36. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

25 Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities ) may still

be retained. For example the ability of the shortened htag7 mutein to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking

5 C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a htag7 mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six htag7 amino acid residues may often evoke an

10 immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the htag7 polypeptide shown in Figure 34 , up to the methionine residue at position number 6, and polynucleotides encoding such polypeptides. In particular, the present invention provides

15 polypeptides comprising the amino acid sequence of residues 1-m1 of Figure 1, where m1 is an integer from 6 to 196 corresponding to the position of the amino acid residue in Figure 34 . Moreover, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of C-terminal deletions of the htag7 polypeptide of the invention shown as SEQ ID NO:36 include

20 polypeptides comprising the amino acid sequence of residues: M-1 to S-195; M-1 to R-194; M-1 to Y-193; M-1 to H-192; M-1 to P-191; M-1 to W-190; M-1 to N-189; M-1 to Q-188; M-1 to I-187; M-1 to L-186; M-1 to H-185; M-1 to Y-184; M-1 to L-183; M-1 to Q-182; M-1 to N-181; M-1 to G-180; M-1 to P-179; M-1 to S-178; M-1 to L-177; M-1 to T-176; M-1 to R-175; M-1 to Q-174; M-1 to V-173; M-1 to D-172; M-1 to R-171; M-1

25 to H-170; M-1 to G-169; M-1 to K-168; M-1 to L-167; M-1 to V-166; M-1 to Y-165; M-1 to N-164; M-1 to S-163; M-1 to R-162; M-1 to L-161; M-1 to A-160; M-1 to G-159; M-1 to Q-158; M-1 to A-157; M-1 to V-156; M-1 to G-155; M-1 to C-154; M-1 to A-

153; M-1 to L-152; M-1 to L-151; M-1 to G-150; M-1 to Q-149; M-1 to A-148; M-1 to A-147; M-1 to R-146; M-1 to I-145; M-1 to A-144; M-1 to Q-143; M-1 to P-142; M-1 to T-141; M-1 to P-140; M-1 to V-139; M-1 to R-138; M-1 to D-137; M-1 to M-136; M-1 to Y-135; M-1 to N-134; M-1 to G-133; M-1 to M-132; M-1 to F-131; M-1 to S-130; M-1 to I-129; M-1 to G-128; M-1 to I-127; M-1 to S-126; M-1 to M-125; M-1 to P-124; M-1 to N-123; M-1 to W-122; M-1 to L-121; M-1 to H-120; M-1 to G-119; M-1 to S-118; M-1 to H-117; M-1 to A-116; M-1 to G-115; M-1 to T-114; M-1 to F-113; M-1 to N-112; M-1 to W-111; M-1 to G-110; M-1 to R-109; M-1 to G-108; M-1 to E-107; M-1 to Y-106; M-1 to V-105; M-1 to L-104; M-1 to G-103; M-1 to D-102; M-1 to E-101; M-1 to G-100; M-1 to I-99; M-1 to L-98; M-1 to F-97; M-1 to N-96; M-1 to Y-95; M-1 to G-94; M-1 to V-93; M-1 to D-92; M-1 to C-91; M-1 to W-90; M-1 to G-89; M-1 to L-88; M-1 to T-87; M-1 to K-86; M-1 to M-85; M-1 to H-84; M-1 to Y-83; M-1 to H-82; M-1 to Q-81; M-1 to V-80; M-1 to N-79; M-1 to R-78; M-1 to A-77; M-1 to Q-76; M-1 to Q-75; M-1 to Q-74; M-1 to C-73; M-1 to S-72; M-1 to A-71; M-1 to P-70; M-1 to T-69; M-1 to N-68; M-1 to C-67; M-1 to S-66; M-1 to S-65; M-1 to G-64; M-1 to A-63; M-1 to T-62; M-1 to H-61; M-1 to S-60; M-1 to V-59; M-1 to V-58; M-1 to V-57; M-1 to Y-56; M-1 to R-55; M-1 to L-54; M-1 to P-53; M-1 to L-52; M-1 to S-51; M-1 to L-50; M-1 to H-49; M-1 to Q-48; M-1 to A-47; M-1 to C-46; M-1 to E-45; M-1 to S-44; M-1 to A-43; M-1 to L-42; M-1 to A-41; M-1 to K-40; M-1 to W-39; M-1 to E-38; M-1 to N-37; M-1 to R-36; M-1 to P-35; M-1 to V-34; M-1 to I-33; M-1 to P-32; M-1 to S-31; M-1 to C-30; M-1 to C-29; M-1 to A-28; M-1 to P-27; M-1 to D-26; M-1 to E-25; M-1 to T-24; M-1 to E-23; M-1 to Q-22; M-1 to A-21; M-1 to A-20; M-1 to G-19; M-1 to L-18; M-1 to R-17; M-1 to L-16; M-1 to L-15; M-1 to S-14; M-1 to P-13; M-1 to L-12; M-1 to A-11; M-1 to W-10; M-1 to A-9; M-1 to L-8; M-1 to L-7; M-1 to M-6; of SEQ ID NO:36.

Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In addition, the invention provides nucleic acid molecules having nucleotide sequences related to extensive portions of SEQ ID NO:36 which have been determined



from the following related cDNA genes: HBMTB79R (SEQ ID NO:115) and HCDDP40R (SEQ ID NO:116).

Based on the sequence similarity to the mouse tag7 and the PGRP-like domain, translation product of this gene is expected to share at least some biological activities with tag7 proteins, and specifically cytokine modulatory proteins. Such activities are known in the art, some of which are described elsewhere herein. Specifically, polynucleotides and polypeptides of the invention are also useful for modulating the differentiation of normal and malignant cells, modulating the proliferation and/or differentiation of cancer and neoplastic cells, and modulating the immune response.

Polynucleotides and polypeptides of the invention may represent a diagnostic marker for hematopoietic and immune diseases and/or disorders. The full-length protein should be a secreted protein, based upon homology to the tag7 protein. Therefore, it is secreted into serum, urine, or feces and thus the levels is assayable from patient samples. Assuming specific expression levels are reflective of the presence of immune disorders, this protein would provide a convenient diagnostic for early detection. In addition, expression of this gene product may also be linked to the progression of immune diseases, and therefore may itself actually represent a therapeutic or therapeutic target for the treatment of cancer.

Polynucleotides and polypeptides of the invention may play an important role in the pathogenesis of human cancers and cellular transformation, particularly those of the immune and hematopoietic systems. Polynucleotides and polypeptides of the invention may also be involved in the pathogenesis of developmental abnormalities based upon its potential effects on proliferation and differentiation of cells and tissue cell types. Due to the potential proliferating and differentiating activity of said polynucleotides and polypeptides, the invention is useful as a therapeutic agent in inducing tissue regeneration, for treating inflammatory conditions (e.g., inflammatory bowel syndrome, diverticulitis, etc.).

Moreover, the invention is useful in modulating the immune response to aberrant polypeptides, as may exist in rapidly proliferating cells and tissue cell types, particularly in adenocarcinoma cells, and other cancers. The translation product of this gene shares sequence homology with Tag7, which is a mouse cytokine that, in soluble form, triggers  
5 apoptosis in mouse L929 cells in vitro.

The translation product of this gene also shares sequence homology with antimicrobial BGP-A, a bovine antimicrobial peptide from bovine neutrophils. Preferred polypeptides of this invention comprise residues 184 to 196 shown in SEQ ID NO: 36. This polypeptide is believed to be the active mature form of the translation product of  
10 this gene.

This gene is expressed primarily in bone marrow and to a lesser extent in human chondrosarcoma and neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
15 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, infections, cancer, and disorders of the immune system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of infected tissues and the  
20 immune system, expression of this gene at significantly higher or lower levels is routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression  
25 level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred polypeptides of the present invention comprise immunogenic epitopes shown in SEQ ID NO: 36 as residues: Ala-63 to Asn-68, Ala-71 to Gln-81, Tyr-135 to

Thr-141, Leu-167 to Gln-174, Pro-191 to Pro-196. Polynucleotides encoding said polypeptides are also provided.

## 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 9

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the use of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides. The polypeptide of the present  
10 invention has been putatively identified as a human butyrophilin homolog derived from a human testes tumor cDNA library. The polypeptide of the present invention is sometimes hereafter referred to as "Butyrophilin and B7-like IgG superfamily receptor", and/or "BBIR II". The invention also relates to inhibiting the action of such polypeptides.

Butyrophilin is a glycoprotein of the immunoglobulin superfamily that is secreted  
15 in association with the milk-fat-globule membrane from mammary epithelial cells. The butyrophilin gene appears to have evolved from a subset of genes in the immunoglobulin superfamily and genes encoding the B30.2 domain, which is conserved in a family of zinc-finger proteins. Furthermore, expression analysis of butyrophilin genes has shown that butyrophilin expression increases during lactation in conjunction with an increase in  
20 milk fat content. These results suggest that the stage-specific expression of milk fat globule membrane glycoproteins in mammary epithelial cells is regulated in a similar but not necessarily identical mechanism to that of a major milk protein, beta-casein.

The polypeptide of the present invention has been putatively identified as a member of the milk fat globule membrane glycoprotein family, and more particularly the  
25 butyrophilin family, and has been termed Butyrophilin and B7-like IgG superfamily receptor ("BBIR II"). This identification has been made as a result of amino acid

sequence homology to the bovine butyrophilin precursor (See Genbank Accession No. gi|162773).

Preferred polypeptides of the invention comprise the following nucleic acid sequence:

5 ACATCCATGGCTCTAATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATC  
AGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGG  
GAGGACGCAGCATTCTCCTGTTTCCTGTCTCCTAAGACCAATGCAGAGGCCA  
TGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGGTCCACCTCTACAG  
GGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGGAC  
10 AAAACTGGTGAAGGATTCTATTGCGGAGGGGGCGCATCTCTCTGAGGCTGGAA  
AACATTACTGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTC  
TTACTACCAGAAGGCCATCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTT  
CCTCTCATTTCCATCACGGGATATGTTGATAGAGACATCCAGCTACTCTGTCA  
GTCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTGGAAGGTCCACAAGGA  
15 CAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTG  
ATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTC  
CATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGG  
AGATAACCTTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGA  
ATACTCTGCTGTGGCCTATTTTTTGGCATTGTTGGACTGAAGATTTTCTTCTCC  
20 AAATTCCAGTGGAAAATCCAGGCGGAACTGGACTGGAGAAGAAAGCACGGA  
CAGGCAGAATTGAGAGACGCCCCGGAACACGCAGTGGAGGTGACTCTGGAT  
CCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCC  
ATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGA  
AGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGT  
25 GGACGGAGGACACAATAAAAGGTGGCGCGTGGGAGTGTGCCGGGATGATGT  
GGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTC  
CTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGTTTTATCAG

CGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCCTGGACTATGAG  
TGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCT  
GACATGTCGGTTTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATA  
ATGAGCAAAATGGA ACTCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAG  
5 GCAACCACGCCCTTCCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCA  
CATTCTTCTTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGC  
AGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCCACATGGG  
AGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTAC  
ATTTAGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTC  
10 AGGTGAAGAACCGTCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAG  
TAGACAAGGAATGTGAATAATGCTTAGATCTTATTGATGACAGAGTGTATCC  
TAATGGTTTGTTCATTATATTACACTTTCAGTAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA (SEQ ID NO:117), and/or  
ATGGCTCTAATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCA  
15 GTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGAC  
GCAGCATTCTCCTGTTTCCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAG  
TGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGG  
GAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGGACAAA ACT  
GGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATT  
20 ACTGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTA  
CCAGAAGGCCATCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCTCTC  
ATTTCCATCACGGGATATGTTGATAGAGACATCCAGCTACTCTGTGTCAGTCCTC  
GGGCTGGTTCCCCCGGCCACAGCGAAGTGGAAGGTCCACAAGGACAGGA  
TTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTG  
25 GAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATGC  
GGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATA  
CCTTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTC

TGCTGTGGCCTATTTTTTGGCATTGTTGGACTGAAGATTTTCTTCTCCAAATTC  
CAGTGGAAAATCCAGGCGGAACTGGACTGGAGAAGAAAGCACGGACAGGCA  
GAATTGAGAGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAGAG  
ACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAAGTGTAAACCCATAGAA  
5 AAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGT  
GGTGGCTTCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGA  
GGACACAATAAAAGGTGGCGCGTGGGAGTGTGCCGGGATGATGTGGACAGG  
AGGAAGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCCTCAGAC  
TGAATGGAGAACATTTGTATTTACATTAAATCCCCGTTTTATCAGCGTCTTC  
10 CCCAGGACCCACCTACAAAAATAGGGGTCTTCCTGGACTATGAGTGTGGGA  
CCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGT  
CGGTTTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGC  
AAAATGGAAGTCCCAGAGACAAGCAACAGTGA (SEQ ID NO:118). Polypeptide  
encoded by these polynucleotides are also provided.

15 Preferred polypeptides of the invention comprise the following amino acid  
sequence:  
MALMLSLVLSLLKLGSQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEV  
RFFRGQFSSVVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVL  
DAGLYGCRISQSYQKAIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFP  
20 TAKWKGPQGQDLSTDSRTNRDMHGLFDVEISLTVQENAGSISCSMRHAHLSREV  
ESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSKFQWKIQAELDWRR  
KHGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVTHRKAQEVPHSEKRFT  
RKS VVASQS FQAGKHYWEVDGGHNRWRVGVCRDDVDRRKEYVTLS PDHGY  
WVLRNLNGEHL YFTLNPRFISVFPRTPTKIGVFLDYECGTISFFNINDQSLIYTLTC  
25 RFEGLLRPYIEYPSYNEQNGTPRDKQQ (SEQ ID NO:119). Polynucleotides encoding  
these polypeptides are also provided.

A preferred polynucleotide splice variant of the invention comprises the following nucleic acid sequence:

ACCTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACT  
CTGCTGTGGCCTATTTTTTGGCATTGTTGGACTGAAGATTTTCTTCTCCAAATT  
5 CCAGTGGAATAATCCAGGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGC  
AGAATTGAGAGACGCCCCGGAACACGCAGTGGAGGTGACTCTGGATCCAGA  
GACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAAGTGTAAACCATAGA  
AAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGT  
GTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACG  
10 GAGGACACAATAAAAGGTGGCGCGTGGGAGTGTGCCGGGATGATGTGGACA  
GGAGGAAGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCTCAG  
ACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGTTTTATCAGCGTCT  
TCCCCAGGACCCACCTACAAAAATAGGGGTCTTCCTGGACTATGAGTGTGG  
GACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACAT  
15 GTCGGTTTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAG  
CAAAATGGAAGTCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAAC  
CACGCCCTTCCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCACATTC  
TTCTTTAGGGATATTAAGGTCTCTCTCCCAGATCCAAAGTCCCGCAGCAGCCG  
GCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCCACATGGGAGTCA  
20 GGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTTAG  
TTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGA  
AGAACCGTCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACA  
AGGAATGTGAATAATGCTTAGATCTTATTGATGACAGAGTGTATCCTAATGG  
TTTGTTTATTATATTACACTTTCAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
25 AAAAAA (SEQ ID NO:120). Polypeptides encoded by these polynucleotides are also  
provided.

Figures 22A-D show the nucleotide (SEQ ID NO:19) and deduced amino acid sequence (SEQ ID NO:37) of BBIR II. Predicted amino acids from about 1 to about 17 constitute the predicted signal peptide (amino acid residues from about 1 to about 17 in SEQ ID NO:37) and are represented by the underlined amino acid regions.

5        Figure 23 shows the regions of similarity between the amino acid sequences of the Butyrophilin and B7-like IgG superfamily receptor (BBIR II) protein (SEQ ID NO:37) and the bovine butyrophilin precursor (SEQ ID NO:121)

Figure 24 shows an analysis of the integrin alpha 11 subunit (BBIR II) amino acid sequence.

10        Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic regions; flexible regions; antigenic index and surface probability are shown.

A polynucleotide encoding a polypeptide of the present invention is obtained from human small intestine, colon tumor, and human testes tumor cells and tissues. The polynucleotide of this invention was discovered in a human testes tumor cDNA library.

15        Its translation product has homology to the B30.2-like domain which is characteristic of proteins containing zinc-binding B-box motifs, and particularly for butyrophilin family members. The polynucleotide contains an open reading frame encoding the BBIR II polypeptide of 318 amino acids. BBIR II exhibits a high degree of homology at the amino acid level to the bovine butyrophilin precursor (as shown in

20        Figure 23). The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding the BBIR II polypeptide having the amino acid sequence shown in Figures 22A-D (SEQ ID NO:37). The nucleotide sequence shown in Figures 22A-D (SEQ ID NO:19) was obtained by sequencing a cloned cDNA (HTTDB46), which was deposited on November 17 at the American Type Culture Collection, and given

25        Accession Number 203484.

The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated DNA molecule having the



nucleotide sequence of the deposited cDNA or the nucleotide sequence shown in SEQ ID NO:19 is intended DNA fragments at least about 15nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length which are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-1500 nt in length are also useful according to the present invention, as are fragments corresponding to most, if not all, of the nucleotide sequence of the deposited cDNA or as shown in SEQ ID NO:19. By a fragment at least 20 nt in length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of the deposited cDNA or the nucleotide sequence as shown in SEQ ID NO:19. In this context "about" includes the particularly recited size, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Representative examples of BBIR II polynucleotide fragments of the invention include, for example, fragments that comprise, or alternatively, consist of, a sequence from about nucleotide 1 to about 50, from about 51 to about 100, from about 101 to about 150, from about 151 to about 200, from about 201 to about 250, from about 251 to about 300, from about 301 to about 350, from about 351 to about 400, from about 401 to about 450, from about 451 to about 500, from about 501 to about 550, from about 551 to about 600, from about 601 to about 650, from about 651 to about 700, from about 701 to about 750, from about 751 to about 800, from about 801 to about 850, from about 851 to about 900, from about 901 to about 950, from about 951 to about 1000, from about 1001 to about 1050, from about 1051 to about 1100, from about 1101 to about 1150, from about 1151 to about 1200, from about 1201 to about 1250, from about 1251 to about 1300, from about 1301 to about 1350, from about 1351 to about 1400, from about 1401 to about 1450, from about 1451 to about 1500, from about 1501 to about 1550, from about 1551 to about 1600, from about 1601 to about 1650, from about 1651 to about 1700, from about 1701 to about 1750, from about 1751 to about 1800, from about 1801 to about 1850, from about 1851 to about 1900, from about 1901 to about 1950, from

about 1951 to about 2000, from about 2001 to about 2050, from about 2051 to about 2100, from about 2101 to about 2150, from about 2151 to about 2200, from about 2201 to about 2250, from about 2251 to about 2300, from about 2301 to about 2350, from about 2351 to about 2400, from about 2401 to about 2450, from about 2451 to about 2500, from about 2501 to about 2550, from about 2551 to about 2600, from about 2601 to about 2650, from about 2651 to about 2700, from about 2701 to about 2750, from about 2751 to about 2800, from about 2801 to about 2850, from about 2851 to about 2900, from about 2901 to about 2950, from about 2951 to about 3000, from about 3001 to about 3050, from about 3051 to about 3059 of SEQ ID NO:19, or the complementary strand thereto, or the cDNA contained in the deposited gene. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini.

Preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding a member selected from the group: a polypeptide comprising or alternatively, consisting of, the mature BBIR II protein (amino acid residues from about 18 to about 318 in Figures 22A-D (amino acids from about 18 to about 318 in SEQ ID NO:37). Since the location of this form of the protein has been predicted by computer analysis, one of ordinary skill would appreciate that the amino acid residues constituting these domains may vary slightly (e.g., by about 1 to 15 amino acid residues) depending on the criteria used to define this location. In additional embodiments, the polynucleotides of the invention encode functional attributes of BBIR II.

Preferred embodiments of the invention in this regard include fragments that comprise alpha-helix and alpha-helix forming regions ("alpha-regions"), beta-sheet and beta-sheet forming regions ("beta-regions"), turn and turn-forming regions ("turn-regions"), coil and coil-forming regions ("coil-regions"), hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions and high antigenic index regions of BBIR II. The data

representing the structural or functional attributes of BBIR II set forth in Figure 24 and/or Table VIII, as described above, was generated using the various modules and algorithms of the DNA\*STAR set on default parameters. In a preferred embodiment, the data presented in columns VIII, IX, XIII, and XIV of Table VIII can be used to

5 determine regions of BBIR II which exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or XIV by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

10 Certain preferred regions in these regards are set out in Figure 24, but may, as shown in Table VIII, be represented or identified by using tabular representations of the data presented in Figure 24. The DNA\*STAR computer algorithm used to generate Figure 24 (set on the original default parameters) was used to present the data in Figure 24 in a tabular format (See Table VIII). The tabular format of the data in Figure 24 is  
15 used to easily determine specific boundaries of a preferred region. The above-mentioned preferred regions set out in Figure 24 and in Table VIII include, but are not limited to, regions of the aforementioned types identified by analysis of the amino acid sequence set out in Figures 22A-D. As set out in Figure 24 and in Table VIII, such preferred regions include Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions,  
20 Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and Hopp-Woods hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schulz flexible regions, Jameson-Wolf regions of high antigenic index and Emmini surface-forming regions. Even if deletion of one or more amino acids from the N-terminus of a protein results in modification of loss of one or more biological  
25 functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, etc.) may still be retained. For example, the ability of shortened BBIR II muteins to induce and/or bind to antibodies which recognize the complete or mature

forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus.

Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods

5 described herein and otherwise known in the art. It is not unlikely that an BBIR II mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six BBIR II amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or  
10 more residues deleted from the amino terminus of the BBIR II amino acid sequence shown in Figures 22A-D, up to the cystein residue at position number 313 and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues n1-318 of Figures 22A-D, where n1 is an integer from 2 to 313 corresponding to the position of the amino acid  
15 residue in Figures 22A-D (which is identical to the sequence shown as SEQ ID NO:37). In another embodiment, N-terminal deletions of the BBIR II polypeptide can be described by the general formula n2-318, where n2 is a number from 2 to 313, corresponding to the position of amino acid identified in Figures 22A-D. N-terminal deletions of the BBIR II polypeptide of the invention shown as SEQ ID NO:37 include  
20 polypeptides comprising the amino acid sequence of residues: N-terminal deletions of the BBIR II polypeptide of the invention shown as SEQ ID NO:37 include polypeptides comprising the amino acid sequence of residues: A-2 to T-318; L-3 to T-318; M-4 to T-318; L-5 to T-318; S-6 to T-318; L-7 to T-318; V-8 to T-318; L-9 to T-318; S-10 to T-318; L-11 to T-318; L-12 to T-318; K-13 to T-318; L-14 to T-318; G-15 to T-318; S-16  
25 to T-318; G-17 to T-318; Q-18 to T-318; W-19 to T-318; Q-20 to T-318; V-21 to T-318; F-22 to T-318; G-23 to T-318; P-24 to T-318; D-25 to T-318; K-26 to T-318; P-27 to T-318; V-28 to T-318; Q-29 to T-318; A-30 to T-318; L-31 to T-318; V-32 to T-318; G-33

to T-318; E-34 to T-318; D-35 to T-318; A-36 to T-318; A-37 to T-318; F-38 to T-318;  
S-39 to T-318; C-40 to T-318; F-41 to T-318; L-42 to T-318; S-43 to T-318; P-44 to T-  
318; K-45 to T-318; T-46 to T-318; N-47 to T-318; A-48 to T-318; E-49 to T-318; A-50  
to T-318; M-51 to T-318; E-52 to T-318; V-53 to T-318; R-54 to T-318; F-55 to T-318;  
5 F-56 to T-318; R-57 to T-318; G-58 to T-318; Q-59 to T-318; F-60 to T-318; S-61 to T-  
318; S-62 to T-318; V-63 to T-318; V-64 to T-318; H-65 to T-318; L-66 to T-318; Y-67  
to T-318; R-68 to T-318; D-69 to T-318; G-70 to T-318; K-71 to T-318; D-72 to T-318;  
Q-73 to T-318; P-74 to T-318; F-75 to T-318; M-76 to T-318; Q-77 to T-318; M-78 to T-  
318; P-79 to T-318; Q-80 to T-318; Y-81 to T-318; Q-82 to T-318; G-83 to T-318; R-84  
10 to T-318; T-85 to T-318; K-86 to T-318; L-87 to T-318; V-88 to T-318; K-89 to T-318;  
D-90 to T-318; S-91 to T-318; I-92 to T-318; A-93 to T-318; E-94 to T-318; G-95 to T-  
318; R-96 to T-318; I-97 to T-318; S-98 to T-318; L-99 to T-318; R-100 to T-318; L-101  
to T-318; E-102 to T-318; N-103 to T-318; I-104 to T-318; T-105 to T-318; V-106 to T-  
318; L-107 to T-318; D-108 to T-318; A-109 to T-318; G-110 to T-318; L-111 to T-318;  
15 Y-112 to T-318; G-113 to T-318; C-114 to T-318; R-115 to T-318; I-116 to T-318; S-117  
to T-318; S-118 to T-318; Q-119 to T-318; S-120 to T-318; Y-121 to T-318; Y-122 to T-  
318; Q-123 to T-318; K-124 to T-318; A-125 to T-318; I-126 to T-318; W-127 to T-318;  
E-128 to T-318; L-129 to T-318; Q-130 to T-318; V-131 to T-318; S-132 to T-318; A-  
133 to T-318; L-134 to T-318; G-135 to T-318; S-136 to T-318; V-137 to T-318; P-138  
20 to T-318; L-139 to T-318; I-140 to T-318; S-141 to T-318; I-142 to T-318; A-143 to T-  
318; G-144 to T-318; Y-145 to T-318; V-146 to T-318; D-147 to T-318; R-148 to T-318;  
D-149 to T-318; I-150 to T-318; Q-151 to T-318; L-152 to T-318; L-153 to T-318; C-154  
to T-318; Q-155 to T-318; S-156 to T-318; S-157 to T-318; G-158 to T-318; W-159 to T-  
318; F-160 to T-318; P-161 to T-318; R-162 to T-318; P-163 to T-318; T-164 to T-318;  
25 A-165 to T-318; K-166 to T-318; W-167 to T-318; K-168 to T-318; G-169 to T-318; P-  
170 to T-318; Q-171 to T-318; G-172 to T-318; Q-173 to T-318; D-174 to T-318; L-175  
to T-318; S-176 to T-318; T-177 to T-318; D-178 to T-318; S-179 to T-318; R-180 to T-

318; T-181 to T-318; N-182 to T-318; R-183 to T-318; D-184 to T-318; M-185 to T-318; H-186 to T-318; G-187 to T-318; L-188 to T-318; F-189 to T-318; D-190 to T-318; V-191 to T-318; E-192 to T-318; I-193 to T-318; S-194 to T-318; L-195 to T-318; T-196 to T-318; V-197 to T-318; Q-198 to T-318; E-199 to T-318; N-200 to T-318; A-201 to T-318; G-202 to T-318; S-203 to T-318; I-204 to T-318; S-205 to T-318; C-206 to T-318; S-207 to T-318; M-208 to T-318; R-209 to T-318; H-210 to T-318; A-211 to T-318; H-212 to T-318; L-213 to T-318; S-214 to T-318; R-215 to T-318; E-216 to T-318; V-217 to T-318; E-218 to T-318; S-219 to T-318; R-220 to T-318; V-221 to T-318; Q-222 to T-318; I-223 to T-318; G-224 to T-318; D-225 to T-318; W-226 to T-318; R-227 to T-318; R-228 to T-318; K-229 to T-318; H-230 to T-318; G-231 to T-318; Q-232 to T-318; A-233 to T-318; G-234 to T-318; K-235 to T-318; R-236 to T-318; K-237 to T-318; Y-238 to T-318; S-239 to T-318; S-240 to T-318; S-241 to T-318; H-242 to T-318; I-243 to T-318; Y-244 to T-318; D-245 to T-318; S-246 to T-318; F-247 to T-318; P-248 to T-318; S-249 to T-318; L-250 to T-318; S-251 to T-318; F-252 to T-318; M-253 to T-318; D-254 to T-318; F-255 to T-318; Y-256 to T-318; I-257 to T-318; L-258 to T-318; R-259 to T-318; P-260 to T-318; V-261 to T-318; G-262 to T-318; P-263 to T-318; C-264 to T-318; R-265 to T-318; A-266 to T-318; K-267 to T-318; L-268 to T-318; V-269 to T-318; M-270 to T-318; G-271 to T-318; T-272 to T-318; L-273 to T-318; K-274 to T-318; L-275 to T-318; Q-276 to T-318; I-277 to T-318; L-278 to T-318; G-279 to T-318; E-280 to T-318; V-281 to T-318; H-282 to T-318; F-283 to T-318; V-284 to T-318; E-285 to T-318; K-286 to T-318; P-287 to T-318; H-288 to T-318; S-289 to T-318; L-290 to T-318; L-291 to T-318; Q-292 to T-318; I-293 to T-318; S-294 to T-318; G-295 to T-318; G-296 to T-318; S-297 to T-318; T-298 to T-318; T-299 to T-318; L-300 to T-318; K-301 to T-318; K-302 to T-318; G-303 to T-318; P-304 to T-318; N-305 to T-318; P-306 to T-318; W-307 to T-318; S-308 to T-318; F-309 to T-318; P-310 to T-318; S-311 to T-318; P-312 to T-318; C-313 to T-318; of SEQ ID NO:37. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities (e.g., ability to illicit mitogenic activity, induce differentiation of normal or malignant cells, ability to multimerize, etc.) may still be retained. For example the ability of the shortened BBIR II mutein to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that an BBIR II mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six BBIR II amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the BBIR II polypeptide shown in Figures 22A-D, up to the serine residue at position number 6, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues 1-m1 of Figure 1, where m1 is an integer from 6 to 318 corresponding to the position of the amino acid residue in Figures 22A-D. Moreover, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of C-terminal deletions of the BBIR II polypeptide of the invention shown as SEQ ID NO:37 include polypeptides comprising the amino acid sequence of residues M-1 to P-317; M-1 to F-316; M-1 to L-315; M-1 to A-314; M-1 to C-313; M-1 to P-312; M-1 to S-311; M-1 to P-310; M-1 to F-309; M-1 to S-308; M-1 to W-307; M-1 to P-306; M-1 to N-305; M-1 to P-304; M-1 to G-303; M-1 to K-302; M-1 to K-301; M-1 to L-300;

M-1 to T-299; M-1 to T-298; M-1 to S-297; M-1 to G-296; M-1 to G-295; M-1 to S-294;  
M-1 to I-293; M-1 to Q-292; M-1 to L-291; M-1 to L-290; M-1 to S-289; M-1 to H-288;  
M-1 to P-287; M-1 to K-286; M-1 to E-285; M-1 to V-284; M-1 to F-283; M-1 to H-282;  
M-1 to V-281; M-1 to E-280; M-1 to G-279; M-1 to L-278; M-1 to I-277; M-1 to Q-276;  
5 M-1 to L-275; M-1 to K-274; M-1 to L-273; M-1 to T-272; M-1 to G-271; M-1 to M-270;  
M-1 to V-269; M-1 to L-268; M-1 to K-267; M-1 to A-266; M-1 to R-265; M-1 to C-264;  
M-1 to P-263; M-1 to G-262; M-1 to V-261; M-1 to P-260; M-1 to R-259; M-1 to L-258;  
M-1 to I-257; M-1 to Y-256; M-1 to F-255; M-1 to D-254; M-1 to M-253; M-1 to F-252;  
M-1 to S-251; M-1 to L-250; M-1 to S-249; M-1 to P-248; M-1 to F-247; M-1 to S-246;  
10 M-1 to D-245; M-1 to Y-244; M-1 to I-243; M-1 to H-242; M-1 to S-241; M-1 to S-240;  
M-1 to S-239; M-1 to Y-238; M-1 to K-237; M-1 to R-236; M-1 to K-235; M-1 to G-234;  
M-1 to A-233; M-1 to Q-232; M-1 to G-231; M-1 to H-230; M-1 to K-229; M-1 to R-  
228; M-1 to R-227; M-1 to W-226; M-1 to D-225; M-1 to G-224; M-1 to I-223; M-1 to  
Q-222; M-1 to V-221; M-1 to R-220; M-1 to S-219; M-1 to E-218; M-1 to V-217; M-1  
15 to E-216; M-1 to R-215; M-1 to S-214; M-1 to L-213; M-1 to H-212; M-1 to A-211; M-1  
to H-210; M-1 to R-209; M-1 to M-208; M-1 to S-207; M-1 to C-206; M-1 to S-205; M-1  
to I-204; M-1 to S-203; M-1 to G-202; M-1 to A-201; M-1 to N-200; M-1 to E-199; M-1  
to Q-198; M-1 to V-197; M-1 to T-196; M-1 to L-195; M-1 to S-194; M-1 to I-193; M-1  
to E-192; M-1 to V-191; M-1 to D-190; M-1 to F-189; M-1 to L-188; M-1 to G-187; M-1  
20 to H-186; M-1 to M-185; M-1 to D-184; M-1 to R-183; M-1 to N-182; M-1 to T-181; M-  
1 to R-180; M-1 to S-179; M-1 to D-178; M-1 to T-177; M-1 to S-176; M-1 to L-175;  
M-1 to D-174; M-1 to Q-173; M-1 to G-172; M-1 to Q-171; M-1 to P-170; M-1 to G-169;  
M-1 to K-168; M-1 to W-167; M-1 to K-166; M-1 to A-165; M-1 to T-164; M-1 to P-  
163; M-1 to R-162; M-1 to P-161; M-1 to F-160; M-1 to W-159; M-1 to G-158; M-1 to  
25 S-157; M-1 to S-156; M-1 to Q-155; M-1 to C-154; M-1 to L-153; M-1 to L-152; M-1 to  
Q-151; M-1 to I-150; M-1 to D-149; M-1 to R-148; M-1 to D-147; M-1 to V-146; M-1 to  
Y-145; M-1 to G-144; M-1 to A-143; M-1 to I-142; M-1 to S-141; M-1 to I-140; M-1



to L-139; M-1 to P-138; M-1 to V-137; M-1 to S-136; M-1 to G-135; M-1 to L-134; M-1 to A-133; M-1 to S-132; M-1 to V-131; M-1 to Q-130; M-1 to L-129; M-1 to E-128; M-1 to W-127; M-1 to I-126; M-1 to A-125; M-1 to K-124; M-1 to Q-123; M-1 to Y-122; M-1 to Y-121; M-1 to S-120; M-1 to Q-119; M-1 to S-118; M-1 to S-117; M-1 to I-116; M-1 to R-115; M-1 to C-114; M-1 to G-113; M-1 to Y-112; M-1 to L-111; M-1 to G-110; M-1 to A-109; M-1 to D-108; M-1 to L-107; M-1 to V-106; M-1 to T-105; M-1 to I-104; M-1 to N-103; M-1 to E-102; M-1 to L-101; M-1 to R-100; M-1 to L-99; M-1 to S-98; M-1 to I-97; M-1 to R-96; M-1 to G-95; M-1 to E-94; M-1 to A-93; M-1 to I-92; M-1 to S-91; M-1 to D-90; M-1 to K-89; M-1 to V-88; M-1 to L-87; M-1 to K-86; M-1 to T-85; M-1 to R-84; M-1 to G-83; M-1 to Q-82; M-1 to Y-81; M-1 to Q-80; M-1 to P-79; M-1 to M-78; M-1 to Q-77; M-1 to M-76; M-1 to F-75; M-1 to P-74; M-1 to Q-73; M-1 to D-72; M-1 to K-71; M-1 to G-70; M-1 to D-69; M-1 to R-68; M-1 to Y-67; M-1 to L-66; M-1 to H-65; M-1 to V-64; M-1 to V-63; M-1 to S-62; M-1 to S-61; M-1 to F-60; M-1 to Q-59; M-1 to G-58; M-1 to R-57; M-1 to F-56; M-1 to F-55; M-1 to R-54; M-1 to V-53; M-1 to E-52; M-1 to M-51; M-1 to A-50; M-1 to E-49; M-1 to A-48; M-1 to N-47; M-1 to T-46; M-1 to K-45; M-1 to P-44; M-1 to S-43; M-1 to L-42; M-1 to F-41; M-1 to C-40; M-1 to S-39; M-1 to F-38; M-1 to A-37; M-1 to A-36; M-1 to D-35; M-1 to E-34; M-1 to G-33; M-1 to V-32; M-1 to L-31; M-1 to A-30; M-1 to Q-29; M-1 to V-28; M-1 to P-27; M-1 to K-26; M-1 to D-25; M-1 to P-24; M-1 to G-23; M-1 to F-22; M-1 to V-21; M-1 to Q-20; M-1 to W-19; M-1 to Q-18; M-1 to G-17; M-1 to S-16; M-1 to G-15; M-1 to L-14; M-1 to K-13; M-1 to L-12; M-1 to L-11; M-1 to S-10; M-1 to L-9; M-1 to V-8; M-1 to L-7; M-1 to S-6; of SEQ ID NO:37. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In addition, the invention provides nucleic acid molecules having nucleotide sequences related to extensive portions of SEQ ID NO:19 which have been determined from the following related cDNA genes: HTTDB46R (SEQ ID NO:122), and HSIEA44R (SEQ ID NO:123).

Based on the sequence similarity to the bovin butyrophilin precursor, translation product of this gene is expected to share at least some biological activities with B30.2-like domain containing proteins, and specifically butyrophilin proteins. Such activities are known in the art, some of which are described elsewhere herein. Specifically,

5 polynucleotides and polypeptides of the invention are also useful for modulating the differentiation of normal and malignant cells, modulating the proliferation and/or differentiation of cancer and neoplastic cells, and regulation of cell growth and differentiation. Polynucleotides and polypeptides of the invention may represent a diagnostic marker for breast diseases and/or disorders, in addition to disorders of

10 secretory organs and tissues (which include, testicular and gastrointestinal disorders, particularly those cells which serve secretory functions for seminal fluid or gastrointestinal hormones, and disorders of the mucosal membranes of such cells and tissues, etc.).

The full-length protein should be a secreted protein, based upon homology to the butyrophilin family of proteins. Therefore, it is secreted into milk, serum, urine, seminal

15 fluid, or feces and thus the levels is assayable from patient samples. Assuming specific expression levels are reflective of the presence of breast disorders (i.e., breast cancer, breast dysfunction, etc.) this protein would provide a convenient diagnostic for early detection of such disorders

20 In addition, expression of this gene product may also be linked to the progression of breast diseases, and therefore may itself actually represent a therapeutic or therapeutic target for the treatment of breast cancer. Polynucleotides and polypeptides of the invention may play an important role in the pathogenesis of human cancers and cellular transformation, particularly those of secretory cells and tissues. Polynucleotides and

25 polypeptides of the invention may also be involved in the pathogenesis of developmental abnormalities based upon its potential effects on proliferation and differentiation of cells and tissue cell types.

Due to the potential proliferating and differentiating activity of said polynucleotides and polypeptides, the invention is useful as a therapeutic agent in inducing tissue regeneration, for treating inflammatory conditions. Moreover, the invention is useful in modulating the immune response to aberrant polypeptides, as may  
5 exist in rapidly proliferating cells and tissue cell types, particularly in cancers. The invention, including agonists and/or antagonists thereof, is useful in modulating the nutritional value of milk, its caloric content, its fat content, and may conceivably be useful in mediating the adaption of breast secretory function as a delivery vehicle for therapeutics (i.e., transgenic breast secretory tissue for transferring therapeutically active  
10 proteins to infants).

Alternatively, the expression within cellular sources marked by proliferating cells indicates this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis, treatment, and/or prevention of developmental diseases and disorders, including cancer, and other proliferative conditions. Representative uses are  
15 described in the "Hyperproliferative Disorders" and "Regeneration" sections below and elsewhere herein. Briefly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation.

Dysregulation of apoptosis can result in inappropriate suppression of cell death, as occurs in the development of some cancers, or in failure to control the extent of cell  
20 death, as is believed to occur in acquired immunodeficiency and certain neurodegenerative disorders, such as spinal muscular atrophy (SMA).

Alternatively, this gene product is involved in the pattern of cellular proliferation that accompanies early embryogenesis. Thus, aberrant expression of this gene product in tissues - particularly adult tissues - may correlate with patterns of abnormal cellular  
25 proliferation, such as found in various cancers. Because of potential roles in proliferation and differentiation, this gene product may have applications in the adult for tissue regeneration and the treatment of cancers. It may also act as a morphogen to control cell

and tissue type specification. Therefore, the polynucleotides and polypeptides of the present invention are useful in treating, detecting, and/or preventing said disorders and conditions, in addition to other types of degenerative conditions. Thus this protein may modulate apoptosis or tissue differentiation and is useful in the detection, treatment,  
5 and/or prevention of degenerative or proliferative conditions and diseases. The protein is useful in modulating the immune response to aberrant polypeptides, as may exist in proliferating and cancerous cells and tissues. The protein can also be used to gain new insight into the regulation of cellular growth and proliferation. Furthermore, the protein may also be used to determine biological activity, to raise antibodies, as tissue markers,  
10 to isolate cognate ligands or receptors, to identify agents that modulate their interactions, in addition to its use as a nutritional supplement. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

This gene is expressed primarily in small intestine, colon tumor, and to a lesser  
15 extent in human testes tumor cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, gastrointestinal diseases and/or disorders, in addition to lactation disorders,  
20 and tumors of the testes. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and reproductive systems, expression of this gene at significantly higher or lower levels is routinely detected in certain tissues or cell types  
25 (e.g. immune, testicular, gastrointestinal, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard

gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred polypeptides of the present invention comprise immunogenic epitopes shown in SEQ ID NO: 37 as residues: Tyr-67 to Pro-74, Ser-117 to Gln-123, Pro-161 to  
5 Met-185, Gly-224 to His-242, Thr-299 to Trp-307. Polynucleotides encoding said polypeptides are also provided.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 10

10

The translation product of this gene contains a serine protease motif and accordingly is believed to possess serine protease activity. Assays for determining such activity are well known in the art. Preferred polypeptides of this invention possess such activity.

15

Included in this invention as preferred domains are serine protease histidine active site domains, which were identified using the ProSite analysis tool (Swiss Institute of Bioinformatics). The catalytic activity of the serine proteases from the trypsin family is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which itself is hydrogen-bonded to a serine. The sequences in the vicinity  
20 of the active site serine and histidine residues are well conserved in this family of proteases [1]. Consensus pattern: [LIVM]-[ST]-A-[STAG]-H-C, H is the active site residue.

25

Preferred polypeptides of the invention comprise the following amino acid sequence: GTLVAEKHVLTAAHCIHDGKTYVKGTQ (SEQ ID NO: 124).

Polynucleotides encoding these polypeptides are also provided.

Further preferred are polypeptides comprising the serine protease histidine active site domain of the sequence referenced in Table XIII for this gene, and at least 5, 10, 15,

20, 25, 30, 50, or 75 additional contiguous amino acid residues of this referenced sequence. The additional contiguous amino acid residues is N-terminal or C-terminal to the serine protease histidine active site domain.

Alternatively, the additional contiguous amino acid residues is both N-terminal  
5 and C-terminal to the serine protease histidine active site domain, wherein the total N- and C-terminal contiguous amino acid residues equal the specified number. The above preferred polypeptide domain is characteristic of a signature specific to serine protease proteins. Based on the sequence similarity, the translation product of this gene is expected to share at least some biological activities with serine proteases. Such activities  
10 are known in the art, some of which are described elsewhere herein.

In another embodiment, polypeptides comprising the amino acid sequence of the open reading frame upstream of the predicted signal peptide are contemplated by the present invention. Specifically, polypeptides of the invention comprise the following amino acid sequence:

15 GTRGQAWEPRLSRRPHLSERRSEPRPGRAARRGTVLGMAGIPGLLFLFF  
LLCAVGQVSPYSAPWKPTWPA YRLPVVLPQSTLNLAKPDFGAEAKLEVSSSCGP  
QCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSG  
KSRRKRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCI  
HDGKTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHV  
20 PKGWIKGNANDIGMDYDYALLELKPKHKRKFMKIGVSPPAKQLPGGRIHFSGYD  
NDRPGNLVYRFCDVKDETYDLLYQQCDSQPGASGSGVYVRMWKRQH QKWER  
KIIGMISGHQWVDMDGSPQEFTRGCSEITPLQYIPDISIGV (SEQ ID NO: 125).

Polynucleotides encoding these polypeptides are also provided.

A preferred polypeptide variant of the invention comprises the following amino  
25 acid sequence:

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPA YRLPVVLPQSTLNLAKPD

FGAEAKLEVSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILS  
SSGDGAQHRDSGSSGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTG  
TLVAEKHVL

AAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRV

5 KRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRI  
HFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGASGSGVYVRMWKRQ  
QQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNYLDCRE  
G (SEQ ID NO: 126). Polynucleotides encoding these polypeptides are also provided.

Figures 25 A-B show the nucleotide (SEQ ID NO:20) and deduced amino acid  
10 sequence (SEQ ID NO:38) of the present invention. Predicted amino acids from about 1  
to about 19 constitute the predicted signal peptide (amino acid residues from about 1 to  
about 19 in SEQ ID NO:38) and are represented by the underlined amino acid regions;  
amino acids from about 162 to about 188 constitutes the predicted serine protease  
histidine active site domain (amino acids residues from about 162 to about 188 in SEQ  
15 ID NO:38) and are represented by the double underlined amino acid regions; and amino  
acid residue 175 (amino acid residue 175 in SEQ ID NO:38) constitutes the predicted  
histidine active site residue and is represented by the bold amino acid.

Figure 26 shows the regions of similarity between the amino acid sequences of  
the present invention SEQ ID NO:38, and the Human Pancreatic Elastase 2 protein  
20 (gi|219620)(SEQ ID NO: 127).

Figure 27 shows an analysis of the amino acid sequence of SEQ ID NO:38.  
Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic  
regions; flexible regions; antigenic index and surface probability are shown.

Northern analysis indicates that this gene is expressed highest in HUVEC,  
25 HUVEC +LPS, smooth muscle, fibroblasts, present in heart, brain, placenta, lung, liver,  
muscle, kidney, pancreas, spleen, thymus, prostate, testes, ovary, small intestine, colon  
and weakly in PBLs.

The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding the polypeptide having the amino acid sequence shown in Figures 25 A-B (SEQ ID NO:38), which was determined by sequencing a cloned cDNA. The nucleotide sequence shown in Figures 25 A-B (SEQ ID NO:20) was obtained by  
5 sequencing a cloned cDNA (HUSAQ05), which was deposited on Nov. 17, 1998 at the American Type Culture Collection, and given Accession Number 203484. The deposited gene is inserted in the pSport plasmid (Life Technologies, Rockville, MD) using the SalI/NotI restriction endonuclease cleavage sites.

The present invention is further directed to fragments of the isolated nucleic acid  
10 molecules described herein. By a fragment of an isolated DNA molecule having the nucleotide sequence of the deposited cDNA or the nucleotide sequence shown in SEQ ID NO:20 is intended DNA fragments at least about 15nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length which are useful as diagnostic probes and primers as discussed herein. Of  
15 course, larger fragments 50-1500 nt in length are also useful according to the present invention, as are fragments corresponding to most, if not all, of the nucleotide sequence of the deposited cDNA or as shown in SEQ ID NO:20. By a fragment at least 20 nt in length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of the deposited cDNA or the nucleotide sequence as  
20 shown in SEQ ID NO:20. In this context "about" includes the particularly recited size, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Representative examples of polynucleotide fragments of the invention include, for example, fragments that comprise, or alternatively, consist of, a sequence from about nucleotide 1 to about 50, from about 51 to about 100, from about 101 to about 150, from  
25 about 151 to about 200, from about 201 to about 250, from about 251 to about 300, from about 301 to about 350, from about 351 to about 400, from about 401 to about 450, from about 451 to about 500, and from about 501 to about 550, and from about 551 to about



600, from about 601 to about 650, from about 651 to about 700, from about 701 to about 750, from about 751 to about 800, from about 801 to about 850, from about 851 to about 900, from about 901 to about 950, from about 951 to about 1000, from about 1001 to about 1050, from about 1051 to about 1100, from about 1101 to about 1150, from about 1151 to about 1200, from about 1201 to about 1250, from about 1251 to about 1300, from about 1301 to about 1350, from about 1351 to about 1400, from about 1401 to about 1450, from about 1451 to about 1500, from about 1501 to about 1550, from about 1551 to about 1600, from about 1601 to about 1650, from about 1651 to about 1699 of SEQ ID NO:20, or the complementary strand thereto, or the cDNA contained in the deposited gene. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. In additional embodiments, the polynucleotides of the invention encode functional attributes of the corresponding protein.

Preferred embodiments of the invention in this regard include fragments that comprise alpha-helix and alpha-helix forming regions ("alpha-regions"), beta-sheet and beta-sheet forming regions ("beta-regions"), turn and turn-forming regions ("turn-regions"), coil and coil-forming regions ("coil-regions"), hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions and high antigenic index regions. The data representing the structural or functional attributes of the protein set forth in Figure 27 and/or Table IX, as described above, was generated using the various modules and algorithms of the DNA\*STAR set on default parameters. In a preferred embodiment, the data presented in columns VIII, IX, XIII, and XIV of Table IX can be used to determine regions of the protein which exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or XIV by choosing values which represent regions of the polypeptide which are likely to

be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Certain preferred regions in these regards are set out in Figure 27, but may, as shown in Table IX, be represented or identified by using tabular representations of the data presented in Figure 27. The DNA\*STAR computer algorithm used to generate Figure 27 (set on the original default parameters) was used to present the data in Figure 27 in a tabular format (See Table IX). The tabular format of the data in Figure 27 is used to easily determine specific boundaries of a preferred region. The above-mentioned preferred regions set out in Figure 27 and in Table IX include, but are not limited to, regions of the aforementioned types identified by analysis of the amino acid sequence set out in Figure 1. As set out in Figure 27 and in Table IX, such preferred regions include Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and Hopp-Woods hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schulz flexible regions, Jameson-Wolf regions of high antigenic index and Emini surface-forming regions. Even if deletion of one or more amino acids from the N-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, etc.) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic

activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence shown in

5 Figures 25A-B, up to the aspartic acid residue at position number 370 and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues n1-375 of Figures 25A-B, where n1 is an integer from 2 to 370 corresponding to the position of the amino acid residue in Figures 25A-B (which is identical to the sequence shown as SEQ ID NO:38).

10 N-terminal deletions of the polypeptide of the invention shown as SEQ ID NO:38 include polypeptides comprising the amino acid sequence of residues: A-2 to V-375; G-3 to V-375; I-4 to V-375; P-5 to V-375; G-6 to V-375; L-7 to V-375; L-8 to V-375; F-9 to V-375; L-10 to V-375; L-11 to V-375; F-12 to V-375; F-13 to V-375; L-14 to V-375; L-15 to V-375; C-16 to V-375; A-17 to V-375; V-18 to V-375; G-19 to V-375; Q-20 to V-

15 375; V-21 to V-375; S-22 to V-375; P-23 to V-375; Y-24 to V-375; S-25 to V-375; A-26 to V-375; P-27 to V-375; W-28 to V-375; K-29 to V-375; P-30 to V-375; T-31 to V-375; W-32 to V-375; P-33 to V-375; A-34 to V-375; Y-35 to V-375; R-36 to V-375; L-37 to V-375; P-38 to V-375; V-39 to V-375; V-40 to V-375; L-41 to V-375; P-42 to V-375; Q-43 to V-375; S-44 to V-375; T-45 to V-375; L-46 to V-375; N-47 to V-375; L-48 to V-

20 375; A-49 to V-375; K-50 to V-375; P-51 to V-375; D-52 to V-375; F-53 to V-375; G-54 to V-375; A-55 to V-375; E-56 to V-375; A-57 to V-375; K-58 to V-375; L-59 to V-375; E-60 to V-375; V-61 to V-375; S-62 to V-375; S-63 to V-375; S-64 to V-375; C-65 to V-375; G-66 to V-375; P-67 to V-375; Q-68 to V-375; C-69 to V-375; H-70 to V-375; K-71 to V-375; G-72 to V-375; T-73 to V-375; P-74 to V-375; L-75 to V-375; P-76 to V-

25 375; T-77 to V-375; Y-78 to V-375; E-79 to V-375; E-80 to V-375; A-81 to V-375; K-82 to V-375; Q-83 to V-375; Y-84 to V-375; L-85 to V-375; S-86 to V-375; Y-87 to V-375; E-88 to V-375; T-89 to V-375; L-90 to V-375; Y-91 to V-375; A-92 to V-375; N-93 to

V-375; G-94 to V-375; S-95 to V-375; R-96 to V-375; T-97 to V-375; E-98 to V-375; T-99 to V-375; Q-100 to V-375; V-101 to V-375; G-102 to V-375; I-103 to V-375; Y-104 to V-375; I-105 to V-375; L-106 to V-375; S-107 to V-375; S-108 to V-375; S-109 to V-375; G-110 to V-375; D-111 to V-375; G-112 to V-375; A-113 to V-375; Q-114 to V-375; H-115 to V-375; R-116 to V-375; D-117 to V-375; S-118 to V-375; G-119 to V-375; S-120 to V-375; S-121 to V-375; G-122 to V-375; K-123 to V-375; S-124 to V-375; R-125 to V-375; R-126 to V-375; K-127 to V-375; R-128 to V-375; Q-129 to V-375; I-130 to V-375; Y-131 to V-375; G-132 to V-375; Y-133 to V-375; D-134 to V-375; S-135 to V-375; R-136 to V-375; F-137 to V-375; S-138 to V-375; I-139 to V-375; F-140 to V-375; G-141 to V-375; K-142 to V-375; D-143 to V-375; F-144 to V-375; L-145 to V-375; L-146 to V-375; N-147 to V-375; Y-148 to V-375; P-149 to V-375; F-150 to V-375; S-151 to V-375; T-152 to V-375; S-153 to V-375; V-154 to V-375; K-155 to V-375; L-156 to V-375; S-157 to V-375; T-158 to V-375; G-159 to V-375; C-160 to V-375; T-161 to V-375; G-162 to V-375; T-163 to V-375; L-164 to V-375; V-165 to V-375; A-166 to V-375; E-167 to V-375; K-168 to V-375; H-169 to V-375; V-170 to V-375; L-171 to V-375; T-172 to V-375; A-173 to V-375; A-174 to V-375; H-175 to V-375; C-176 to V-375; I-177 to V-375; H-178 to V-375; D-179 to V-375; G-180 to V-375; K-181 to V-375; T-182 to V-375; Y-183 to V-375; V-184 to V-375; K-185 to V-375; G-186 to V-375; T-187 to V-375; Q-188 to V-375; K-189 to V-375; L-190 to V-375; R-191 to V-375; V-192 to V-375; G-193 to V-375; F-194 to V-375; L-195 to V-375; K-196 to V-375; P-197 to V-375; K-198 to V-375; F-199 to V-375; K-200 to V-375; D-201 to V-375; G-202 to V-375; G-203 to V-375; R-204 to V-375; G-205 to V-375; A-206 to V-375; N-207 to V-375; D-208 to V-375; S-209 to V-375; T-210 to V-375; S-211 to V-375; A-212 to V-375; M-213 to V-375; P-214 to V-375; E-215 to V-375; Q-216 to V-375; M-217 to V-375; K-218 to V-375; F-219 to V-375; Q-220 to V-375; W-221 to V-375; I-222 to V-375; R-223 to V-375; V-224 to V-375; K-225 to V-375; R-226 to V-375; T-227 to V-375; H-228 to V-375; V-229 to V-375; P-230 to V-

375; K-231 to V-375; G-232 to V-375; W-233 to V-375; I-234 to V-375; K-235 to V-375; G-236 to V-375; N-237 to V-375; A-238 to V-375; N-239 to V-375; D-240 to V-375; I-241 to V-375; G-242 to V-375; M-243 to V-375; D-244 to V-375; Y-245 to V-375; D-246 to V-375; Y-247 to V-375; A-248 to V-375; L-249 to V-375; L-250 to V-375; E-251 to V-375; L-252 to V-375; K-253 to V-375; K-254 to V-375; P-255 to V-375; H-256 to V-375; K-257 to V-375; R-258 to V-375; K-259 to V-375; F-260 to V-375; M-261 to V-375; K-262 to V-375; I-263 to V-375; G-264 to V-375; V-265 to V-375; S-266 to V-375; P-267 to V-375; P-268 to V-375; A-269 to V-375; K-270 to V-375; Q-271 to V-375; L-272 to V-375; P-273 to V-375; G-274 to V-375; G-275 to V-375; R-276 to V-375; I-277 to V-375; H-278 to V-375; F-279 to V-375; S-280 to V-375; G-281 to V-375; Y-282 to V-375; D-283 to V-375; N-284 to V-375; D-285 to V-375; R-286 to V-375; P-287 to V-375; G-288 to V-375; N-289 to V-375; L-290 to V-375; V-291 to V-375; Y-292 to V-375; R-293 to V-375; F-294 to V-375; C-295 to V-375; D-296 to V-375; V-297 to V-375; K-298 to V-375; D-299 to V-375; E-300 to V-375; T-301 to V-375; Y-302 to V-375; D-303 to V-375; L-304 to V-375; L-305 to V-375; Y-306 to V-375; Q-307 to V-375; Q-308 to V-375; C-309 to V-375; D-310 to V-375; S-311 to V-375; Q-312 to V-375; P-313 to V-375; G-314 to V-375; A-315 to V-375; S-316 to V-375; G-317 to V-375; S-318 to V-375; G-319 to V-375; V-320 to V-375; Y-321 to V-375; V-322 to V-375; R-323 to V-375; M-324 to V-375; W-325 to V-375; K-326 to V-375; R-327 to V-375; Q-328 to V-375; H-329 to V-375; Q-330 to V-375; K-331 to V-375; W-332 to V-375; E-333 to V-375; R-334 to V-375; K-335 to V-375; I-336 to V-375; I-337 to V-375; G-338 to V-375; M-339 to V-375; I-340 to V-375; S-341 to V-375; G-342 to V-375; H-343 to V-375; Q-344 to V-375; W-345 to V-375; V-346 to V-375; D-347 to V-375; M-348 to V-375; D-349 to V-375; G-350 to V-375; S-351 to V-375; P-352 to V-375; Q-353 to V-375; E-354 to V-375; F-355 to V-375; T-356 to V-375; R-357 to V-375; G-358 to V-375; C-359 to V-375; S-360 to V-375; E-361 to V-375; I-362 to V-375; T-363 to V-375; P-364 to V-375; L-365 to V-375; Q-366 to V-375; Y-367 to V-

375; I-368 to V-375; P-369 to V-375; D-370 to V-375; of SEQ ID NO:38. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities such as ability to modulate the extracellular matrix, etc.) may still be retained. For example the ability to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the polypeptide shown in Figures 25A-B, up to the glycine residue at position number 6, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues 1-m1 of Figures 25A-B, where m1 is an integer from 6 to 375 corresponding to the position of the amino acid residue in Figures 25A-B. Moreover, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of C-terminal deletions of the polypeptide of the invention shown as SEQ ID NO:38 include polypeptides comprising the amino acid sequence of residues: M-1 to G-374; M-1 to I-373; M-1 to S-372; M-1 to I-371; M-1 to D-370; M-1 to P-369; M-1 to I-368; M-1 to Y-367; M-1 to Q-366; M-1 to L-365; M-1 to P-364; M-1 to T-363; M-1 to I-362; M-1 to E-

361; M-1 to S-360; M-1 to C-359; M-1 to G-358; M-1 to R-357; M-1 to T-356; M-1 to  
F-355; M-1 to E-354; M-1 to Q-353; M-1 to P-352; M-1 to S-351; M-1 to G-350; M-1 to  
D-349; M-1 to M-348; M-1 to D-347; M-1 to V-346; M-1 to W-345; M-1 to Q-344; M-1  
to H-343; M-1 to G-342; M-1 to S-341; M-1 to I-340; M-1 to M-339; M-1 to G-338; M-  
5 1 to I-337; M-1 to I-336; M-1 to K-335; M-1 to R-334; M-1 to E-333; M-1 to W-332; M-  
1 to K-331; M-1 to Q-330; M-1 to H-329; M-1 to Q-328; M-1 to R-327; M-1 to K-326;  
M-1 to W-325; M-1 to M-324; M-1 to R-323; M-1 to V-322; M-1 to Y-321; M-1 to V-  
320; M-1 to G-319; M-1 to S-318; M-1 to G-317; M-1 to S-316; M-1 to A-315; M-1 to  
G-314; M-1 to P-313; M-1 to Q-312; M-1 to S-311; M-1 to D-310; M-1 to C-309; M-1  
10 to Q-308; M-1 to Q-307; M-1 to Y-306; M-1 to L-305; M-1 to L-304; M-1 to D-303; M-  
1 to Y-302; M-1 to T-301; M-1 to E-300; M-1 to D-299; M-1 to K-298; M-1 to V-297;  
M-1 to D-296; M-1 to C-295; M-1 to F-294; M-1 to R-293; M-1 to Y-292; M-1 to V-  
291; M-1 to L-290; M-1 to N-289; M-1 to G-288; M-1 to P-287; M-1 to R-286; M-1 to  
D-285; M-1 to N-284; M-1 to D-283; M-1 to Y-282; M-1 to G-281; M-1 to S-280; M-1  
15 to F-279; M-1 to H-278; M-1 to I-277; M-1 to R-276; M-1 to G-275; M-1 to G-274; M-1  
to P-273; M-1 to L-272; M-1 to Q-271; M-1 to K-270; M-1 to A-269; M-1 to P-268; M-1  
to P-267; M-1 to S-266; M-1 to V-265; M-1 to G-264; M-1 to I-263; M-1 to K-262; M-1  
to M-261; M-1 to F-260; M-1 to K-259; M-1 to R-258; M-1 to K-257; M-1 to H-256; M-  
1 to P-255; M-1 to K-254; M-1 to K-253; M-1 to L-252; M-1 to E-251; M-1 to L-250;  
20 M-1 to L-249; M-1 to A-248; M-1 to Y-247; M-1 to D-246; M-1 to Y-245; M-1 to D-  
244; M-1 to M-243; M-1 to G-242; M-1 to I-241; M-1 to D-240; M-1 to N-239; M-1 to  
A-238; M-1 to N-237; M-1 to G-236; M-1 to K-235; M-1 to I-234; M-1 to W-233; M-1  
to G-232; M-1 to K-231; M-1 to P-230; M-1 to V-229; M-1 to H-228; M-1 to T-227; M-  
1 to R-226; M-1 to K-225; M-1 to V-224; M-1 to R-223; M-1 to I-222; M-1 to W-221;  
25 M-1 to Q-220; M-1 to F-219; M-1 to K-218; M-1 to M-217; M-1 to Q-216; M-1 to E-  
215; M-1 to P-214; M-1 to M-213; M-1 to A-212; M-1 to S-211; M-1 to T-210; M-1 to  
S-209; M-1 to D-208; M-1 to N-207; M-1 to A-206; M-1 to G-205; M-1 to R-204; M-1

to G-203; M-1 to G-202; M-1 to D-201; M-1 to K-200; M-1 to F-199; M-1 to K-198; M-1 to P-197; M-1 to K-196; M-1 to L-195; M-1 to F-194; M-1 to G-193; M-1 to V-192; M-1 to R-191; M-1 to L-190; M-1 to K-189; M-1 to Q-188; M-1 to T-187; M-1 to G-186; M-1 to K-185; M-1 to V-184; M-1 to Y-183; M-1 to T-182; M-1 to K-181; M-1 to  
5 G-180; M-1 to D-179; M-1 to H-178; M-1 to I-177; M-1 to C-176; M-1 to H-175; M-1 to A-174; M-1 to A-173; M-1 to T-172; M-1 to L-171; M-1 to V-170; M-1 to H-169; M-1 to K-168; M-1 to E-167; M-1 to A-166; M-1 to V-165; M-1 to L-164; M-1 to T-163; M-1 to G-162; M-1 to T-161; M-1 to C-160; M-1 to G-159; M-1 to T-158; M-1 to S-157; M-1 to L-156; M-1 to K-155; M-1 to V-154; M-1 to S-153; M-1 to T-152; M-1 to S-151;  
10 M-1 to F-150; M-1 to P-149; M-1 to Y-148; M-1 to N-147; M-1 to L-146; M-1 to L-145; M-1 to F-144; M-1 to D-143; M-1 to K-142; M-1 to G-141; M-1 to F-140; M-1 to I-139; M-1 to S-138; M-1 to F-137; M-1 to R-136; M-1 to S-135; M-1 to D-134; M-1 to Y-133; M-1 to G-132; M-1 to Y-131; M-1 to I-130; M-1 to Q-129; M-1 to R-128; M-1 to K-127; M-1 to R-126; M-1 to R-125; M-1 to S-124; M-1 to K-123; M-1 to G-122; M-1 to S-121;  
15 M-1 to S-120; M-1 to G-119; M-1 to S-118; M-1 to D-117; M-1 to R-116; M-1 to H-115; M-1 to Q-114; M-1 to A-113; M-1 to G-112; M-1 to D-111; M-1 to G-110; M-1 to S-109; M-1 to S-108; M-1 to S-107; M-1 to L-106; M-1 to I-105; M-1 to Y-104; M-1 to I-103; M-1 to G-102; M-1 to V-101; M-1 to Q-100; M-1 to T-99; M-1 to E-98; M-1 to T-97; M-1 to R-96; M-1 to S-95; M-1 to G-94; M-1 to N-93; M-1 to A-92; M-1 to Y-91;  
20 M-1 to L-90; M-1 to T-89; M-1 to E-88; M-1 to Y-87; M-1 to S-86; M-1 to L-85; M-1 to Y-84; M-1 to Q-83; M-1 to K-82; M-1 to A-81; M-1 to E-80; M-1 to E-79; M-1 to Y-78; M-1 to T-77; M-1 to P-76; M-1 to L-75; M-1 to P-74; M-1 to T-73; M-1 to G-72; M-1 to K-71; M-1 to H-70; M-1 to C-69; M-1 to Q-68; M-1 to P-67; M-1 to G-66; M-1 to C-65; M-1 to S-64; M-1 to S-63; M-1 to S-62; M-1 to V-61; M-1 to E-60; M-1 to L-59; M-1 to  
25 K-58; M-1 to A-57; M-1 to E-56; M-1 to A-55; M-1 to G-54; M-1 to F-53; M-1 to D-52; M-1 to P-51; M-1 to K-50; M-1 to A-49; M-1 to L-48; M-1 to N-47; M-1 to L-46; M-1 to T-45; M-1 to S-44; M-1 to Q-43; M-1 to P-42; M-1 to L-41; M-1 to V-40; M-1 to V-



39; M-1 to P-38; M-1 to L-37; M-1 to R-36; M-1 to Y-35; M-1 to A-34; M-1 to P-33; M-1 to W-32; M-1 to T-31; M-1 to P-30; M-1 to K-29; M-1 to W-28; M-1 to P-27; M-1 to A-26; M-1 to S-25; M-1 to Y-24; M-1 to P-23; M-1 to S-22; M-1 to V-21; M-1 to Q-20; M-1 to G-19; M-1 to V-18; M-1 to A-17; M-1 to C-16; M-1 to L-15; M-1 to L-14; M-1 to F-13; M-1 to F-12; M-1 to L-11; M-1 to L-10; M-1 to F-9; M-1 to L-8; M-1 to L-7; M-1 to G-6; of SEQ ID NO:38. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In addition, the invention provides nucleic acid molecules having nucleotide sequences related to extensive portions of SEQ ID NO:20 which have been determined from the following related cDNA genes: HFKCF40F (SEQ ID NO:128), HSRDF26R (SEQ ID NO:129), HTEBE07R (SEQ ID NO:130), HFTBP82R (SEQ ID NO:131), HAQBJ11R (SEQ ID NO:132), HAFBB11R (SEQ ID NO:133), HOEFO85R (SEQ ID NO:134), and HUVGY95R (SEQ ID NO:135).

The gene encoding the disclosed cDNA is believed to reside on chromosome 12. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 12.

This gene is expressed primarily in endothelial cells, fibroblasts, smooth muscle, and osteoblasts, and to a lesser extent in brain, heart, placental tissues, lung, and many other tissues. Moreover, the transcript is present in HUVEC, HUVEC +LPS, smooth muscle, fibroblasts; present in heart, brain, placenta, lung, liver, muscle, kidney, pancreas, spleen, thymus, prostate, testes, ovary, small intestine, colon and weakly in PBLs.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, disorders of vascularized tissues. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for

differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular tissues, expression of this gene at significantly higher or lower levels is routinely detected in certain tissues or cell types (e.g. vascular, skeletal, developmental, neural, cardiovascular, pulmonary, renal, immune, hematopoietic, reproductive, gastrointestinal, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, seminal, fluid, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 Preferred polypeptides of the present invention comprise immunogenic epitopes shown in SEQ ID NO: 38 as residues: Pro-67 to Thr-73, Pro-76 to Gln-83, Asn-93 to Thr-99, His-115 to Arg-128, His-178 to Lys-189, Pro-197 to Ala-212, Val-224 to Trp-233, Lys-253 to Lys-259, Ser-280 to Asn-289, Asp-296 to Tyr-302, Gln-308 to Ala-315, Arg-327 to Lys-335, Asp-349 to Gly-358. Polynucleotides encoding said polypeptides  
15 are also provided.

The tissue distribution in the vascularized endothelial cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of diseases of vascularized tissues, such as atherosclerosis, ataxia malabsortion, and hyperlipidemia. These and other factors often result in other  
20 cardiovascular disease. Furthermore, translation product of this gene is useful for the treatment of wounds, and may facilitate the wound healing process. Moreover, the protein is useful in the detection, treatment, and/or prevention of a variety of vascular disorders and conditions, which include, but are not limited to microvascular disease, vascular leak syndrome, aneurysm, stroke, embolism, thrombosis, coronary artery  
25 disease, arteriosclerosis, and/or atherosclerosis. Based upon the tissue distribution of this protein, antagonists directed against this protein is useful in blocking the activity of this

protein. Accordingly, preferred are antibodies which specifically bind a portion of the translation product of this gene.

Also provided is a kit for detecting tumors in which expression of this protein occurs. Such a kit comprises in one embodiment an antibody specific for the translation  
5 product of this gene bound to a solid support. Also provided is a method of detecting these tumors in an individual which comprises a step of contacting an antibody specific for the translation product of this gene to a bodily fluid from the individual, preferably serum, and ascertaining whether antibody binds to an antigen found in the bodily fluid. Preferably the antibody is bound to a solid support and the bodily fluid is serum. The  
10 above embodiments, as well as other treatments and diagnostic tests (kits and methods), are more particularly described elsewhere herein. Furthermore, the protein may also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions, in addition to its use as a nutritional supplement. Protein, as well as, antibodies directed  
15 against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:20 and may have been publicly available prior to conception of the present  
20 invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-  
b, where a is any integer between 1 to 1685 of SEQ ID NO:20, b is an integer of 15 to  
25 1699, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:20, and where b is greater than or equal to a + 14.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 11**

The translation product of this gene shares sequence homology with Cytotoxic-  
 5 Regulatory T-Cell Associated Molecule (CRTAM) protein, which is thought to be  
 important in the regulation of cellular physiology, development, differentiation or  
 function of various cell types, including haematopoietic cells and various T-cell  
 progenitors. See for example, PCT publication WO 96/34102 incorporated herein by  
 reference in its entirety. Moreover, the protein product of this gene also shares homology  
 10 with the thymocyte activation and developmental protein and the class-I MHC-restricted  
 T cell associated molecule (See Genbank Accession Nos. gi|2665790, gb|AAB88491.1,  
 gb|AAC80267.1, and gi|3930163; all information and references contained within these  
 accessions are hereby incorporated herein by reference). Based on the sequence  
 similarity, the translation product of this gene is expected to share at least some  
 15 biological activities with T-cell modulatory proteins. Such activities are known in the art,  
 some of which are described elsewhere herein.

Preferred polypeptides of the invention comprise the following amino acid  
 sequence:

MASVVLPSGSQCAAAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVI  
 20 EGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSL  
 TNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCT  
 AMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQMLMLKVHKEDDGVPVIC  
 QVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQ  
 PVMVTWVRVDDMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDY  
 25 MLYVYDPPTTIPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAV  
 VVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEK

KEYFI (SEQ ID NO: 136). Polynucleotides encoding these polypeptides are also provided.

The polypeptide of this latter embodiment has been determined to have a transmembrane domain at about amino acid position 379 - 395 of the amino acid sequence referenced in Table XIII for this gene. Moreover, a cytoplasmic tail encompassing amino acids 396 to 442 of this protein has also been determined. Based upon these characteristics, it is believed that the protein product of this gene shares structural features to type Ia membrane proteins.

Preferred polynucleotides comprise the following sequence:

10 ATGGCGAGTGTAGTGC  
TGCCGAGCGGATCCCAGTGTGCGGCGGCAGCGGCGGCGGCGGCCTCCCCG  
GGCTCCGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGGCACTGATCCCC  
ACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA  
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTC  
15 AGCTACTGAATCCCAACAGGCAGACCATTTATTTTCAGGGACTTCAGGCCTTT  
GAAGGACAGCAGGTTTCAGTTGCTGAATTTTTCTAGCAGTGAAGTCAAAGTA  
TCATTGACAAACGTCTCAATTTCTGATGAAGGAAGATACTTTTGCCAGCTCTA  
TACCGATCCCCCACAGGAAAGTTACACCACCATCACAGTCCTGGTCCCACCA  
CGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGGAG  
20 ATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGT  
GGTTCAAAGGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGT  
CAGACATGTACACTGTGACCAGTCAGCTGATGCTGAAGGTGCACAAGGAGG  
ACGATGGGGTCCCAGTGATCTGCCAGGTGGAGCACCCCTGCGGTCACTGGAAA  
CCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCTCAAGTGCACATT  
25 CAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGAGT  
TAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAG  
AGTCGATGATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTC

ATCAATAACCTAAACAAAACAGATAATGGTACATACCGCTGTGAAGCTTCAA  
ACATAGTGGGGAAAGCTCACTCGGATTATATGCTGTATGTATACGATCCCCC  
CACAACCTATCCCTCCTCCCACAACAACCACCACCACCACCACCACCACC  
ACCACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGCTCGA  
5 TCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTT  
CGCCATGCTGTGCTTGCTCATCTTCTGGGGCGCTATTTTGCCAGACATAAAG  
GTACATACTTCACTCATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAG  
ACACAGCTATAATCAATGCAGAAGGAGGACAGAACAACCTCCGAAGAAAAGA  
AAGAGTACTTCATCTAG (SEQ ID NO:137). Also preferred are the polypeptides  
10 encoded by these polynucleotides.

Figures 28A-B shows the nucleotide (SEQ ID NO:21) and deduced amino acid  
sequence (SEQ ID NO:39) of the present invention. Predicted amino acids from about 1  
to about 44 constitute the predicted signal peptide (amino acid residues from about 1 to  
about 44 in SEQ ID NO:39) and are represented by the underlined amino acid regions.

15 Figure 29 shows the regions of similarity between the amino acid sequences of  
the present invention SEQ ID NO:39, the human poliovirus receptor protein (gi|1524088)  
(SEQ ID NO: 138), the human class-I MHC-restricted T cell associated molecule  
(WO9634102) (SEQ ID NO:144), and the Gallus gallus thymocyte activation and  
developmental protein (gb|AAB88491.1) (SEQ ID NO:145).

20 Figure 30 shows an analysis of the amino acid sequence of SEQ ID NO:39.  
Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic  
regions; flexible regions; antigenic index and surface probability are shown.

The present invention provides isolated nucleic acid molecules comprising a  
polynucleotide encoding the polypeptide having the amino acid sequence shown in  
25 Figures 28A-B (SEQ ID NO:39), which was determined by sequencing a cloned cDNA.  
The nucleotide sequence shown in Figures 28A-B (SEQ ID NO:21) was obtained by  
sequencing a cloned cDNA (HOUDJ81), which was deposited on Nov. 17, 1998 at the

American Type Culture Collection, and given Accession Number 203484. The deposited gene is inserted in the pSport plasmid (Life Technologies, Rockville, MD) using the SalI/NotI restriction endonuclease cleavage sites.

The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated DNA molecule having the nucleotide sequence of the deposited cDNA or the nucleotide sequence shown in SEQ ID NO:21 is intended DNA fragments at least about 15nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length which are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-1500 nt in length are also useful according to the present invention, as are fragments corresponding to most, if not all, of the nucleotide sequence of the deposited cDNA or as shown in SEQ ID NO:21. By a fragment at least 20 nt in length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of the deposited cDNA or the nucleotide sequence as shown in SEQ ID NO:21. In this context "about" includes the particularly recited size, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Representative examples of polynucleotide fragments of the invention include, for example, fragments that comprise, or alternatively, consist of, a sequence from about nucleotide 1 to about 50, from about 51 to about 100, from about 101 to about 150, from about 151 to about 200, from about 201 to about 250, from about 251 to about 300, from about 301 to about 350, from about 351 to about 400, from about 401 to about 450, from about 451 to about 500, and from about 501 to about 550, and from about 551 to about 600, from about 601 to about 650, from about 651 to about 700, from about 701 to about 750, from about 751 to about 800, from about 801 to about 850, from about 851 to about 900, from about 901 to about 950, from about 951 to about 1000, from about 1001 to about 1050, from about 1051 to about 1100, from about 1101 to about 1150, from about 1151 to about 1200, from about 1201 to about 1250, from about 1251 to about 1300,

from about 1301 to about 1350, from about 1351 to about 1400, from about 1401 to about 1450, from about 1451 to about 1500, from about 1501 to about 1520 of SEQ ID NO:21, or the complementary strand thereto, or the cDNA contained in the deposited gene. In this context "about" includes the particularly recited ranges, larger or smaller by  
5 several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. In additional embodiments, the polynucleotides of the invention encode functional attributes of the corresponding protein.

Preferred embodiments of the invention in this regard include fragments that comprise alpha-helix and alpha-helix forming regions ("alpha-regions"), beta-sheet and  
10 beta-sheet forming regions ("beta-regions"), turn and turn-forming regions ("turn-regions"), coil and coil-forming regions ("coil-regions"), hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions and high antigenic index regions. The data representing the structural or functional attributes of the protein set forth in Figure 30 and/or Table X,  
15 as described above, was generated using the various modules and algorithms of the DNA\*STAR set on default parameters. In a preferred embodiment, the data presented in columns VIII, IX, XIII, and XIV of Table X can be used to determine regions of the protein which exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or  
20 XIV by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Certain preferred regions in these regards are set out in Figure 30, but may, as shown in Table X, be represented or identified by using tabular representations of the  
25 data presented in Figure 30. The DNA\*STAR computer algorithm used to generate Figure 30 (set on the original default parameters) was used to present the data in Figure 30 in a tabular format (See Table X). The tabular format of the data in Figure 30 is used



to easily determine specific boundaries of a preferred region. The above-mentioned preferred regions set out in Figure 30 and in Table X include, but are not limited to, regions of the aforementioned types identified by analysis of the amino acid sequence set out in Figures 28A-B. As set out in Figure 30 and in Table X, such preferred regions

5 include Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and Hopp-Woods hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schulz flexible regions, Jameson-Wolf regions of high antigenic index and Emini surface-forming regions. Even if deletion of one or more amino acids from the

10 N-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, etc.) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the

15 complete or mature polypeptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic

20 activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence shown in Figures 28A-B, up to the threonine residue at position number 359 and polynucleotides

25 encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues n1-364 of Figures 28A-B, where n1 is an integer from 2 to 359 corresponding to the position of the amino acid residue in Figures

28A-B (which is identical to the sequence shown as SEQ ID NO:39). N-terminal deletions of the polypeptide of the invention shown as SEQ ID NO:39 include polypeptides comprising the amino acid sequence of residues: A-2 to R-364; S-3 to R-364; V-4 to R-364; V-5 to R-364; L-6 to R-364; P-7 to R-364; S-8 to R-364; G-9 to R-364; S-10 to R-364; Q-11 to R-364; C-12 to R-364; A-13 to R-364; A-14 to R-364; A-15 to R-364; A-16 to R-364; A-17 to R-364; A-18 to R-364; A-19 to R-364; A-20 to R-364; P-21 to R-364; P-22 to R-364; G-23 to R-364; L-24 to R-364; R-25 to R-364; L-26 to R-364; R-27 to R-364; L-28 to R-364; L-29 to R-364; L-30 to R-364; L-31 to R-364; L-32 to R-364; F-33 to R-364; S-34 to R-364; A-35 to R-364; A-36 to R-364; A-37 to R-364; L-38 to R-364; I-39 to R-364; P-40 to R-364; T-41 to R-364; G-42 to R-364; D-43 to R-364; G-44 to R-364; Q-45 to R-364; N-46 to R-364; L-47 to R-364; F-48 to R-364; T-49 to R-364; K-50 to R-364; D-51 to R-364; V-52 to R-364; T-53 to R-364; V-54 to R-364; I-55 to R-364; E-56 to R-364; G-57 to R-364; E-58 to R-364; V-59 to R-364; A-60 to R-364; T-61 to R-364; I-62 to R-364; S-63 to R-364; C-64 to R-364; Q-65 to R-364; V-66 to R-364; N-67 to R-364; K-68 to R-364; S-69 to R-364; D-70 to R-364; D-71 to R-364; S-72 to R-364; V-73 to R-364; I-74 to R-364; Q-75 to R-364; L-76 to R-364; L-77 to R-364; N-78 to R-364; P-79 to R-364; N-80 to R-364; R-81 to R-364; Q-82 to R-364; T-83 to R-364; I-84 to R-364; Y-85 to R-364; F-86 to R-364; R-87 to R-364; D-88 to R-364; F-89 to R-364; R-90 to R-364; P-91 to R-364; L-92 to R-364; K-93 to R-364; D-94 to R-364; S-95 to R-364; R-96 to R-364; F-97 to R-364; Q-98 to R-364; L-99 to R-364; L-100 to R-364; N-101 to R-364; F-102 to R-364; S-103 to R-364; S-104 to R-364; S-105 to R-364; E-106 to R-364; L-107 to R-364; K-108 to R-364; V-109 to R-364; S-110 to R-364; L-111 to R-364; T-112 to R-364; N-113 to R-364; V-114 to R-364; S-115 to R-364; I-116 to R-364; S-117 to R-364; D-118 to R-364; E-119 to R-364; G-120 to R-364; R-121 to R-364; Y-122 to R-364; F-123 to R-364; C-124 to R-364; Q-125 to R-364; L-126 to R-364; Y-127 to R-364; T-128 to R-364; D-129 to R-364; P-130 to R-364; P-131 to R-364; Q-132 to R-364; E-133 to R-364; S-134 to R-364; Y-135 to R-364; T-136 to R-364;

T-137 to R-364; I-138 to R-364; T-139 to R-364; V-140 to R-364; L-141 to R-364; V-142 to R-364; P-143 to R-364; P-144 to R-364; R-145 to R-364; N-146 to R-364; L-147 to R-364; M-148 to R-364; I-149 to R-364; D-150 to R-364; I-151 to R-364; Q-152 to R-364; K-153 to R-364; D-154 to R-364; T-155 to R-364; A-156 to R-364; V-157 to R-364; E-158 to R-364; G-159 to R-364; E-160 to R-364; E-161 to R-364; I-162 to R-364; E-163 to R-364; V-164 to R-364; N-165 to R-364; C-166 to R-364; T-167 to R-364; A-168 to R-364; M-169 to R-364; A-170 to R-364; S-171 to R-364; K-172 to R-364; P-173 to R-364; A-174 to R-364; T-175 to R-364; T-176 to R-364; I-177 to R-364; R-178 to R-364; W-179 to R-364; F-180 to R-364; K-181 to R-364; G-182 to R-364; N-183 to R-364; T-184 to R-364; E-185 to R-364; L-186 to R-364; K-187 to R-364; G-188 to R-364; K-189 to R-364; S-190 to R-364; E-191 to R-364; V-192 to R-364; E-193 to R-364; E-194 to R-364; W-195 to R-364; S-196 to R-364; D-197 to R-364; M-198 to R-364; Y-199 to R-364; T-200 to R-364; V-201 to R-364; T-202 to R-364; S-203 to R-364; Q-204 to R-364; L-205 to R-364; M-206 to R-364; L-207 to R-364; K-208 to R-364; V-209 to R-364; H-210 to R-364; K-211 to R-364; E-212 to R-364; D-213 to R-364; D-214 to R-364; G-215 to R-364; V-216 to R-364; P-217 to R-364; V-218 to R-364; I-219 to R-364; C-220 to R-364; Q-221 to R-364; V-222 to R-364; E-223 to R-364; H-224 to R-364; P-225 to R-364; A-226 to R-364; V-227 to R-364; T-228 to R-364; G-229 to R-364; N-230 to R-364; L-231 to R-364; Q-232 to R-364; T-233 to R-364; Q-234 to R-364; R-235 to R-364; Y-236 to R-364; L-237 to R-364; E-238 to R-364; V-239 to R-364; Q-240 to R-364; Y-241 to R-364; K-242 to R-364; P-243 to R-364; Q-244 to R-364; V-245 to R-364; H-246 to R-364; I-247 to R-364; Q-248 to R-364; M-249 to R-364; T-250 to R-364; Y-251 to R-364; P-252 to R-364; L-253 to R-364; Q-254 to R-364; G-255 to R-364; L-256 to R-364; T-257 to R-364; R-258 to R-364; E-259 to R-364; G-260 to R-364; D-261 to R-364; A-262 to R-364; L-263 to R-364; E-264 to R-364; L-265 to R-364; T-266 to R-364; C-267 to R-364; E-268 to R-364; A-269 to R-364; I-270 to R-364; G-271 to R-364; K-272 to R-364; P-273 to R-364; Q-274 to R-364; P-275 to R-364; V-276 to R-364;

M-277 to R-364; V-278 to R-364; T-279 to R-364; W-280 to R-364; V-281 to R-364; R-282 to R-364; V-283 to R-364; D-284 to R-364; D-285 to R-364; E-286 to R-364; M-287 to R-364; P-288 to R-364; Q-289 to R-364; H-290 to R-364; A-291 to R-364; V-292 to R-364; L-293 to R-364; S-294 to R-364; G-295 to R-364; P-296 to R-364; N-297 to  
5 R-364; L-298 to R-364; F-299 to R-364; I-300 to R-364; N-301 to R-364; N-302 to R-364; L-303 to R-364; N-304 to R-364; K-305 to R-364; T-306 to R-364; D-307 to R-364; N-308 to R-364; G-309 to R-364; T-310 to R-364; Y-311 to R-364; R-312 to R-364; C-313 to R-364; E-314 to R-364; A-315 to R-364; S-316 to R-364; N-317 to R-364; I-318 to R-364; V-319 to R-364; G-320 to R-364; K-321 to R-364; A-322 to R-364; H-  
10 323 to R-364; S-324 to R-364; D-325 to R-364; Y-326 to R-364; M-327 to R-364; L-328 to R-364; Y-329 to R-364; V-330 to R-364; Y-331 to R-364; D-332 to R-364; P-333 to R-364; P-334 to R-364; T-335 to R-364; T-336 to R-364; I-337 to R-364; P-338 to R-364; P-339 to R-364; P-340 to R-364; T-341 to R-364; T-342 to R-364; T-343 to R-364; T-344 to R-364; T-345 to R-364; T-346 to R-364; T-347 to R-364; T-348 to R-364; T-  
15 349 to R-364; T-350 to R-364; T-351 to R-364; T-352 to R-364; T-353 to R-364; I-354 to R-364; L-355 to R-364; T-356 to R-364; I-357 to R-364; I-358 to R-364; T-359 to R-364; of SEQ ID NO:39. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the  
20 C-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities such as ability to modulate the extracellular matrix, etc.) may still be retained. For example the ability to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues  
25 of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein

and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

5           Accordingly, the present invention further provides polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the polypeptide shown in Figures 28A-B, up to the leucine residue at position number 6, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues 1-m1 of Figures 28A-B,  
10       where m1 is an integer from 6 to 364 corresponding to the position of the amino acid residue in Figures 28A-B. Moreover, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of C-terminal deletions of the polypeptide of the invention shown as SEQ ID NO:39 include polypeptides comprising the amino acid sequence of residues: M-1 to A-363; M-1 to R-  
15       362; M-1 to S-361; M-1 to D-360; M-1 to T-359; M-1 to I-358; M-1 to I-357; M-1 to T-356; M-1 to L-355; M-1 to I-354; M-1 to T-353; M-1 to T-352; M-1 to T-351; M-1 to T-350; M-1 to T-349; M-1 to T-348; M-1 to T-347; M-1 to T-346; M-1 to T-345; M-1 to T-344; M-1 to T-343; M-1 to T-342; M-1 to T-341; M-1 to P-340; M-1 to P-339; M-1 to P-338; M-1 to I-337; M-1 to T-336; M-1 to T-335; M-1 to P-334; M-1 to P-333; M-1 to D-  
20       332; M-1 to Y-331; M-1 to V-330; M-1 to Y-329; M-1 to L-328; M-1 to M-327; M-1 to Y-326; M-1 to D-325; M-1 to S-324; M-1 to H-323; M-1 to A-322; M-1 to K-321; M-1 to G-320; M-1 to V-319; M-1 to I-318; M-1 to N-317; M-1 to S-316; M-1 to A-315; M-1 to E-314; M-1 to C-313; M-1 to R-312; M-1 to Y-311; M-1 to T-310; M-1 to G-309; M-1 to N-308; M-1 to D-307; M-1 to T-306; M-1 to K-305; M-1 to N-304; M-1 to L-303;  
25       M-1 to N-302; M-1 to N-301; M-1 to I-300; M-1 to F-299; M-1 to L-298; M-1 to N-297; M-1 to P-296; M-1 to G-295; M-1 to S-294; M-1 to L-293; M-1 to V-292; M-1 to A-291; M-1 to H-290; M-1 to Q-289; M-1 to P-288; M-1 to M-287; M-1 to E-286; M-1 to D-

285; M-1 to D-284; M-1 to V-283; M-1 to R-282; M-1 to V-281; M-1 to W-280; M-1 to  
T-279; M-1 to V-278; M-1 to M-277; M-1 to V-276; M-1 to P-275; M-1 to Q-274; M-1  
to P-273; M-1 to K-272; M-1 to G-271; M-1 to I-270; M-1 to A-269; M-1 to E-268; M-1  
to C-267; M-1 to T-266; M-1 to L-265; M-1 to E-264; M-1 to L-263; M-1 to A-262; M-1  
5 to D-261; M-1 to G-260; M-1 to E-259; M-1 to R-258; M-1 to T-257; M-1 to L-256; M-  
1 to G-255; M-1 to Q-254; M-1 to L-253; M-1 to P-252; M-1 to Y-251; M-1 to T-250;  
M-1 to M-249; M-1 to Q-248; M-1 to I-247; M-1 to H-246; M-1 to V-245; M-1 to Q-  
244; M-1 to P-243; M-1 to K-242; M-1 to Y-241; M-1 to Q-240; M-1 to V-239; M-1 to  
E-238; M-1 to L-237; M-1 to Y-236; M-1 to R-235; M-1 to Q-234; M-1 to T-233; M-1  
10 to Q-232; M-1 to L-231; M-1 to N-230; M-1 to G-229; M-1 to T-228; M-1 to V-227; M-  
1 to A-226; M-1 to P-225; M-1 to H-224; M-1 to E-223; M-1 to V-222; M-1 to Q-221;  
M-1 to C-220; M-1 to I-219; M-1 to V-218; M-1 to P-217; M-1 to V-216; M-1 to G-215;  
M-1 to D-214; M-1 to D-213; M-1 to E-212; M-1 to K-211; M-1 to H-210; M-1 to V-  
209; M-1 to K-208; M-1 to L-207; M-1 to M-206; M-1 to L-205; M-1 to Q-204; M-1 to  
15 S-203; M-1 to T-202; M-1 to V-201; M-1 to T-200; M-1 to Y-199; M-1 to M-198; M-1  
to D-197; M-1 to S-196; M-1 to W-195; M-1 to E-194; M-1 to E-193; M-1 to V-192; M-  
1 to E-191; M-1 to S-190; M-1 to K-189; M-1 to G-188; M-1 to K-187; M-1 to L-186;  
M-1 to E-185; M-1 to T-184; M-1 to N-183; M-1 to G-182; M-1 to K-181; M-1 to F-  
180; M-1 to W-179; M-1 to R-178; M-1 to I-177; M-1 to T-176; M-1 to T-175; M-1 to  
20 A-174; M-1 to P-173; M-1 to K-172; M-1 to S-171; M-1 to A-170; M-1 to M-169; M-1  
to A-168; M-1 to T-167; M-1 to C-166; M-1 to N-165; M-1 to V-164; M-1 to E-163; M-  
1 to I-162; M-1 to E-161; M-1 to E-160; M-1 to G-159; M-1 to E-158; M-1 to V-157; M-  
1 to A-156; M-1 to T-155; M-1 to D-154; M-1 to K-153; M-1 to Q-152; M-1 to I-151;  
M-1 to D-150; M-1 to I-149; M-1 to M-148; M-1 to L-147; M-1 to N-146; M-1 to R-  
25 145; M-1 to P-144; M-1 to P-143; M-1 to V-142; M-1 to L-141; M-1 to V-140; M-1 to  
T-139; M-1 to I-138; M-1 to T-137; M-1 to T-136; M-1 to Y-135; M-1 to S-134; M-1 to  
E-133; M-1 to Q-132; M-1 to P-131; M-1 to P-130; M-1 to D-129; M-1 to T-128; M-1 to

Y-127; M-1 to L-126; M-1 to Q-125; M-1 to C-124; M-1 to F-123; M-1 to Y-122; M-1 to R-121; M-1 to G-120; M-1 to E-119; M-1 to D-118; M-1 to S-117; M-1 to I-116; M-1 to S-115; M-1 to V-114; M-1 to N-113; M-1 to T-112; M-1 to L-111; M-1 to S-110; M-1 to V-109; M-1 to K-108; M-1 to L-107; M-1 to E-106; M-1 to S-105; M-1 to S-104; M-1 to S-103; M-1 to F-102; M-1 to N-101; M-1 to L-100; M-1 to L-99; M-1 to Q-98; M-1 to F-97; M-1 to R-96; M-1 to S-95; M-1 to D-94; M-1 to K-93; M-1 to L-92; M-1 to P-91; M-1 to R-90; M-1 to F-89; M-1 to D-88; M-1 to R-87; M-1 to F-86; M-1 to Y-85; M-1 to I-84; M-1 to T-83; M-1 to Q-82; M-1 to R-81; M-1 to N-80; M-1 to P-79; M-1 to N-78; M-1 to L-77; M-1 to L-76; M-1 to Q-75; M-1 to I-74; M-1 to V-73; M-1 to S-72; M-1 to D-71; M-1 to D-70; M-1 to S-69; M-1 to K-68; M-1 to N-67; M-1 to V-66; M-1 to Q-65; M-1 to C-64; M-1 to S-63; M-1 to I-62; M-1 to T-61; M-1 to A-60; M-1 to V-59; M-1 to E-58; M-1 to G-57; M-1 to E-56; M-1 to I-55; M-1 to V-54; M-1 to T-53; M-1 to V-52; M-1 to D-51; M-1 to K-50; M-1 to T-49; M-1 to F-48; M-1 to L-47; M-1 to N-46; M-1 to Q-45; M-1 to G-44; M-1 to D-43; M-1 to G-42; M-1 to T-41; M-1 to P-40; M-1 to I-39; M-1 to L-38; M-1 to A-37; M-1 to A-36; M-1 to A-35; M-1 to S-34; M-1 to F-33; M-1 to L-32; M-1 to L-31; M-1 to L-30; M-1 to L-29; M-1 to L-28; M-1 to R-27; M-1 to L-26; M-1 to R-25; M-1 to L-24; M-1 to G-23; M-1 to P-22; M-1 to P-21; M-1 to A-20; M-1 to A-19; M-1 to A-18; M-1 to A-17; M-1 to A-16; M-1 to A-15; M-1 to A-14; M-1 to A-13; M-1 to C-12; M-1 to Q-11; M-1 to S-10; M-1 to G-9; M-1 to S-8; M-1 to P-7; M-1 to L-6; of SEQ ID NO:39. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

In addition, the invention provides nucleic acid molecules having nucleotide sequences related to extensive portions of SEQ ID NO:21 which have been determined from the following related cDNA genes: HSQFJ92R (SEQ ID NO:139), HFLAB18F (SEQ ID NO:140), HAQBH82R (SEQ ID NO:141), HLHTM10R (SEQ ID NO:142), and HLHAL65R (SEQ ID NO:143).

This gene is expressed primarily in immune system related tissues such as ulcerative colitis, rejected kidney tissues, and to a lesser extent in thymus and bone marrow. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune and hematopoietic diseases and/or disorders, particularly ulcerative colitis and rejected organs. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels is routinely detected in certain tissues or cell types (e.g. transplanted kidney, immune, hematopoietic, renal, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Preferred polypeptides of the present invention comprise immunogenic epitopes shown in SEQ ID NO: 39 as residues: Gly-42 to Phe-48, Val-66 to Asp-71, Asn-78 to Thr-83, Asp-88 to Arg-96, Tyr-127 to Tyr-135, Lys-181 to Trp-195, His-210 to Gly-215, Leu-303 to Thr-310, Thr-341 to Thr-350. Polynucleotides encoding said polypeptides are also provided.

The tissue distribution primarily in immune cells and tissues, combined with the homology to the CRTAM, thymocyte activation and developmental protein, the class-I MHC-restricted T cell associated molecule protein, and the polivirus receptor, indicates that the protein products of this gene are useful for the regulation of cellular physiology, development, differentiation or function of various cell types, including haematopoietic cells and particularly T-cell progenitors. Representative uses are described in the



"Immune Activity" and "infectious disease" sections below, in Example 11, 13, 14, 16, 18, 19, 20, and 27, and elsewhere herein. The proteins can be used to develop products for the diagnosis and treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancers, or degenerative conditions.

5 The physiology or development of a cell can be modulated by contacting the cell with an agonist or antagonist (i.e. an anti- CRTAM-like peptide antibody). Further the CRTAM-like polypeptides of the present invention include treatment of ulcerative colitis, organ rejection and other immune system related disorders. Agonists or antagonists may treat or prevent such disorders as ulcerative colitis and rejected organs, such as kidney. Based  
10 upon the tissue distribution of this protein, antagonists directed against this protein is useful in blocking the activity of this protein. Accordingly, preferred are antibodies which specifically bind a portion of the translation product of this gene.

Also provided is a kit for detecting tumors in which expression of this protein occurs. Such a kit comprises in one embodiment an antibody specific for the translation  
15 product of this gene bound to a solid support. Also provided is a method of detecting these tumors in an individual which comprises a step of contacting an antibody specific for the translation product of this gene to a bodily fluid from the individual, preferably serum, and ascertaining whether antibody binds to an antigen found in the bodily fluid. Preferably the antibody is bound to a solid support and the bodily fluid is serum. The  
20 above embodiments, as well as other treatments and diagnostic tests (kits and methods), are more particularly described elsewhere herein. Furthermore, the protein may also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions, in addition to its use as a nutritional supplement. Protein, as well as, antibodies directed  
25 against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:21 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of  $a-b$ , where  $a$  is any integer between 1 to 1506 of SEQ ID NO:21,  $b$  is an integer of 15 to 1520, where both  $a$  and  $b$  correspond to the positions of nucleotide residues shown in SEQ ID NO:21, and where  $b$  is greater than or equal to  $a + 14$ .

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 12

Figure 31 shows the nucleotide (SEQ ID NO:22) and deduced amino acid sequence (SEQ ID NO:40) of the present invention. Predicted amino acids from about 1 to about 23 constitute the predicted signal peptide (amino acid residues from about 1 to about 23 in SEQ ID NO:40) and are represented by the underlined amino acid regions.

Figure 32 shows the regions of similarity between the amino acid sequences of the present invention SEQ ID NO:40 and the human FAP protein (gi|1890647) (SEQ ID NO:146).

Figure 33 shows an analysis of the amino acid sequence of SEQ ID NO:40.

Alpha, beta, turn and coil regions; hydrophilicity and hydrophobicity; amphipathic regions; flexible regions; antigenic index and surface probability are shown.

The present invention provides isolated nucleic acid molecules comprising a polynucleotide encoding the polypeptide having the amino acid sequence shown in Figure 31 (SEQ ID NO:40), which was determined by sequencing a cloned cDNA. The

nucleotide sequence shown in Figure 31 (SEQ ID NO:22) was obtained by sequencing a cloned cDNA (HPWCM76), which was deposited on Nov. 17, 1998 at the American Type Culture Collection, and given Accession Number 203484. The deposited gene is inserted in the pSport plasmid (Life Technologies, Rockville, MD) using the Sall/NotI  
5 restriction endonuclease cleavage sites.

The present invention is further directed to fragments of the isolated nucleic acid molecules described herein. By a fragment of an isolated DNA molecule having the nucleotide sequence of the deposited cDNA or the nucleotide sequence shown in SEQ ID NO:22 is intended DNA fragments at least about 15nt, and more preferably at least about  
10 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length which are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments 50-1500 nt in length are also useful according to the present invention, as are fragments corresponding to most, if not all, of the nucleotide sequence of the deposited cDNA or as shown in SEQ ID NO:22. By a fragment at least 20 nt in  
15 length, for example, is intended fragments which include 20 or more contiguous bases from the nucleotide sequence of the deposited cDNA or the nucleotide sequence as shown in SEQ ID NO:22. In this context "about" includes the particularly recited size, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Representative examples of polynucleotide fragments of the invention include,  
20 for example, fragments that comprise, or alternatively, consist of, a sequence from about nucleotide 1 to about 50, from about 51 to about 100, from about 101 to about 150, from about 151 to about 200, from about 201 to about 250, from about 251 to about 300, from about 301 to about 350, from about 351 to about 400, from about 401 to about 450, from about 451 to about 500, and from about 501 to about 550, and from about 551 to about  
25 600, from about 601 to about 650, from about 651 to about 700, from about 701 to about 750, from about 751 to about 800, from about 801 to about 807 of SEQ ID NO:22, or the

complementary strand thereto, or the cDNA contained in the deposited gene. In this context "about" includes the particularly recited ranges, larger or smaller

by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. In additional embodiments, the polynucleotides of the invention encode functional

5 attributes of the corresponding protein.

Preferred embodiments of the invention in this regard include fragments that comprise alpha-helix and alpha-helix forming regions ("alpha-regions"), beta-sheet and beta-sheet forming regions ("beta-regions"), turn and turn-forming regions ("turn-regions"), coil and coil-forming regions ("coil-regions"), hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions and high antigenic index regions. The data representing the structural or functional attributes of the protein set forth in Figure 33 and/or Table XI, as described above, was generated using the various modules and algorithms of the DNA\*STAR set on default parameters. In a preferred embodiment, the data presented in columns VIII, IX, XIII, and XIV of Table XI can be used to determine regions of the protein which exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from the data presented in columns VIII, IX, XIII, and/or XIV by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Certain preferred regions in these regards are set out in Figure 33, but may, as shown in Table XI, be represented or identified by using tabular representations of the data presented in Figure 33. The DNA\*STAR computer algorithm used to generate Figure 33 (set on the original default parameters) was used to present the data in Figure 33 in a tabular format (See Table XI). The tabular format of the data in Figure 33 is used to easily determine specific boundaries of a preferred region. The above-mentioned preferred regions set out in Figure 33 and in Table XI include, but are not limited to,

regions of the aforementioned types identified by analysis of the amino acid sequence set out in Figure 31. As set out in Figure 33 and in Table XI, such preferred regions include Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and Hopp-Woods hydrophobic regions, Eisenberg alpha- and beta-amphipathic regions, Karplus-Schulz flexible regions, Jameson-Wolf regions of high antigenic index and Emini surface-forming regions. Even if deletion of one or more amino acids from the N-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, etc.) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence shown in Figure 31, up to the arginine residue at position number 61 and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues n1-66 of Figure 31, where n1 is an integer from 2 to 61 corresponding to the position of the amino acid residue in Figure 31 (which is identical to the sequence shown as SEQ ID NO:40). N-terminal deletions of the polypeptide of the invention shown as SEQ ID NO:40 include polypeptides comprising

the amino acid sequence of residues: S-2 to N-66; S-3 to N-66; S-4 to N-66; S-5 to N-66; L-6 to N-66; K-7 to N-66; H-8 to N-66; L-9 to N-66; L-10 to N-66; C-11 to N-66; M-12 to N-66; A-13 to N-66; L-14 to N-66; S-15 to N-66; W-16 to N-66; F-17 to N-66; S-18 to N-66; S-19 to N-66; F-20 to N-66; I-21 to N-66; S-22 to N-66; G-23 to N-66; E-24 to N-66; T-25 to N-66; S-26 to N-66; F-27 to N-66; S-28 to N-66; L-29 to N-66; L-30 to N-66; N-31 to N-66; S-32 to N-66; F-33 to N-66; F-34 to N-66; L-35 to N-66; P-36 to N-66; Y-37 to N-66; P-38 to N-66; S-39 to N-66; S-40 to N-66; R-41 to N-66; C-42 to N-66; C-43 to N-66; C-44 to N-66; F-45 to N-66; S-46 to N-66; V-47 to N-66; Q-48 to N-66; C-49 to N-66; S-50 to N-66; I-51 to N-66; L-52 to N-66; D-53 to N-66; P-54 to N-66; F-55 to N-66; S-56 to N-66; C-57 to N-66; N-58 to N-66; S-59 to N-66; M-60 to N-66; R-61 to N-66; of SEQ ID NO:40. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities such as ability to modulate the extracellular matrix, etc.) may still be retained. For example the ability to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues deleted from the carboxy terminus of the amino acid sequence of the

polypeptide shown in Figure 31, up to the leucine residue at position number 6, and polynucleotides encoding such polypeptides. In particular, the present invention provides polypeptides comprising the amino acid sequence of residues 1-m1 of Figure 31, where m1 is an integer from 6 to 66 corresponding to the position of the amino acid residue in

5 Figure 31. Moreover, the invention provides polynucleotides encoding polypeptides comprising, or alternatively consisting of, the amino acid sequence of C-terminal deletions of the polypeptide of the invention shown as SEQ ID NO:40 include polypeptides comprising the amino acid sequence of residues: M-1 to E-65; M-1 to W-64; M-1 to P-63; M-1 to F-62; M-1 to R-61; M-1 to M-60; M-1 to S-59; M-1 to N-58;

10 M-1 to C-57; M-1 to S-56; M-1 to F-55; M-1 to P-54; M-1 to D-53; M-1 to L-52; M-1 to I-51; M-1 to S-50; M-1 to C-49; M-1 to Q-48; M-1 to V-47; M-1 to S-46; M-1 to F-45; M-1 to C-44; M-1 to C-43; M-1 to C-42; M-1 to R-41; M-1 to S-40; M-1 to S-39; M-1 to P-38; M-1 to Y-37; M-1 to P-36; M-1 to L-35; M-1 to F-34; M-1 to F-33; M-1 to S-32; M-1 to N-31; M-1 to L-30; M-1 to L-29; M-1 to S-28; M-1 to F-27; M-1 to S-26; M-1 to

15 T-25; M-1 to E-24; M-1 to G-23; M-1 to S-22; M-1 to I-21; M-1 to F-20; M-1 to S-19; M-1 to S-18; M-1 to F-17; M-1 to W-16; M-1 to S-15; M-1 to L-14; M-1 to A-13; M-1 to M-12; M-1 to C-11; M-1 to L-10; M-1 to L-9; M-1 to H-8; M-1 to K-7; M-1 to L-6; of SEQ ID NO:40. Polypeptides encoded by these polynucleotides are also encompassed by the invention.

20 In addition, the invention provides nucleic acid molecules having nucleotide sequences related to extensive portions of SEQ ID NO:22 which have been determined from the following related cDNA genes: HPWCM76R (SEQ ID NO:147).

This gene is expressed primarily in prostate BPH (benign prostatic hyperplasia) tissue. Therefore, polynucleotides and polypeptides of the invention are useful as

25 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, inflammation of the prostate, or related tissues. Similarly, polypeptides and

antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate, expression of this gene at significantly higher or lower levels is routinely detected in certain tissues or cell types (e.g. prostate, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10           The tissue distribution in prostate BPH tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of inflammatory conditions which result in an enlargement of the prostate, or related tissues. Polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of conditions concerning proper testicular function (e.g. endocrine function, sperm maturation), as well as cancer. Therefore, this gene product is useful in 15 the treatment of male infertility and/or impotence. This gene product is also useful in assays designed to identify binding agents, as such agents (antagonists) are useful as male contraceptive agents. Similarly, the protein is believed to be useful in the treatment and/or diagnosis of testicular cancer. The testes are also a site of active gene expression 20 of transcripts that is expressed, particularly at low levels, in other tissues of the body. Therefore, this gene product is expressed in other specific tissues or organs where it may play related functional roles in other processes, such as hematopoiesis, inflammation, bone formation, and kidney function, to name a few possible target indications. Based upon the tissue distribution of this protein, antagonists directed against this protein is 25 useful in blocking the activity of this protein. Accordingly, preferred are antibodies which specifically bind a portion of the translation product of this gene.



Also provided is a kit for detecting tumors in which expression of this protein occurs. Such a kit comprises in one embodiment an antibody specific for the translation product of this gene bound to a solid support. Also provided is a method of detecting these tumors in an individual which comprises a step of contacting an antibody specific  
5 for the translation product of this gene to a bodily fluid from the individual, preferably serum, and ascertaining whether antibody binds to an antigen found in the bodily fluid. Preferably the antibody is bound to a solid support and the bodily fluid is serum. The above embodiments, as well as other treatments and diagnostic tests (kits and methods), are more particularly described elsewhere herein. The homology to the FAP protein  
10 indicates that the protein product of this gene is useful in treating, detecting, and/or preventing iron metabolism disorders, particularly those resulting in high oxidative states, tissue damage, atherosclerosis, free radical damage, vascular disorders, iron binding protein dysfunction, nitric oxide synthase dysfunction or aberration, vasodilation disorders, and tissue edema. Based on the sequence similarity, the translation product of  
15 this gene is expected to share at least some biological activities with iron metabolism modulatory proteins. Such activities are known in the art, some of which are described elsewhere herein. Furthermore, the protein may also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions, in addition to its use as a nutritional  
20 supplement. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:22 and may have been publicly available prior to conception of the present  
25 invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more

polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 793 of SEQ ID NO:22, b is an integer of 15 to 807, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:22, and where b is greater than or equal to a + 14.

Table I

	Res Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
5	Met 1	.	.	B	.	.	.	.	-0.10	0.44	.	.	.	-0.40 0.48	
	Val 2	.	.	B	.	.	.	.	0.08	0.01	.	.	.	0.15 0.63	
	Ala 3	.	.	B	.	.	.	.	0.47	0.01	.	.	.	0.40 0.76	
	Gln 4	.	.	B	.	.	.	.	0.51	-0.01	.	.	.	1.40 1.33	
	Asp 5	.	.	.	.	.	T	C	0.23	-0.20	.	.	F	2.20 1.77	
10	Pro 6	.	.	.	.	T	T	.	0.02	-0.27	*	*	F	2.50 0.94	
	Gln 7	.	.	.	.	T	T	.	0.88	-0.09	*	*	F	2.25 0.45	
	Gly 8	.	.	.	.	T	T	.	0.66	-0.09	.	*	F	2.00 0.47	
	Cys 9	.	A	B	.	.	.	.	-0.01	0.60	.	*	.	-0.10 0.25	
	Leu 10	.	A	B	.	.	.	.	-0.82	0.74	.	*	.	-0.35 0.08	
15	Gln 11	.	A	B	.	.	.	.	-0.91	1.03	.	*	.	-0.60 0.06	
	Leu 12	.	A	B	.	.	.	.	-0.91	0.99	.	*	.	-0.60 0.16	
	Cys 13	.	A	B	.	.	.	.	-1.42	0.41	.	*	.	-0.60 0.34	
	Leu 14	.	A	B	.	.	.	.	-1.34	0.37	*	.	.	-0.30 0.14	
	Ser 15	.	A	B	.	.	.	.	-0.53	0.47	*	*	.	-0.60 0.18	
20	Glu 16	.	A	B	.	.	.	.	-0.88	0.19	*	.	.	-0.30 0.53	
	Val 17	.	.	B	.	.	T	.	-0.88	0.04	*	*	.	0.10 0.63	
	Ala 18	A	.	.	.	.	T	.	-0.10	0.04	*	.	.	0.10 0.39	
	Asn 19	.	.	.	.	T	T	.	0.71	-0.34	*	.	.	1.31 0.44	
	Gly 20	.	.	.	.	T	T	.	0.80	0.06	*	*	F	1.07 0.96	
25	Leu 21	.	.	.	.	.	.	C	-0.06	-0.16	*	*	F	1.63 1.47	
	Arg 22	.	.	.	.	.	.	C	0.50	-0.01	*	*	F	1.69 0.68	
	Asn 23	.	.	.	.	.	T	C	0.49	-0.03	*	.	F	2.10 0.92	
	Pro 24	.	.	B	.	.	T	.	-0.37	0.16	*	.	F	1.24 1.10	
	Val 25	.	.	B	.	.	T	.	-0.06	0.11	*	*	.	0.73 0.42	
30	Ser 26	.	.	B	.	.	T	.	0.17	0.61	*	*	.	0.22 0.35	
	Met 27	.	.	B	B	.	.	.	-0.29	0.71	*	.	.	-0.39 0.23	
	Val 28	.	.	B	B	.	.	.	-0.29	0.71	.	.	.	-0.60 0.31	
	His 29	.	.	B	B	.	.	.	-0.42	0.07	.	.	.	0.00 0.38	
	Ala 30	A	.	B	.	.	.	.	0.12	0.11	.	.	.	0.50 0.38	
35	Gly 31	.	.	.	.	T	T	.	0.39	-0.01	*	.	F	2.15 0.74	
	Asp 32	.	.	.	.	T	T	.	1.10	-0.16	*	*	F	2.45 0.74	
	Gly 33	.	.	.	.	.	T	C	1.26	-0.66	*	*	F	3.00 1.44	
	Thr 34	.	.	.	.	.	T	C	0.59	-0.37	*	*	F	2.40 1.26	
	His 35	.	.	B	B	.	.	.	0.32	-0.01	*	*	.	1.20 0.65	
40	Arg 36	.	.	B	B	.	.	.	0.08	0.63	.	*	.	0.00 0.49	
	Phe 37	.	.	B	B	.	.	.	0.08	0.70	.	*	.	-0.30 0.34	
	Phe 38	.	.	B	B	.	.	.	0.42	0.21	.	*	.	-0.30 0.44	

	Val	39	A	.	.	B	.	.	.	-0.12	0.11	.	*	.	-0.30	0.39
	Ala	40	A	.	.	B	.	.	.	-0.43	0.76	.	*	.	-0.60	0.33
	Glu	41	A	.	.	B	.	.	.	-1.40	0.40	.	*	.	-0.60	0.38
	Gln	42	A	.	.	B	.	.	.	-1.56	0.26	.	.	.	-0.30	0.38
5	Val	43	A	.	.	B	.	.	.	-1.14	0.26	.	.	.	-0.30	0.28
	Gly	44	.	.	B	B	.	.	.	-1.14	0.67	.	.	.	-0.60	0.17
	Val	45	.	.	B	B	.	.	.	-0.80	1.31	.	.	.	-0.60	0.07
	Val	46	.	.	B	B	.	.	.	-1.61	1.67	.	.	.	-0.60	0.15
	Trp	47	.	.	B	B	.	.	.	-1.82	1.71	.	.	.	-0.60	0.13
10	Val	48	.	.	B	B	.	.	.	-0.97	1.71	.	.	.	-0.60	0.27
	Tyr	49	.	.	B	.	.	.	.	-0.97	1.07	.	.	.	-0.16	0.60
	Leu	50	.	.	B	.	.	T	.	-0.41	0.86	*	.	.	0.28	0.56
	Pro	51	.	.	.	.	T	T	.	0.56	0.33	*	*	F	1.52	1.01
	Asp	52	.	.	.	.	T	T	.	0.03	-0.31	.	*	F	2.36	1.27
15	Gly	53	.	.	.	.	.	T	C	0.89	-0.39	*	*	F	2.40	1.27
	Ser	54	.	A	.	.	.	.	C	1.13	-1.07	*	.	F	2.06	1.42
	Arg	55	.	A	B	.	.	.	.	1.73	-1.10	*	*	F	1.62	1.47
	Leu	56	.	A	B	.	.	.	.	1.24	-0.67	*	.	F	1.38	2.30
	Glu	57	.	A	B	.	.	.	.	0.43	-0.31	*	.	F	0.84	1.49
20	Gln	58	.	A	B	.	.	.	.	0.78	-0.01	*	*	F	0.45	0.63
	Pro	59	A	A	.	.	.	.	.	0.27	-0.01	*	*	F	0.60	1.27
	Phe	60	A	A	.	.	.	.	.	0.20	-0.01	*	*	.	0.30	0.60
	Leu	61	A	A	.	.	.	.	.	1.01	-0.01	*	.	.	0.30	0.70
	Asp	62	A	A	.	.	.	.	.	0.12	-0.01	*	.	.	0.30	0.73
25	Leu	63	A	.	.	B	.	.	.	-0.73	0.24	*	.	.	-0.30	0.59
	Lys	64	A	.	.	B	.	.	.	-1.33	0.10	.	.	.	-0.30	0.53
	Asn	65	.	.	B	B	.	.	.	-0.94	0.10	.	.	.	-0.30	0.26
	Ile	66	.	.	B	B	.	.	.	-0.44	0.59	.	*	.	-0.60	0.46
	Val	67	.	.	B	B	.	.	.	-0.66	0.39	.	.	.	-0.30	0.33
30	Leu	68	.	.	B	B	.	.	.	-0.13	0.81	*	.	.	-0.60	0.32
	Thr	69	.	.	B	B	.	.	.	-1.07	1.33	.	.	F	-0.45	0.48
	Thr	70	.	.	B	B	.	.	.	-1.41	1.33	.	.	F	-0.45	0.45
	Pro	71	.	.	B	B	.	.	.	-0.52	1.11	.	.	F	-0.45	0.54
	Trp	72	.	.	.	B	T	.	.	0.33	0.43	.	.	.	-0.20	0.62
35	Ile	73	.	.	B	B	.	.	.	1.26	-0.06	.	*	.	0.61	0.75
	Gly	74	.	.	B	B	.	.	.	1.22	-0.54	.	.	F	1.37	0.95
	Asp	75	.	.	.	.	.	T	C	0.83	-0.54	.	.	F	2.28	0.89
	Glu	76	.	.	B	.	.	T	.	0.23	-0.67	.	.	F	2.54	1.10
	Arg	77	.	.	.	.	T	T	.	0.18	-0.67	.	*	F	3.10	0.92
40	Gly	78	.	.	.	.	T	T	.	0.26	-0.67	.	.	F	2.79	0.54
	Phe	79	A	.	.	.	.	.	.	0.01	0.01	.	*	.	0.83	0.26

	Leu	80	A	.	.	.	.	.	-0.69	0.51	.	*	.	0.22	0.13
	Gly	81	A	.	.	.	.	.	-0.72	1.30	.	*	.	-0.09	0.12
	Leu	82	A	.	.	.	.	.	-1.04	1.37	*	*	.	-0.40	0.18
	Ala	83	A	.	.	.	.	.	-0.66	1.01	.	*	.	-0.40	0.34
5	Phe	84	A	.	.	.	.	.	-0.66	0.33	.	*	.	-0.10	0.70
	His	85	A	.	.	.	.	T	0.27	0.69	*	*	.	-0.20	0.73
	Pro	86	A	.	.	.	.	T	0.58	0.00	.	*	.	0.25	1.42
	Lys	87	A	.	.	.	.	T	1.39	0.00	.	*	.	0.56	2.23
	Phe	88	A	.	.	.	.	T	2.09	-0.39	*	*	.	1.47	2.63
10	Arg	89	A	.	.	.	.	.	2.83	-0.89	*	*	.	1.88	3.33
	His	90	A	.	.	.	T	T	2.17	-1.31	*	*	.	2.79	3.33
	Asn	91	.	.	.	.	T	T	2.13	-0.53	.	*	.	3.10	3.33
	Arg	92	.	.	.	.	T	T	1.20	-0.56	.	*	.	2.79	2.67
	Lys	93	.	.	.	.	T	T	1.66	0.13	*	*	.	1.58	1.37
15	Phe	94	.	.	.	B	T	.	1.30	0.39	*	*	.	0.87	1.34
	Tyr	95	.	.	B	B	.	.	1.03	0.74	.	.	.	-0.14	1.07
	Ile	96	.	.	B	B	.	.	0.37	1.13	*	.	.	-0.60	0.72
	Tyr	97	.	.	B	.	.	T	-0.56	1.70	*	.	.	-0.20	0.44
	Tyr	98	.	.	B	.	.	T	-0.60	1.60	.	*	.	-0.20	0.23
20	Ser	99	.	.	B	.	.	T	0.14	0.84	.	.	.	-0.20	0.56
	Cys	100	A	.	.	.	.	T	0.43	0.16	.	.	.	0.10	0.71
	Leu	101	A	A	.	.	.	.	1.37	-0.60	.	.	.	0.60	0.91
	Asp	102	A	A	.	.	.	.	0.76	-1.36	.	.	F	0.90	1.35
	Lys	103	A	A	.	.	.	.	1.00	-1.10	.	.	F	0.90	1.87
25	Lys	104	A	A	.	.	.	.	1.34	-1.67	.	.	F	0.90	3.94
	Lys	105	A	A	.	.	.	.	1.12	-2.36	*	*	F	0.90	4.71
	Val	106	A	A	.	.	.	.	2.04	-1.67	.	*	F	0.90	1.65
	Glu	107	A	A	.	.	.	.	1.16	-1.67	.	*	F	0.90	1.62
	Lys	108	A	A	.	.	.	.	0.81	-0.99	.	*	F	0.75	0.57
30	Ile	109	A	A	.	.	.	.	0.77	-0.60	.	*	F	0.90	1.02
	Arg	110	A	A	.	.	.	.	0.12	-1.24	.	.	.	0.75	1.02
	Ile	111	A	A	.	.	.	.	1.02	-0.63	.	*	.	0.60	0.51
	Ser	112	A	A	.	.	.	.	0.17	-0.63	.	*	F	0.90	1.45
	Glu	113	A	A	.	.	.	.	-0.18	-0.67	*	*	F	0.75	0.55
35	Met	114	A	A	.	.	.	.	0.82	-0.29	*	*	F	0.60	1.05
	Lys	115	A	A	.	.	.	.	0.12	-0.97	*	.	F	0.90	1.53
	Val	116	.	A	B	.	.	.	1.01	-0.86	.	.	F	0.75	0.89
	Ser	117	A	A	.	.	.	.	1.10	-0.86	.	*	F	0.90	1.51
	Arg	118	A	A	.	.	.	.	1.10	-1.04	.	.	F	0.90	1.17
40	Ala	119	A	A	.	.	.	.	1.74	-0.64	*	.	F	0.90	2.52
	Asp	120	A	.	.	.	.	T	1.11	-1.29	*	.	F	1.30	3.77

	Pro	121	A	.	.	.	.	T	.	1.97	-1.17	*	.	F	1.30	1.94
	Asn	122	A	.	.	.	.	T	.	1.46	-1.17	.	*	F	1.30	3.21
	Lys	123	A	.	.	.	.	T	.	1.39	-0.99	.	*	F	1.30	1.59
	Ala	124	A	A	.	.	.	.	.	1.68	-0.99	.	*	F	0.90	2.05
5	Asp	125	A	A	.	.	.	.	.	1.68	-1.03	*	.	F	0.90	1.71
	Leu	126	A	A	.	.	.	.	.	2.00	-1.43	*	*	F	0.90	1.48
	Lys	127	A	A	.	.	.	.	.	1.14	-1.43	*	*	F	0.90	2.87
	Ser	128	A	A	.	.	.	.	.	0.21	-1.29	*	*	F	0.90	1.28
	Glu	129	A	A	.	.	.	.	.	-0.01	-0.60	*	*	F	0.90	1.08
10	Arg	130	A	A	.	.	.	.	.	-0.01	-0.60	*	*	F	0.75	0.45
	Val	131	A	A	.	.	.	.	.	-0.09	-0.60	*	*	.	0.60	0.58
	Ile	132	A	A	.	.	.	.	.	-0.13	-0.30	*	*	.	0.30	0.23
	Leu	133	A	A	.	.	.	.	.	0.17	-0.30	*	*	.	0.30	0.21
	Glu	134	A	A	.	.	.	.	.	-0.04	-0.30	*	*	.	0.30	0.48
15	Ile	135	A	A	.	.	.	.	.	-0.74	-0.51	*	*	.	0.75	1.06
	Glu	136	A	A	.	.	.	.	.	-0.19	-0.70	*	*	F	0.90	1.30
	Glu	137	A	A	.	.	.	.	.	0.70	-1.00	*	.	F	0.90	1.01
	Pro	138	A	.	.	.	.	T	.	1.48	-0.60	.	*	F	1.30	2.31
	Ala	139	A	.	.	.	.	T	.	1.48	-0.79	.	.	F	1.58	1.82
20	Ser	140	A	.	.	.	.	T	.	2.02	-0.39	.	.	F	1.56	1.69
	Asn	141	.	.	.	.	.	T	C	1.68	0.04	.	.	F	1.44	1.08
	His	142	.	.	.	.	.	T	C	1.68	0.04	.	.	F	1.72	1.06
	Asn	143	.	.	.	.	T	T	.	1.08	-0.06	.	.	F	2.80	1.37
	Gly	144	.	.	.	.	T	T	.	0.86	0.24	.	.	F	1.77	0.70
25	Gly	145	.	.	.	.	T	T	.	0.46	0.53	.	.	F	1.19	0.43
	Gln	146	.	A	B	B	.	.	.	0.11	0.81	.	.	F	0.11	0.23
	Leu	147	.	A	B	B	.	.	.	-0.67	0.84	.	*	.	-0.32	0.23
	Leu	148	.	A	B	B	.	.	.	-0.67	1.10	.	*	.	-0.60	0.19
	Phe	149	.	A	B	B	.	.	.	-0.67	0.67	.	*	.	-0.60	0.18
30	Gly	150	.	.	B	B	.	.	.	-0.57	0.70	.	*	.	-0.60	0.22
	Leu	151	.	.	B	.	.	T	.	-1.17	0.77	.	*	.	-0.20	0.42
	Asp	152	.	.	.	.	T	T	.	-0.60	0.70	.	*	.	0.20	0.48
	Gly	153	.	.	.	.	T	T	.	-0.68	0.67	.	.	.	0.20	0.76
	Tyr	154	.	.	B	.	.	T	.	-0.68	0.93	.	*	.	-0.20	0.65
35	Met	155	.	.	B	B	.	.	.	-0.64	1.03	.	.	.	-0.60	0.33
	Tyr	156	.	.	B	B	.	.	.	-0.18	1.51	.	*	.	-0.60	0.49
	Ile	157	.	.	B	B	.	.	.	-0.18	1.51	.	.	.	-0.60	0.31
	Phe	158	.	.	B	B	.	.	.	-0.18	0.76	.	.	.	-0.60	0.52
	Thr	159	.	.	B	B	.	.	.	-0.28	0.57	.	.	F	-0.45	0.33
40	Gly	160	.	.	.	.	T	T	.	0.32	0.24	.	.	F	0.88	0.46
	Asp	161	.	.	.	.	T	T	.	-0.02	-0.04	.	.	F	1.71	0.93

	Gly	162	.	.	.	.	.	T	C	0.52	-0.33	.	.	F	1.74	0.65
	Gly	163	.	.	.	.	.	T	C	1.22	-0.39	.	.	F	1.97	0.65
	Gln	164	.	.	.	.	.	.	C	1.32	-0.81	*	.	F	2.30	0.65
	Ala	165	.	.	.	.	.	.	C	0.97	-0.39	*	.	F	1.92	1.01
5	Gly	166	.	.	B	.	.	.	.	0.62	-0.03	.	.	F	1.34	0.89
	Asp	167	.	.	B	.	.	T	.	0.16	-0.03	.	.	F	1.31	0.51
	Pro	168	.	.	B	.	.	T	.	-0.20	0.26	.	.	F	0.48	0.41
	Phe	169	.	.	B	.	.	T	.	-0.54	0.54	*	.	.	-0.20	0.36
	Gly	170	.	.	B	.	.	T	.	0.04	0.54	*	.	.	-0.20	0.21
10	Leu	171	.	.	B	.	.	.	.	-0.20	0.94	.	.	.	-0.40	0.22
	Phe	172	.	.	B	.	.	.	.	-0.20	1.01	.	.	.	-0.40	0.26
	Gly	173	.	.	B	.	.	.	.	0.01	0.63	.	*	.	-0.10	0.46
	Asn	174	.	.	.	.	.	.	C	0.76	0.60	.	*	F	0.55	0.89
	Ala	175	.	.	.	.	.	.	C	0.80	-0.09	.	.	F	1.90	2.05
15	Gln	176	.	.	.	.	.	.	C	1.31	-0.49	.	*	F	2.20	2.78
	Asn	177	.	.	.	.	.	T	C	1.20	-0.53	.	.	F	3.00	2.32
	Lys	178	.	.	.	.	T	T	.	0.73	-0.24	.	*	F	2.60	1.89
	Ser	179	.	.	B	.	.	T	.	0.39	-0.06	.	*	F	1.75	0.90
	Ser	180	.	.	B	.	.	T	.	1.02	-0.03	*	*	F	1.45	0.55
20	Leu	181	.	.	B	.	.	.	.	0.17	-0.43	*	*	F	0.95	0.55
	Leu	182	.	.	B	B	.	.	.	-0.64	0.21	*	.	F	-0.15	0.31
	Gly	183	.	.	B	B	.	.	.	-0.58	0.51	*	*	F	-0.45	0.19
	Lys	184	.	.	B	B	.	.	.	-1.17	0.13	*	*	.	-0.30	0.45
	Val	185	.	.	B	B	.	.	.	-0.87	0.13	*	*	.	-0.30	0.38
25	Leu	186	.	.	B	B	.	.	.	-0.91	-0.56	*	*	.	0.60	0.64
	Arg	187	.	.	B	B	.	.	.	-0.10	-0.34	*	*	.	0.30	0.24
	Ile	188	.	.	B	B	.	.	.	0.36	0.06	*	.	.	-0.30	0.52
	Asp	189	.	.	B	.	.	T	.	-0.28	-0.59	*	*	.	1.15	1.23
	Val	190	.	.	B	.	.	T	.	0.23	-0.77	*	*	.	1.00	0.63
30	Asn	191	.	.	B	.	.	T	.	0.74	-0.34	*	*	F	0.85	0.89
	Arg	192	.	.	B	.	.	T	.	0.60	-0.64	.	*	F	1.49	0.72
	Ala	193	.	.	.	.	T	.	.	1.14	-0.14	*	*	F	1.88	1.32
	Gly	194	.	.	.	.	T	T	.	1.19	-0.36	*	.	F	2.27	0.81
	Ser	195	.	.	.	.	.	T	C	2.16	-0.76	*	.	F	2.71	0.83
35	His	196	.	.	.	.	T	T	.	1.91	-0.76	*	*	F	3.40	1.60
	Gly	197	.	.	.	.	T	T	.	1.91	-0.50	*	*	F	3.06	2.54
	Lys	198	.	.	B	.	.	.	.	1.64	-0.93	.	*	F	2.12	3.71
	Arg	199	.	.	B	B	.	.	.	1.78	-0.67	.	*	F	1.58	2.02
	Tyr	200	.	.	B	B	.	.	.	1.78	-0.74	.	*	.	1.43	3.16
40	Arg	201	.	.	B	B	.	.	.	1.81	-0.79	.	*	.	1.43	2.12
	Val	202	.	.	B	B	.	.	.	2.16	-0.79	.	*	F	1.92	1.81

5	Pro	203	.	.	B	.	.	T	.	1.90	-0.39	.	*	F	2.36	1.85
	Ser	204	.	.	.	.	T	T	.	1.09	-0.71	.	*	F	3.40	1.46
	Asp	205	.	.	.	.	.	T	C	0.48	0.07	.	*	F	1.96	1.71
	Asn	206	.	.	.	.	.	T	C	0.07	0.07	.	*	F	1.47	0.82
	Pro	207	.	.	.	.	.	.	C	0.92	0.03	.	.	F	0.93	0.82
10	Phe	208	.	.	B	.	.	.	.	0.92	-0.36	.	.	F	0.99	0.85
	Val	209	.	.	B	.	.	.	.	0.88	0.07	.	.	F	0.33	0.82
	Ser	210	.	.	B	.	.	.	.	0.29	0.10	.	.	F	0.61	0.52
	Glu	211	.	.	B	.	.	T	.	0.26	0.17	.	.	F	1.09	0.61
	Pro	212	.	.	.	.	T	T	.	0.26	-0.11	.	.	F	2.52	1.12
15	Gly	213	.	.	.	.	T	T	.	0.37	-0.33	.	.	F	2.80	1.29
	Ala	214	.	.	.	.	.	T	C	0.33	-0.21	.	.	.	2.02	0.75
	His	215	.	.	.	.	.	.	C	0.39	0.47	.	.	.	0.64	0.34
	Pro	216	.	.	B	B	.	.	.	-0.20	0.80	.	.	.	-0.04	0.54
	Ala	217	.	.	B	B	.	.	.	-0.23	0.87	.	.	.	-0.32	0.54
20	Ile	218	.	.	B	B	.	.	.	-0.23	1.13	.	.	.	-0.60	0.62
	Tyr	219	.	.	B	.	.	T	.	-0.53	1.06	.	*	.	-0.20	0.40
	Ala	220	.	.	B	.	.	T	.	-0.39	1.31	.	.	.	-0.20	0.28
	Tyr	221	.	.	B	.	.	T	.	-0.18	0.81	*	.	.	-0.20	0.77
	Gly	222	.	.	B	.	.	T	.	-0.19	0.53	*	.	.	-0.20	0.79
25	Ile	223	.	.	B	B	.	.	.	0.41	0.39	*	*	.	-0.30	0.78
	Arg	224	.	.	B	B	.	.	.	0.77	0.80	*	*	.	-0.60	0.52
	Asn	225	.	.	.	B	T	.	.	0.69	0.04	*	*	.	0.25	1.03
	Met	226	.	.	.	B	T	.	.	0.34	0.19	*	*	.	0.10	0.79
	Trp	227	.	.	B	B	.	.	.	-0.17	0.00	*	*	.	0.30	0.41
30	Arg	228	.	.	B	.	.	.	.	0.72	0.64	*	*	.	-0.40	0.19
	Cys	229	.	.	B	.	.	.	.	0.72	0.24	*	*	.	0.24	0.32
	Ala	230	.	.	B	.	.	.	.	0.38	-0.37	*	.	.	1.18	0.59
	Val	231	.	.	B	.	.	.	.	0.98	-0.86	*	.	.	1.82	0.30
	Asp	232	.	.	.	.	T	T	.	1.06	-0.86	*	.	F	2.91	0.93
35	Arg	233	.	.	.	.	T	T	.	0.06	-1.00	*	.	F	3.40	1.42
	Gly	234	.	.	.	.	T	T	.	0.41	-0.81	*	*	F	3.06	1.34
	Asp	235	.	.	.	.	.	T	C	1.11	-0.97	*	.	F	2.52	1.16
	Pro	236	.	.	B	.	.	.	.	1.97	-0.97	*	.	F	1.78	1.16
	Ile	237	.	.	B	.	.	.	.	1.62	-0.57	*	*	F	1.78	2.03
40	Thr	238	.	.	B	.	.	.	.	1.62	-0.57	*	*	F	1.78	1.20
	Arg	239	.	.	B	.	.	.	.	1.62	-0.57	*	*	F	2.12	1.52
	Gln	240	.	.	B	.	.	.	.	1.73	-0.57	*	*	F	2.46	2.15
	Gly	241	.	.	.	.	T	T	.	1.06	-1.26	.	*	F	3.40	2.92
	Arg	242	.	.	.	.	T	T	.	1.24	-1.06	.	*	F	3.06	1.05
	Gly	243	.	.	.	.	T	T	.	0.89	-0.27	.	*	F	2.27	0.52



	Arg	244	.	.	B	.	.	T	.	0.43	-0.10	.	*	F	1.53	0.28
	Ile	245	.	.	B	.	.	.	.	0.43	-0.10	.	*	.	0.84	0.14
	Phe	246	.	.	B	.	.	.	.	-0.08	-0.10	.	*	.	0.50	0.24
	Cys	247	.	.	B	.	.	T	.	-0.53	0.11	.	*	.	0.40	0.09
5	Gly	248	.	.	B	.	.	T	.	-0.19	0.54	.	.	.	0.40	0.13
	Asp	249	.	.	.	.	T	T	.	-0.30	0.26	.	.	F	1.55	0.26
	Val	250	.	.	.	.	.	T	C	0.70	-0.13	.	.	F	2.25	0.77
	Gly	251	.	.	.	.	.	T	C	0.70	-0.70	.	*	F	3.00	1.53
	Gln	252	.	.	.	.	.	T	C	1.37	-0.34	*	.	F	2.25	0.80
10	Asn	253	.	.	.	.	.	T	C	1.71	-0.34	*	.	F	2.10	1.86
	Arg	254	.	.	B	.	.	T	.	0.86	-0.99	*	.	F	1.90	3.25
	Phe	255	A	A	.	.	.	.	.	1.71	-0.77	.	.	F	1.20	1.39
	Glu	256	A	A	.	.	.	.	.	1.24	-1.17	.	*	F	0.90	1.45
	Glu	257	A	A	.	.	.	.	.	0.36	-0.89	.	*	.	0.60	0.61
15	Val	258	A	A	.	B	.	.	.	-0.46	-0.20	*	*	.	0.30	0.49
	Asp	259	A	A	.	B	.	.	.	-0.52	-0.30	.	*	.	0.30	0.23
	Leu	260	A	A	.	B	.	.	.	-0.17	-0.30	*	*	.	0.30	0.27
	Ile	261	A	A	.	B	.	.	.	-0.51	0.13	*	*	.	-0.30	0.36
	Leu	262	A	.	.	.	.	T	.	-0.51	-0.09	*	*	.	0.70	0.21
20	Lys	263	.	.	.	.	T	T	.	0.10	0.31	*	*	F	0.65	0.42
	Gly	264	.	.	.	.	T	T	.	-0.24	0.39	*	.	F	0.65	0.93
	Gly	265	.	.	.	.	T	T	.	0.28	0.13	*	*	F	0.80	1.12
	Asn	266	.	.	.	.	.	T	C	1.28	0.36	*	*	F	0.45	0.59
	Tyr	267	.	.	.	.	.	T	C	1.50	0.36	*	*	.	0.45	1.17
25	Gly	268	.	.	.	.	.	T	C	1.50	0.43	*	*	.	0.15	1.19
	Trp	269	.	.	B	.	.	T	.	1.84	0.00	*	*	.	0.85	1.48
	Arg	270	.	A	B	.	.	.	.	1.84	-0.40	*	*	.	0.45	1.63
	Ala	271	.	A	B	.	.	.	.	1.14	-0.73	*	*	F	0.90	1.63
	Lys	272	A	A	.	.	.	.	.	0.80	-0.37	*	*	F	0.60	1.35
30	Glu	273	A	A	.	.	.	.	.	0.48	-0.79	*	*	F	0.75	0.69
	Gly	274	A	A	.	.	.	.	.	0.52	-0.21	.	*	F	0.45	0.37
	Phe	275	A	A	.	.	.	.	.	0.41	0.04	*	*	.	-0.30	0.29
	Ala	276	A	A	.	.	.	.	.	1.04	0.04	*	.	.	-0.30	0.28
	Cys	277	A	.	.	.	.	T	.	1.04	0.04	*	.	.	0.10	0.56
35	Tyr	278	A	.	.	.	.	T	.	0.23	-0.39	*	.	.	0.85	1.30
	Asp	279	A	.	.	.	.	T	.	-0.09	-0.49	*	.	F	1.00	1.06
	Lys	280	A	.	.	.	.	T	.	0.58	-0.41	*	.	F	1.00	1.06
	Lys	281	A	A	.	.	.	.	.	1.17	-0.49	.	.	F	0.45	0.92
	Leu	282	A	A	.	.	.	.	.	1.24	-0.84	.	.	.	0.60	0.89
40	Cys	283	A	A	.	.	.	.	.	1.19	-0.34	.	*	.	0.30	0.45
	His	284	.	A	B	.	.	.	.	0.38	0.04	.	*	.	-0.30	0.30

	Asn	285	.	.	B	.	.	T	.	0.33	0.73	.	*	.	-0.20	0.30
	Ala	286	A	.	.	.	.	T	.	0.29	0.04	.	*	.	0.10	0.94
	Ser	287	A	.	.	.	.	T	.	0.24	-0.53	.	.	.	1.15	1.15
	Leu	288	A	.	.	.	.	T	.	0.10	-0.39	.	.	F	0.85	0.53
5	Asp	289	.	.	B	B	.	.	.	-0.08	-0.10	.	.	F	0.45	0.43
	Asp	290	.	.	B	B	.	.	.	-0.97	-0.17	.	*	F	0.45	0.50
	Val	291	.	.	B	B	.	.	.	-0.62	0.13	.	.	.	-0.30	0.42
	Leu	292	.	.	B	B	.	.	.	-0.91	0.20	.	.	.	-0.30	0.40
	Pro	293	.	.	B	B	.	.	.	-0.34	0.70	*	.	.	-0.60	0.24
10	Ile	294	.	.	B	B	.	.	.	-0.69	1.46	.	.	.	-0.60	0.51
	Tyr	295	.	.	B	.	.	T	.	-0.72	1.24	.	.	.	-0.20	0.61
	Ala	296	.	.	B	.	.	T	.	-0.46	1.06	.	.	.	-0.20	0.54
	Tyr	297	.	.	B	.	.	T	.	-0.50	1.13	.	*	.	-0.20	0.77
	Gly	298	.	.	B	.	.	T	.	-0.63	1.09	*	.	.	-0.20	0.37
15	His	299	.	.	B	B	.	.	.	0.30	0.76	*	.	.	-0.60	0.36
	Ala	300	.	.	B	B	.	.	.	0.24	0.26	*	.	.	-0.30	0.46
	Val	301	.	.	B	B	.	.	.	-0.02	-0.11	*	.	.	0.30	0.62
	Gly	302	.	.	B	.	.	T	.	-0.09	0.10	*	.	F	0.25	0.34
	Lys	303	.	.	B	.	.	T	.	-0.09	0.09	*	.	F	0.25	0.48
20	Ser	304	.	.	B	.	.	T	.	-0.40	0.01	*	.	F	0.25	0.64
	Val	305	.	.	B	.	.	T	.	-0.06	-0.20	.	.	F	0.85	0.64
	Thr	306	.	.	B	.	.	T	.	-0.06	0.13	.	.	F	0.25	0.50
	Gly	307	.	.	B	.	.	T	.	0.04	0.77	.	.	F	-0.05	0.28
	Gly	308	.	.	B	.	.	T	.	0.11	1.14	.	.	F	-0.05	0.59
25	Tyr	309	.	.	B	.	.	T	.	0.07	0.50	.	.	.	-0.20	0.80
	Val	310	.	.	B	.	.	.	.	0.26	0.44	*	.	.	-0.40	0.80
	Tyr	311	.	.	B	.	.	T	.	0.57	0.59	*	.	.	-0.20	0.43
	Arg	312	.	.	B	.	.	T	.	0.61	0.16	*	.	.	0.10	0.48
	Gly	313	.	.	B	.	.	T	.	0.74	-0.21	*	.	F	1.13	0.87
30	Cys	314	.	.	B	.	.	T	.	0.99	-0.43	*	*	F	1.41	0.85
	Glu	315	.	.	B	.	.	.	.	1.03	-0.79	*	*	F	1.79	0.70
	Ser	316	.	.	.	.	.	T	C	1.28	-0.10	.	*	F	2.17	0.58
	Pro	317	.	.	.	.	T	T	.	0.82	-0.13	.	*	F	2.80	1.75
	Asn	318	.	.	.	.	T	T	.	0.36	-0.27	.	.	F	2.52	1.00
35	Leu	319	.	.	.	.	T	T	.	0.78	0.41	.	.	F	1.19	0.62
	Asn	320	.	.	.	B	T	.	.	-0.11	0.79	.	.	.	0.36	0.63
	Gly	321	.	.	B	B	.	.	.	-0.51	1.04	.	.	.	-0.32	0.27
	Leu	322	.	.	B	B	.	.	.	-0.64	1.43	.	.	.	-0.60	0.29
	Tyr	323	.	.	B	B	.	.	.	-0.64	1.17	.	*	.	-0.60	0.18
40	Ile	324	.	.	B	B	.	.	.	-0.53	0.77	*	.	.	-0.60	0.30
	Phe	325	.	.	B	B	.	.	.	-1.13	1.13	*	.	.	-0.60	0.31

5	Gly	326	.	.	B	B	.	.	.	-1.09	1.06	*	.	.	-0.60	0.20
	Asp	327	.	.	B	.	.	.	.	-0.62	0.69	.	*	.	-0.40	0.38
	Phe	328	.	.	B	.	.	.	.	-0.27	0.43	.	*	.	-0.40	0.43
	Met	329	A	.	.	.	.	T	.	-0.19	-0.36	.	*	.	0.70	0.85
	Ser	330	.	.	.	.	.	T	C	-0.09	-0.10	.	*	F	1.05	0.42
10	Gly	331	A	.	.	.	.	T	.	-0.33	0.51	.	.	F	-0.05	0.48
	Arg	332	A	.	.	.	.	T	.	-1.14	0.23	.	.	.	0.10	0.49
	Leu	333	A	A	.	.	.	.	.	-0.44	0.30	.	.	.	-0.30	0.30
	Met	334	A	A	.	.	.	.	.	0.16	0.31	.	*	.	-0.30	0.53
	Ala	335	A	A	.	.	.	.	.	0.46	-0.11	.	*	.	0.30	0.47
15	Leu	336	A	A	.	.	.	.	.	0.91	-0.11	.	*	.	0.30	0.95
	Gln	337	A	A	.	.	.	.	.	0.84	-0.80	.	.	.	0.75	1.87
	Glu	338	A	A	.	.	.	.	.	1.66	-1.41	.	.	F	0.90	3.71
	Asp	339	A	A	.	.	.	.	.	2.30	-1.51	*	.	F	0.90	7.23
	Arg	340	A	A	.	.	.	.	.	2.93	-2.20	*	.	F	0.90	8.35
20	Lys	341	A	A	.	.	.	.	.	3.46	-2.60	.	*	F	0.90	9.64
	Asn	342	A	.	.	.	.	T	.	3.50	-1.69	*	.	F	1.30	6.07
	Lys	343	A	.	.	.	.	T	.	3.54	-1.69	*	.	F	1.30	6.20
	Lys	344	A	.	.	.	.	T	.	3.54	-1.69	*	.	F	1.30	6.20
	Trp	345	A	.	.	.	.	T	.	3.43	-1.29	*	.	F	1.30	6.68
25	Lys	346	A	A	.	.	.	.	.	2.58	-1.69	.	.	F	0.90	5.58
	Lys	347	A	A	.	.	.	.	.	1.91	-1.00	.	.	F	0.90	2.30
	Gln	348	.	A	B	.	.	.	.	1.06	-0.43	*	.	F	0.60	1.17
	Asp	349	.	A	B	.	.	.	.	0.67	-0.66	.	.	F	0.75	0.48
	Leu	350	.	A	B	.	.	.	.	0.66	-0.23	.	.	F	0.45	0.24
30	Cys	351	.	A	B	.	.	.	.	0.30	0.16	.	.	F	-0.15	0.19
	Leu	352	.	A	B	.	.	.	.	-0.06	0.24	.	.	F	-0.15	0.16
	Gly	353	.	A	.	.	T	.	.	-0.36	0.73	.	.	F	-0.05	0.28
	Ser	354	.	.	.	.	T	T	.	-1.02	0.43	.	.	F	0.35	0.70
	Thr	355	.	.	.	.	T	T	.	-0.80	0.43	.	.	F	0.35	0.45
35	Thr	356	.	.	B	.	.	T	.	-0.83	0.24	.	.	F	0.25	0.46
	Ser	357	.	.	B	.	.	T	.	-0.23	0.60	.	.	F	-0.05	0.30
	Cys	358	.	.	B	.	.	.	.	-0.23	0.64	.	.	.	-0.40	0.32
	Ala	359	.	.	B	.	.	.	.	-0.74	0.59	.	.	.	-0.40	0.22
	Phe	360	.	.	B	.	.	T	.	-1.32	0.79	.	.	.	-0.20	0.14
40	Pro	361	.	.	B	.	.	T	.	-1.31	1.09	.	.	.	-0.20	0.18
	Gly	362	.	.	.	.	T	T	.	-1.32	0.90	.	.	.	0.20	0.24
	Leu	363	.	.	B	.	.	T	.	-0.69	0.89	.	.	.	-0.20	0.39
	Ile	364	.	.	B	.	.	.	.	-0.40	0.60	*	.	.	-0.40	0.35
	Ser	365	A	.	.	.	.	T	.	0.34	0.56	*	*	.	-0.20	0.47
	Thr	366	A	.	.	.	.	T	.	-0.14	0.13	*	.	F	0.40	1.13

	His	367	A	.	.	.	.	T	.	-0.69	0.23	*	*	F	0.40	1.40
	Ser	368	.	.	B	.	.	T	.	-0.77	0.23	*	*	F	0.25	0.73
	Lys	369	.	.	B	B	.	.	.	-0.18	0.53	*	*	.	-0.60	0.36
	Phe	370	.	.	B	B	.	.	.	-0.58	0.43	*	*	.	-0.60	0.35
5	Ile	371	.	.	B	B	.	.	.	-0.86	0.71	*	*	.	-0.60	0.23
	Ile	372	.	.	B	B	.	.	.	-0.82	0.83	*	*	.	-0.60	0.11
	Ser	373	.	A	B	.	.	.	.	-0.52	0.83	*	.	.	-0.60	0.23
	Phe	374	A	A	.	.	.	.	.	-0.57	0.04	*	*	.	-0.30	0.54
	Ala	375	A	A	.	.	.	.	.	-0.46	-0.64	.	.	.	0.75	1.35
10	Glu	376	A	A	.	.	.	.	.	0.09	-0.83	*	.	.	0.75	1.01
	Asp	377	A	A	.	.	.	.	.	0.98	-0.79	*	.	F	0.90	1.16
	Glu	378	A	A	.	.	.	.	.	0.47	-1.57	.	.	F	0.90	1.99
	Ala	379	A	A	.	.	.	.	.	0.92	-1.39	.	.	F	0.75	0.95
	Gly	380	A	A	.	.	.	.	.	0.81	-0.63	.	.	F	0.75	0.89
15	Glu	381	A	A	.	B	.	.	.	0.00	0.16	.	.	.	-0.30	0.44
	Leu	382	A	A	.	B	.	.	.	-0.59	0.84	.	.	.	-0.60	0.36
	Tyr	383	A	A	.	B	.	.	.	-0.90	0.84	.	.	.	-0.60	0.37
	Phe	384	A	A	.	B	.	.	.	-0.61	0.90	.	.	.	-0.60	0.31
	Leu	385	.	A	B	B	.	.	.	-0.51	1.29	.	.	.	-0.60	0.50
20	Ala	386	.	A	B	B	.	.	.	-0.72	1.36	.	.	.	-0.60	0.50
	Thr	387	.	A	B	B	.	.	.	-0.21	1.03	.	.	.	-0.60	0.89
	Ser	388	.	A	.	.	.	.	C	-0.56	0.63	.	.	F	-0.10	1.45
	Tyr	389	.	.	.	.	.	T	C	-0.10	0.44	.	.	F	0.30	1.45
	Pro	390	.	.	.	.	T	T	.	0.12	0.70	.	.	F	0.50	1.58
25	Ser	391	.	.	.	.	T	T	.	0.50	0.71	.	.	.	0.35	1.19
	Ala	392	.	.	B	.	.	T	.	0.92	0.76	.	.	.	0.08	1.17
	Tyr	393	.	.	B	.	.	.	.	0.88	0.00	.	.	.	0.91	1.49
	Ala	394	.	.	B	.	.	T	.	0.82	0.00	.	*	.	1.24	1.10
	Pro	395	.	.	B	.	.	T	.	0.14	0.00	.	*	F	1.52	1.46
30	Arg	396	.	.	.	.	T	T	.	0.20	0.19	.	.	F	1.30	0.65
	Gly	397	.	.	B	.	.	T	.	0.83	0.19	.	.	F	0.92	1.01
	Ser	398	.	.	B	B	.	.	.	0.38	-0.31	.	.	F	0.99	1.31
	Ile	399	.	.	B	B	.	.	.	0.11	0.04	*	.	.	-0.04	0.58
	Tyr	400	.	.	B	B	.	.	.	0.32	0.69	*	*	.	-0.47	0.43
35	Lys	401	.	.	B	B	.	.	.	0.00	0.26	*	*	.	-0.30	0.54
	Phe	402	.	.	B	B	.	.	.	0.04	0.30	*	.	.	0.19	1.19
	Val	403	.	.	B	B	.	.	.	0.46	0.00	*	.	F	1.28	1.02
	Asp	404	.	.	B	.	.	T	.	1.46	-0.76	*	.	F	2.17	1.00
	Pro	405	.	.	B	.	.	T	.	1.11	-0.76	*	.	F	2.66	2.26
40	Ser	406	.	.	.	.	T	T	.	0.86	-1.04	*	.	F	3.40	3.07
	Arg	407	.	.	.	.	T	T	.	1.34	-1.26	*	.	F	3.06	2.85

	Arg	408	.	.	.	.	T	.	.	1.86	-0.83	.	.	F	2.86	2.85
	Ala	409	.	.	.	.	.	.	C	1.90	-0.83	.	.	F	2.66	2.10
	Pro	410	.	.	.	.	.	T	C	1.44	-1.21	*	.	F	2.86	2.15
	Pro	411	.	.	.	.	T	T	.	1.79	-0.64	*	*	F	2.91	0.59
5	Gly	412	.	.	.	.	T	T	.	1.43	-0.64	.	*	F	3.40	1.16
	Lys	413	.	.	.	.	T	T	.	1.37	-0.39	.	*	F	2.76	1.18
	Cys	414	.	.	.	.	T	T	.	1.74	-0.81	.	*	F	2.72	1.52
	Lys	415	.	.	B	.	.	T	.	1.10	-0.81	.	*	F	1.98	2.38
	Tyr	416	.	.	B	.	.	T	.	1.10	-0.60	.	*	F	1.49	0.88
10	Lys	417	.	.	B	.	.	T	.	0.59	-0.17	.	*	F	1.00	2.55
	Pro	418	.	.	B	B	.	.	.	0.66	-0.10	.	*	F	0.45	0.95
	Val	419	.	.	B	B	.	.	.	1.01	-0.10	.	*	F	0.60	1.18
	Pro	420	.	.	B	B	.	.	.	1.01	-0.37	.	*	F	0.79	0.85
	Val	421	.	.	B	B	.	.	.	0.96	-0.37	.	*	F	1.28	1.10
15	Arg	422	.	.	B	B	.	.	.	0.96	-0.41	.	*	F	1.62	1.99
	Thr	423	.	.	B	.	.	T	.	1.28	-1.06	*	*	F	2.66	2.58
	Lys	424	.	.	.	.	T	T	.	1.24	-1.49	*	*	F	3.40	6.80
	Ser	425	.	.	.	.	T	T	.	1.24	-1.44	*	*	F	3.06	2.43
	Lys	426	.	.	.	.	T	T	.	1.40	-1.01	*	*	F	2.72	2.61
20	Arg	427	.	.	B	.	.	.	.	1.40	-0.71	.	*	F	1.78	1.13
	Ile	428	.	.	B	.	.	.	.	1.50	-0.71	*	*	F	1.44	1.65
	Pro	429	.	.	B	.	.	.	.	0.64	-0.67	*	*	.	0.95	1.28
	Phe	430	.	.	B	.	.	.	.	0.36	0.01	*	*	.	-0.10	0.54
	Arg	431	.	A	B	.	.	.	.	0.36	0.51	*	*	.	-0.60	0.77
25	Pro	432	.	A	B	.	.	.	.	-0.07	-0.17	*	*	F	0.60	1.00
	Leu	433	A	A	.	.	.	.	.	-0.03	-0.11	*	*	F	0.60	1.67
	Ala	434	A	A	.	.	.	.	.	-0.63	-0.26	*	*	F	0.45	0.63
	Lys	435	A	A	.	.	.	.	.	0.07	0.43	*	*	F	-0.45	0.34
	Thr	436	A	A	.	.	.	.	.	-0.86	0.00	*	*	.	0.30	0.68
30	Val	437	A	A	.	.	.	.	.	-1.46	0.00	*	.	.	0.30	0.56
	Leu	438	A	A	.	.	.	.	.	-0.60	0.19	*	.	.	-0.30	0.23
	Asp	439	A	A	.	.	.	.	.	-0.01	0.19	*	.	.	-0.30	0.32
	Leu	440	A	A	.	.	.	.	.	-0.06	-0.30	*	.	.	0.30	0.74
	Leu	441	A	A	.	.	.	.	.	-0.04	-0.54	*	.	F	0.90	1.56
35	Lys	442	A	A	.	.	.	.	.	0.81	-0.84	*	.	F	0.90	1.25
	Glu	443	A	A	.	.	.	.	.	1.67	-0.84	*	.	F	0.90	2.63
	Gln	444	A	A	.	.	.	.	.	1.08	-1.53	*	.	F	0.90	6.38
	Ser	445	A	A	.	.	.	.	.	1.30	-1.71	*	.	F	0.90	3.22
	Glu	446	A	A	.	.	.	.	.	2.22	-1.21	*	.	F	0.90	1.88
40	Lys	447	A	A	.	.	.	.	.	2.22	-1.21	*	.	F	0.90	2.13
	Ala	448	A	A	.	.	.	.	.	1.92	-1.61	*	.	F	0.90	3.17

	Ala	449	A	A	.	.	.	.	.	1.62	-1.61	*	.	F	0.90	2.46
	Arg	450	A	A	.	.	.	.	.	1.62	-1.23	*	.	F	0.90	1.65
	Lys	451	A	A	.	.	.	.	.	1.03	-0.84	*	.	F	0.90	2.18
	Ser	452	A	.	.	.	.	T	.	0.68	-0.84	*	.	F	1.30	2.18
5	Ser	453	A	.	.	.	.	T	.	0.46	-0.86	.	.	F	1.30	1.61
	Ser	454	.	.	B	.	.	T	.	0.46	-0.17	.	.	F	0.85	0.66
	Ala	455	.	.	B	.	.	T	.	0.04	0.33	.	.	F	0.25	0.50
	Thr	456	.	.	B	.	.	.	.	-0.34	0.33	.	.	.	-0.10	0.50
	Leu	457	.	.	B	.	.	.	.	-0.26	0.37	.	.	.	-0.10	0.37
10	Ala	458	.	.	B	.	.	T	.	-0.54	0.41	.	.	F	-0.05	0.57
	Ser	459	.	.	B	.	.	T	.	-0.24	0.41	.	.	F	-0.05	0.40
	Gly	460	.	.	.	.	.	T	C	0.00	0.33	.	.	F	0.45	0.83
	Pro	461	.	.	.	.	.	T	C	-0.50	0.07	*	.	F	0.45	0.81
	Ala	462	.	.	.	.	.	.	C	0.01	0.26	*	.	F	0.25	0.50
15	Gln	463	A	.	.	.	.	.	.	0.60	0.26	.	.	F	0.05	0.68
	Gly	464	.	.	B	.	.	.	.	0.94	-0.17	.	.	F	0.65	0.76
	Leu	465	.	.	B	.	.	.	.	0.94	-0.60	.	.	F	1.10	1.50
	Ser	466	A	.	.	.	.	.	.	0.86	-0.67	*	.	F	0.95	0.86
	Glu	467	A	.	.	.	.	.	.	1.14	-0.69	.	*	F	1.10	1.16
20	Lys	468	A	.	.	.	.	.	.	1.19	-0.73	.	.	F	1.10	1.89
	Gly	469	A	.	.	.	T	T	.	1.58	-1.41	.	.	F	1.70	2.82
	Ser	470	A	.	.	.	.	T	.	1.58	-1.80	.	.	F	1.30	3.26
	Ser	471	A	.	.	.	.	T	.	1.29	-1.11	.	.	F	1.30	1.34
	Lys	472	A	.	.	.	.	T	.	0.99	-0.61	.	.	F	1.30	1.37
25	Lys	473	.	.	B	.	.	.	.	0.73	-0.66	.	.	F	1.10	1.37
	Leu	474	.	.	B	.	.	.	.	0.77	-0.61	.	.	F	1.10	1.58
	Ala	475	.	.	B	.	.	.	.	0.77	-0.51	*	.	F	1.40	1.14
	Ser	476	.	.	B	.	.	T	.	0.77	-0.13	.	.	F	1.45	0.77
	Pro	477	.	.	B	.	.	T	.	0.77	0.26	.	.	F	1.30	1.24
30	Thr	478	.	.	.	.	T	T	.	0.72	-0.43	.	.	F	2.60	2.46
	Ser	479	.	.	.	.	.	T	C	1.22	-0.53	.	.	F	3.00	2.95
	Ser	480	.	.	.	.	T	T	.	1.00	-0.43	*	*	F	2.60	2.76
	Lys	481	.	.	B	.	.	T	.	1.41	-0.17	*	*	F	1.90	1.58
	Asn	482	.	.	B	.	.	T	.	1.28	-0.66	*	*	F	1.90	2.30
35	Thr	483	.	.	B	.	.	T	.	1.38	-0.61	*	*	F	1.94	1.70
	Leu	484	.	.	B	.	.	.	.	1.33	-0.57	*	*	F	1.78	1.32
	Arg	485	.	.	B	.	.	.	.	1.32	-0.14	*	*	F	1.67	0.81
	Gly	486	.	.	B	.	.	T	.	1.32	-0.06	.	*	F	2.21	0.81
	Pro	487	.	.	.	.	T	T	.	1.37	-0.54	.	*	F	3.40	1.96
40	Gly	488	.	.	.	.	T	T	.	1.72	-1.23	.	*	F	3.06	2.00
	Thr	489	.	.	.	.	.	T	C	1.94	-1.23	.	*	F	2.52	4.05

5	Lys	490	.	A	B	.	.	.	1.94	-1.16	.	*	F	1.58	2.65	
	Lys	491	.	A	B	.	.	.	1.43	-1.59	*	*	F	1.24	5.24	
	Lys	492	.	A	B	.	.	.	1.30	-1.37	*	*	F	0.90	2.69	
	Ala	493	.	A	B	.	.	.	1.43	-1.43	*	*	F	0.90	1.33	
	Arg	494	.	A	B	.	.	.	1.71	-1.00	*	*	F	0.90	1.03	
	Val	495	.	A	B	.	.	.	0.81	-0.50	*	*	F	0.75	0.70	
	Gly	496	.	.	B	.	.	T	0.88	0.14	*	*	F	0.25	0.52	
10	Pro	497	.	.	B	.	.	T	0.83	-0.36	*	*	F	0.85	0.52	
	His	498	.	.	B	.	.	T	1.08	0.04	*	*	F	0.74	1.20	
	Val	499	.	.	B	.	.	T	1.01	-0.17	*	*	F	1.68	1.20	
	Arg	500	.	.	B	.	.	T	1.98	-0.60	*	*	F	2.32	1.55	
	Gln	501	.	.	B	.	.	T	2.43	-1.03	*	.	F	2.66	2.24	
15	Gly	502	.	.	.	.	T	T	2.69	-1.53	*	.	F	3.40	5.90	
	Lys	503	A	.	.	.	.	T	2.42	-2.17	.	.	F	2.66	6.03	
	Arg	504	A	.	.	.	.	.	2.47	-1.79	.	*	F	2.12	4.66	
	Arg	505	.	.	B	.	.	.	2.40	-1.50	.	.	F	1.78	3.89	
	Lys	506	.	.	B	.	.	.	2.10	-1.93	.	*	F	1.44	3.89	
	Ser	507	.	.	B	.	.	.	2.41	-1.54	.	.	F	1.44	2.66	
	Leu	508	.	.	B	.	.	.	2.07	-1.04	.	.	F	1.78	1.85	
20	Lys	509	.	.	B	.	.	.	1.61	-0.66	.	.	F	2.12	1.24	
	Ser	510	.	.	.	.	.	C	1.61	-0.23	*	*	F	2.21	0.91	
	His	511	.	.	.	.	T	T	0.97	-0.61	*	*	F	3.40	2.17	
25	Ser	512	.	.	.	.	.	T	C	1.38	-0.69	.	*	F	2.86	1.07
	Gly	513	.	.	.	.	T	T	1.98	-0.69	.	*	F	3.02	1.57	
	Arg	514	.	.	.	.	T	T	1.63	-0.64	.	*	F	2.98	1.78	
	Met	515	.	.	.	.	.	.	C	1.34	-0.76	.	*	F	2.54	1.78
	Arg	516	.	.	.	.	.	T	C	1.38	-0.64	.	*	F	2.70	1.82
	Pro	517	.	.	.	.	.	T	C	1.68	-1.07	.	*	F	3.00	1.61
	Ser	518	A	.	.	.	.	T	.	2.07	-0.67	.	*	F	2.50	2.82
30	Ala	519	A	.	.	.	.	T	.	2.07	-1.29	.	*	F	2.20	2.88
	Glu	520	A	A	.	.	.	.	2.08	-1.29	*	*	F	1.50	3.65	
	Gln	521	A	A	.	.	.	.	1.62	-1.21	*	*	F	1.51	2.75	
35	Lys	522	A	A	.	.	.	.	1.94	-1.17	*	.	F	1.52	2.69	
	Arg	523	A	A	.	.	.	.	1.94	-1.67	*	.	F	1.83	3.04	
	Ala	524	.	A	.	.	T	.	1.72	-1.29	*	.	F	2.54	2.36	
	Gly	525	.	.	.	.	T	T	1.51	-1.00	*	.	F	3.10	0.97	
	Arg	526	.	.	.	.	T	T	1.12	-0.57	*	.	F	2.79	0.77	
40	Ser	527	.	.	.	.	.	T	C	0.69	-0.14	*	.	F	1.98	0.97
	Leu	528	.	.	.	.	.	T	C	0.19	-0.21	*	.	.	1.67	1.25
	Pro	529	.	.	B	.	.	.	0.39	-0.21	*	.	.	0.81	0.82	
	Ter	530	.	.	.	.	T	.	0.34	0.21	*	.	.	0.30	0.78	

**PAGE INTENTIONALLY LEFT BLANK**



Table II

	Res Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
5	Met 1	.	.	.	.	.	.	C	0.69	-0.24	.	*	.	1.19	1.74
	Arg 2	.	.	.	.	.	.	C	0.38	-0.24	.	*	.	1.53	1.34
	Pro 3	.	.	.	.	.	T	C	0.88	0.11	.	.	.	1.32	0.91
	Pro 4	.	.	.	.	T	T	.	1.27	-0.31	.	.	.	2.61	1.80
	Gly 5	.	.	.	.	T	T	.	0.96	-0.53	.	.	F	3.40	1.48
10	Phe 6	.	.	.	.	T	T	.	0.74	0.26	.	.	F	2.01	0.83
	Arg 7	.	A	B	.	.	.	.	-0.18	0.51	.	.	.	0.42	0.44
	Asn 8	.	A	B	.	.	.	.	-0.78	0.77	*	.	.	0.08	0.37
	Phe 9	.	A	B	.	.	.	.	-1.16	1.03	*	.	.	-0.26	0.35
	Leu 10	.	A	B	.	.	.	.	-1.11	0.74	*	.	.	-0.60	0.18
15	Leu 11	.	A	.	.	.	.	C	-0.71	1.13	*	.	.	-0.40	0.15
	Leu 12	.	A	.	.	.	.	C	-1.63	1.11	*	.	.	-0.40	0.23
	Ala 13	.	A	.	.	.	.	C	-2.44	1.01	.	.	.	-0.40	0.23
	Ser 14	.	A	.	.	.	.	C	-2.44	1.01	.	.	.	-0.40	0.23
	Ser 15	.	A	.	.	.	.	C	-2.22	1.11	.	.	.	-0.40	0.24
20	Leu 16	.	A	B	.	.	.	.	-1.76	0.93	.	.	.	-0.60	0.24
	Leu 17	.	A	B	.	.	.	.	-1.76	0.86	.	.	.	-0.60	0.18
	Phe 18	.	A	B	.	.	.	.	-1.47	1.16	.	.	.	-0.60	0.11
	Ala 19	.	A	.	.	.	.	C	-1.76	1.16	.	.	.	-0.40	0.18
	Gly 20	.	A	.	.	.	.	C	-2.31	0.97	.	.	.	-0.40	0.22
25	Leu 21	.	A	.	.	.	.	C	-1.71	0.93	*	.	.	-0.40	0.19
	Ser 22	.	A	.	.	.	.	C	-0.90	0.57	*	.	.	-0.40	0.29
	Ala 23	.	A	.	.	.	.	C	-0.50	0.47	*	.	.	-0.40	0.51
	Val 24	.	A	.	.	.	.	C	-0.61	0.43	*	.	.	-0.40	0.83
	Pro 25	.	.	.	.	.	T	C	-0.57	0.53	*	.	F	0.15	0.53
30	Gln 26	.	.	.	.	T	T	.	0.03	0.53	*	.	F	0.35	0.71
	Ser 27	.	.	.	.	T	T	.	0.03	0.46	*	.	F	0.50	1.48
	Phe 28	.	.	.	.	.	T	C	-0.19	0.20	*	*	F	0.60	1.28
	Ser 29	.	.	.	.	.	T	C	0.78	0.46	*	*	F	0.15	0.61
	Pro 30	.	.	.	.	.	T	C	0.69	0.06	*	*	F	0.45	0.89
35	Ser 31	.	.	.	.	T	T	.	0.40	0.06	*	*	F	0.80	1.38
	Leu 32	.	.	.	.	T	T	.	0.49	0.19	*	*	F	0.80	1.08
	Arg 33	.	.	.	.	T	.	.	0.84	0.23	*	*	F	0.60	1.08
	Ser 34	.	.	.	.	T	.	.	0.56	0.23	*	*	F	0.45	0.80
	Trp 35	.	.	.	.	.	T	C	0.18	0.34	*	*	F	0.45	0.98
40	Pro 36	.	.	.	.	.	T	C	-0.19	0.16	*	*	F	0.45	0.50
	Gly 37	.	.	.	.	T	T	.	0.73	0.73	*	*	.	0.20	0.20

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	Ala	38	.	.	.	.	T	T	.	-0.19	0.34	*	*	.	0.50	0.38
	Ala	39	.	.	.	.	.	.	C	-0.19	0.11	*	.	.	0.10	0.20
	Cys	40	.	.	B	.	T	.	.	0.21	0.07	*	.	.	0.30	0.27
	Arg	41	.	A	B	.	.	.	.	-0.17	-0.36	*	.	.	0.30	0.53
5	Leu	42	.	A	.	.	.	.	C	0.18	-0.36	*	.	.	0.50	0.53
	Ser	43	.	A	.	.	.	.	C	0.47	-0.86	*	*	.	0.95	1.70
	Arg	44	.	A	.	.	.	.	C	1.06	-1.04	*	.	F	1.10	1.16
	Ala	45	.	A	.	.	.	.	C	1.83	-1.04	.	*	F	1.10	2.44
	Glu	46	.	A	.	.	T	.	.	1.83	-1.73	.	*	F	1.30	3.57
10	Ser	47	.	A	.	.	T	.	.	1.98	-2.11	.	*	F	1.30	3.57
	Glu	48	.	A	.	.	T	.	.	2.39	-1.54	.	*	F	1.30	1.89
	Arg	49	.	A	.	.	T	.	.	1.69	-2.04	.	*	F	1.30	2.14
	Arg	50	.	A	.	.	T	.	.	2.07	-1.54	*	*	F	1.58	1.62
	Cys	51	.	A	.	.	T	.	.	1.72	-1.50	*	*	.	1.71	1.44
15	Arg	52	.	A	.	.	T	.	.	2.02	-1.07	*	*	F	1.99	0.73
	Ala	53	.	.	.	.	.	T	C	1.81	-0.67	*	*	F	2.47	0.64
	Pro	54	.	.	.	.	T	T	.	1.49	-0.24	*	*	F	2.80	1.86
	Gly	55	.	.	.	.	T	T	.	1.03	-0.39	.	*	F	2.52	1.47
	Gln	56	.	.	.	.	.	T	C	1.11	0.04	*	*	F	1.44	1.44
20	Pro	57	.	.	.	.	.	T	C	0.41	0.04	*	*	F	1.01	0.94
	Pro	58	.	.	.	.	T	T	.	0.19	0.11	.	.	F	0.93	0.96
	Gly	59	.	.	.	.	T	T	.	-0.27	0.37	.	.	F	0.65	0.46
	Ala	60	.	.	B	.	.	T	.	0.04	0.54	.	.	.	-0.20	0.16
	Ala	61	.	.	B	.	.	.	.	-0.30	0.61	.	*	.	-0.40	0.14
25	Leu	62	.	.	B	.	.	.	.	0.02	0.61	.	*	.	-0.40	0.14
	Cys	63	.	.	.	.	T	.	.	-0.11	0.19	.	*	.	0.61	0.27
	His	64	.	.	.	.	T	T	.	0.34	0.11	.	*	.	1.12	0.26
	Gly	65	.	.	.	.	T	T	.	0.27	-0.39	.	*	F	2.18	0.63
	Arg	66	.	.	.	.	T	T	.	0.86	-0.50	.	*	F	2.49	0.63
30	Gly	67	.	.	.	.	T	T	.	1.00	-1.07	.	*	F	3.10	0.77
	Arg	68	.	.	.	.	T	.	.	1.32	-1.00	.	*	F	2.59	0.42
	Cys	69	.	.	.	.	T	T	.	0.50	-1.00	.	*	.	2.33	0.21
	Asp	70	.	.	.	.	T	T	.	0.18	-0.36	.	*	.	1.72	0.16
	Cys	71	.	.	.	.	T	T	.	-0.82	-0.21	.	*	.	1.41	0.04
35	Gly	72	.	.	.	.	T	T	.	-1.14	0.47	.	*	.	0.20	0.06
	Val	73	.	.	.	B	T	.	.	-1.29	0.47	.	*	.	-0.20	0.02
	Cys	74	.	.	B	B	.	.	.	-1.48	0.97	.	.	.	-0.60	0.05
	Ile	75	.	.	B	B	.	.	.	-1.79	1.04	*	.	.	-0.60	0.03
	Cys	76	.	.	B	B	.	.	.	-1.12	1.10	.	.	.	-0.60	0.07
40	His	77	.	.	B	B	.	.	.	-0.99	0.46	.	.	.	-0.60	0.22
	Val	78	.	.	.	B	T	.	.	-0.48	0.31	.	.	.	0.10	0.48

	Thr	79	.	.	.	B	.	.	C	-0.41	0.06	.	.	F	0.05 0.89
	Glu	80	.	.	.	.	.	T	C	-0.22	0.10	*	.	F	0.45 0.64
	Pro	81	.	.	.	.	T	T	.	-0.26	0.39	.	.	F	0.65 0.75
	Gly	82	.	.	.	.	T	T	.	-0.57	0.53	.	.	.	0.20 0.45
5	Met	83	.	.	.	.	T	T	.	0.08	0.47	*	.	.	0.20 0.26
	Phe	84	.	.	.	.	T	.	.	-0.42	0.90	.	.	.	0.00 0.26
	Phe	85	.	.	.	.	T	.	.	-1.09	1.16	.	.	.	0.00 0.21
	Gly	86	.	.	.	.	.	T	C	-0.88	1.30	.	.	.	0.00 0.12
	Pro	87	.	.	.	.	.	T	C	-1.20	0.69	.	.	.	0.00 0.23
10	Leu	88	.	.	.	.	T	T	.	-0.63	0.47	*	.	.	0.20 0.14
	Cys	89	.	.	.	.	T	T	.	0.07	0.19	*	.	.	0.50 0.20
	Glu	90	.	A	.	.	T	.	.	0.48	-0.24	*	.	.	0.70 0.22
	Cys	91	.	A	.	.	T	.	.	-0.03	0.24	.	.	.	0.10 0.28
	His	92	.	A	.	.	T	.	.	-0.49	0.20	*	.	.	0.10 0.39
15	Glu	93	.	A	.	.	T	.	.	0.32	0.20	*	.	.	0.10 0.12
	Trp	94	.	A	.	.	T	.	.	0.68	0.20	*	.	.	0.10 0.39
	Val	95	.	A	.	.	T	.	.	0.43	0.11	*	.	.	0.10 0.42
	Cys	96	.	A	.	.	T	.	.	1.10	0.37	*	.	.	0.38 0.38
	Glu	97	.	A	.	.	T	.	.	0.79	0.37	*	.	.	0.66 0.60
20	Thr	98	.	A	.	.	T	.	.	0.49	-0.11	*	.	F	1.69 0.80
	Tyr	99	.	.	.	.	T	T	.	0.47	-0.37	.	.	F	2.52 1.99
	Asp	100	.	.	.	.	T	T	.	0.66	-0.46	.	.	F	2.80 1.66
	Gly	101	.	.	.	.	T	T	.	0.73	0.11	.	.	F	1.77 0.62
	Ser	102	.	.	.	.	T	T	.	0.39	0.13	.	.	F	1.49 0.40
25	Thr	103	.	.	.	.	T	.	.	0.67	-0.20	.	.	F	1.61 0.24
	Cys	104	.	.	.	.	T	T	.	0.57	0.30	.	*	.	0.78 0.32
	Ala	105	.	.	.	.	T	T	.	0.61	0.30	.	*	.	0.50 0.24
	Gly	106	.	.	.	.	T	T	.	0.29	-0.09	.	*	.	1.10 0.33
	His	107	.	.	.	.	T	T	.	0.59	0.00	.	*	.	0.50 0.33
30	Gly	108	.	.	.	.	T	.	.	0.23	-0.57	.	*	F	1.35 0.55
	Lys	109	.	.	.	.	T	.	.	0.56	-0.50	.	*	F	1.36 0.30
	Cys	110	.	.	.	.	T	T	.	1.19	-0.50	.	.	.	1.72 0.22
	Asp	111	.	.	.	.	T	T	.	0.87	-1.00	.	*	.	2.33 0.44
	Cys	112	.	.	.	.	T	T	.	0.94	-0.86	.	*	.	2.64 0.12
35	Gly	113	.	.	.	.	T	T	.	0.62	-0.86	.	*	F	3.10 0.44
	Lys	114	.	.	.	.	T	.	.	0.58	-0.86	.	*	F	2.59 0.14
	Cys	115	.	.	.	.	T	.	.	1.24	-0.86	.	*	F	2.28 0.44
	Lys	116	.	.	.	.	T	.	.	0.90	-1.03	.	*	F	1.97 0.76
	Cys	117	.	.	.	.	T	.	.	1.28	-1.03	.	*	F	1.94 0.38
40	Asp	118	.	.	.	.	T	T	.	1.38	-0.11	.	*	F	1.81 0.74
	Gln	119	.	.	.	.	T	T	.	0.99	0.07	.	*	F	1.49 0.58

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	Gly	120	.	.	.	.	T	T	.	1.66	0.50	.	*	F	1.62	1.07
	Trp	121	.	.	.	.	T	T	.	1.02	-0.07	.	*	F	2.80	1.07
	Tyr	122	.	.	.	.	T	.	.	1.02	0.43	.	.	.	1.12	0.62
	Gly	123	.	.	.	.	T	.	.	1.02	0.60	.	.	.	0.84	0.34
5	Asp	124	.	.	.	.	T	.	.	0.78	0.57	.	.	.	0.56	0.56
	Ala	125	.	.	.	.	T	.	.	0.91	0.41	.	.	.	0.28	0.56
	Cys	126	.	.	.	.	T	.	.	0.89	0.09	*	.	.	0.30	0.87
	Gln	127	.	.	.	.	T	.	.	1.13	0.14	*	.	.	0.30	0.75
	Tyr	128	.	.	.	.	.	.	C	0.81	0.54	.	.	.	-0.05	1.20
10	Pro	129	.	.	.	.	T	T	.	0.81	0.61	.	*	F	0.50	1.20
	Thr	130	.	.	.	.	T	T	.	0.59	0.04	.	*	F	0.80	1.15
	Asn	131	.	.	.	.	T	T	.	0.94	0.33	.	*	F	0.65	0.61
	Cys	132	.	.	.	.	T	T	.	0.99	0.06	.	*	.	0.50	0.57
	Asp	133	.	.	.	.	T	.	.	1.28	-0.37	.	.	.	0.90	0.79
15	Leu	134	.	.	.	.	T	.	.	1.53	-0.86	.	.	F	1.69	0.98
	Thr	135	.	.	.	.	T	.	.	1.54	-1.26	.	.	F	2.18	3.64
	Lys	136	.	.	.	.	T	.	.	1.54	-1.44	.	.	F	2.52	2.92
	Lys	137	.	.	.	.	T	.	.	2.21	-1.04	*	.	F	2.86	5.70
	Lys	138	.	.	.	.	T	T	.	1.61	-1.33	*	.	F	3.40	6.84
20	Ser	139	.	.	.	.	T	T	.	1.76	-1.20	*	.	F	3.06	3.39
	Asn	140	.	.	.	.	T	T	.	2.11	-0.63	*	.	F	2.57	0.91
	Gln	141	.	.	.	.	T	T	.	2.07	-0.63	*	.	F	2.57	0.91
	Met	142	.	.	.	.	T	.	.	1.72	-0.23	*	.	.	2.07	1.09
	Cys	143	.	.	.	.	T	T	.	1.68	-0.23	*	.	.	2.12	0.91
25	Lys	144	.	.	.	.	T	T	.	1.98	-0.23	*	.	F	2.61	0.91
	Asn	145	.	.	.	.	T	T	.	1.09	-0.63	*	.	F	3.40	1.53
	Ser	146	.	.	.	.	T	T	.	0.20	-0.56	*	.	F	3.06	2.00
	Gln	147	.	.	.	B	T	.	.	0.13	-0.44	*	.	F	1.87	0.70
	Asp	148	.	.	.	B	T	.	.	0.50	0.13	*	.	F	0.93	0.23
30	Ile	149	.	.	B	B	.	.	.	0.46	0.11	*	.	.	0.04	0.23
	Ile	150	.	.	B	B	.	.	.	-0.13	0.13	.	.	.	-0.30	0.22
	Cys	151	.	.	B	.	.	T	.	-0.18	0.23	.	.	.	0.10	0.13
	Ser	152	.	.	.	.	T	T	.	-0.49	0.66	.	.	.	0.20	0.19
	Asn	153	.	.	.	.	T	T	.	-1.16	0.46	.	.	F	0.35	0.38
35	Ala	154	.	.	.	.	T	T	.	-0.30	0.34	.	.	F	0.65	0.38
	Gly	155	.	.	.	.	T	.	.	-0.08	0.27	.	.	F	0.45	0.39
	Thr	156	.	.	.	.	T	.	.	0.24	0.46	.	.	.	0.00	0.13
	Cys	157	.	.	.	.	T	T	.	0.66	0.49	.	.	.	0.20	0.13
	His	158	.	.	.	.	T	T	.	-0.01	-0.01	.	*	.	1.10	0.25
40	Cys	159	.	.	.	.	T	T	.	0.62	0.13	.	*	.	0.50	0.09
	Gly	160	.	.	.	.	T	T	.	0.30	-0.36	.	*	.	1.10	0.35

	Arg	161	.	.	.	.	T	.	.	0.61	-0.36	.	*	.	1.24	0.14
	Cys	162	.	.	.	.	T	T	.	1.28	-0.86	.	*	F	2.23	0.43
	Lys	163	.	.	.	.	T	T	.	1.01	-1.03	.	*	F	2.57	0.69
	Cys	164	.	.	.	.	T	T	.	1.68	-1.07	.	*	F	2.91	0.47
5	Asp	165	.	.	.	.	T	T	.	1.68	-1.07	.	*	F	3.40	1.48
	Asn	166	.	.	.	.	T	T	.	1.27	-1.21	.	*	F	2.91	0.73
	Ser	167	.	.	.	.	T	T	.	1.59	-0.83	.	.	F	2.72	1.83
	Asp	168	.	.	.	.	T	T	.	0.73	-0.97	.	.	F	2.38	1.08
	Gly	169	.	.	.	.	T	T	.	0.54	-0.29	.	.	F	1.59	0.56
10	Ser	170	.	.	.	B	T	.	.	0.30	-0.04	.	.	F	0.85	0.31
	Gly	171	.	.	.	B	T	.	.	-0.04	0.33	.	*	F	0.25	0.29
	Leu	172	.	.	B	B	.	.	.	0.30	0.76	.	*	F	-0.45	0.29
	Val	173	.	.	B	B	.	.	.	-0.40	0.33	.	*	.	-0.30	0.43
	Tyr	174	.	.	.	B	T	.	.	-0.72	0.73	.	*	.	-0.20	0.38
15	Gly	175	.	.	.	.	T	T	.	-0.42	0.87	.	.	.	0.20	0.24
	Lys	176	.	.	.	.	T	T	.	-0.74	0.19	.	.	.	0.50	0.57
	Phe	177	.	.	.	.	T	T	.	0.07	0.11	.	.	.	0.84	0.20
	Cys	178	.	.	.	.	T	T	.	0.92	-0.64	*	*	.	2.08	0.33
	Glu	179	.	.	.	.	T	.	.	1.28	-1.07	*	.	.	2.22	0.28
20	Cys	180	.	.	.	.	T	T	.	1.62	-1.07	*	.	.	2.76	0.62
	Asp	181	.	.	.	.	T	T	.	0.91	-1.86	*	*	F	3.40	2.01
	Asp	182	.	.	.	.	T	T	.	0.72	-1.86	*	*	F	2.91	0.62
	Arg	183	.	.	.	.	T	T	.	1.39	-1.17	.	*	F	2.88	0.81
	Glu	184	.	.	.	.	T	.	.	1.39	-1.74	.	*	.	2.50	0.81
25	Cys	185	.	.	.	.	T	.	.	2.06	-1.74	.	*	.	2.47	0.81
	Ile	186	.	.	.	.	T	.	.	1.74	-1.74	*	*	.	2.44	0.72
	Asp	187	.	.	.	.	T	T	.	1.74	-1.26	.	*	F	3.10	0.60
	Asp	188	.	.	.	.	.	T	C	1.63	-1.26	*	*	F	2.74	1.94
	Glu	189	A	.	.	.	.	T	.	0.74	-1.83	*	.	F	2.23	4.79
30	Thr	190	A	.	.	.	.	T	.	0.74	-1.83	*	.	F	1.92	2.01
	Glu	191	A	.	.	.	.	.	.	1.29	-1.26	*	.	F	1.26	0.65
	Glu	192	A	.	.	.	.	.	.	0.94	-0.83	.	.	F	0.95	0.37
	Ile	193	.	.	.	.	T	.	.	0.91	-0.40	.	.	.	1.15	0.25
	Cys	194	.	.	.	.	T	T	.	0.57	-0.39	.	.	.	1.60	0.20
35	Gly	195	.	.	.	.	T	T	.	0.92	0.04	.	.	.	1.25	0.11
	Gly	196	.	.	.	.	T	T	.	0.26	0.04	*	.	F	1.65	0.32
	His	197	.	.	.	.	T	T	.	0.01	-0.07	.	.	F	2.50	0.32
	Gly	198	.	.	.	.	T	T	.	0.23	0.11	.	.	F	1.65	0.51
	Lys	199	.	.	.	.	T	T	.	0.56	0.26	.	.	.	1.25	0.28
40	Cys	200	.	.	.	.	T	T	.	0.90	0.26	.	.	.	1.00	0.20
	Tyr	201	.	.	.	.	T	T	.	0.58	0.16	.	.	.	0.75	0.33

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	Cys	202	.	.	.	.	T	T	.	0.37	0.30	.	.	.	0.50 0.09
	Gly	203	.	.	.	.	T	T	.	0.04	1.06	.	*	.	0.20 0.26
	Asn	204	.	.	.	.	T	T	.	0.04	1.06	.	*	.	0.20 0.09
	Cys	205	.	.	.	.	T	T	.	0.12	0.30	*	*	.	0.50 0.33
5	Tyr	206	.	.	.	.	T	.	.	0.02	0.23	.	*	.	0.30 0.34
	Cys	207	.	.	.	.	T	T	.	0.40	0.23	*	*	.	0.50 0.21
	Lys	208	.	.	.	.	T	T	.	0.71	0.74	*	*	.	0.20 0.40
	Ala	209	.	.	.	.	T	T	.	0.37	0.67	*	*	.	0.20 0.35
	Gly	210	.	.	.	.	T	T	.	1.03	0.34	*	*	.	0.81 0.65
10	Trp	211	.	.	.	.	T	.	.	1.32	-0.23	*	*	.	1.52 0.54
	His	212	.	.	.	.	.	T	C	1.32	-0.23	*	*	.	1.98 1.07
	Gly	213	.	.	.	.	T	T	.	1.28	-0.16	.	*	F	2.49 0.58
	Asp	214	.	.	.	.	T	T	.	1.17	-0.59	.	*	F	3.10 0.96
	Lys	215	.	.	.	.	T	T	.	1.51	-0.71	.	*	F	2.79 0.61
15	Cys	216	.	A	.	.	T	.	.	1.13	-0.81	.	*	.	2.08 1.07
	Glu	217	.	A	.	.	T	.	.	1.17	-0.67	.	*	.	1.62 0.34
	Phe	218	.	A	.	.	T	.	.	0.62	-0.67	.	*	.	1.31 0.29
	Gln	219	.	A	.	.	T	.	.	0.31	0.01	.	*	.	0.10 0.37
	Cys	220	.	A	.	.	T	.	.	0.06	-0.07	.	*	.	0.70 0.31
20	Asp	221	.	A	.	.	T	.	.	0.43	0.36	.	*	.	0.10 0.56
	Ile	222	.	A	.	.	.	.	C	0.43	0.49	.	*	.	-0.06 0.34
	Thr	223	.	.	.	.	.	T	C	0.83	0.09	.	*	F	1.28 1.09
	Pro	224	.	.	.	.	T	T	.	0.88	-0.10	.	.	F	2.27 0.88
	Trp	225	.	.	.	.	T	T	.	1.66	-0.10	.	*	F	2.76 2.50
25	Glu	226	.	.	.	.	T	T	.	1.77	-0.79	.	*	F	3.40 3.39
	Ser	227	.	.	.	.	T	T	.	1.99	-1.27	.	.	F	3.06 4.29
	Lys	228	.	.	.	.	T	T	.	1.99	-1.13	*	*	F	2.72 2.19
	Arg	229	.	.	.	.	T	T	.	1.90	-1.56	*	*	F	2.38 1.82
	Arg	230	.	.	.	.	T	T	.	1.98	-1.17	.	*	F	2.38 1.82
30	Cys	231	.	.	.	.	T	.	.	1.98	-1.13	.	.	F	2.18 1.41
	Thr	232	.	.	.	.	T	.	.	1.93	-1.13	.	*	F	2.52 1.20
	Ser	233	.	.	.	.	.	T	C	1.93	-0.70	*	*	F	2.71 0.61
	Pro	234	.	.	.	.	T	T	.	0.93	-0.70	*	*	F	3.40 2.27
	Asp	235	.	.	.	.	T	T	.	0.16	-0.59	*	*	F	3.06 1.10
35	Gly	236	.	.	.	.	T	T	.	0.52	-0.50	.	*	F	2.58 0.44
	Lys	237	.	.	.	.	T	.	.	0.83	-0.50	.	*	F	2.35 0.38
	Ile	238	.	.	.	.	T	.	.	1.24	-0.53	.	*	.	2.47 0.37
	Cys	239	.	.	.	.	T	T	.	1.11	-0.53	.	*	.	2.64 0.73
	Ser	240	.	.	.	.	T	T	.	0.80	-0.53	.	*	F	3.10 0.36
40	Asn	241	.	.	.	.	T	T	.	0.48	-0.04	.	.	F	2.49 0.74
	Arg	242	.	.	.	.	T	T	.	-0.42	-0.16	.	.	F	2.18 0.74

	Gly	243	.	.	.	B	T	.	.	-0.20	-0.09	.	.	F	1.47	0.41
	Thr	244	.	.	.	B	T	.	.	0.12	0.10	*	.	F	0.56	0.14
	Cys	245	.	.	.	B	T	.	.	0.42	0.13	*	.	.	0.10	0.07
	Val	246	.	.	.	B	T	.	.	-0.24	0.13	*	.	.	0.10	0.12
5	Cys	247	.	.	.	.	T	T	.	-0.67	0.27	*	*	.	0.50	0.04
	Gly	248	.	.	.	.	T	T	.	-0.99	0.27	.	.	.	0.50	0.12
	Glu	249	.	.	.	.	T	T	.	-0.71	0.27	.	.	.	0.50	0.09
	Cys	250	.	.	.	.	T	T	.	-0.04	0.13	.	.	.	0.50	0.22
	Thr	251	.	.	.	.	T	.	.	-0.04	-0.44	.	*	.	0.90	0.37
10	Cys	252	.	.	.	.	T	.	.	0.62	-0.23	.	.	.	0.90	0.16
	His	253	.	.	.	.	T	.	.	0.76	-0.23	.	.	.	1.24	0.50
	Asp	254	.	.	.	.	T	.	.	0.44	-0.37	.	*	.	1.58	0.54
	Val	255	.	.	.	.	T	.	.	0.77	-0.37	.	*	.	2.07	1.44
	Asp	256	.	.	.	.	.	T	C	1.08	-0.51	.	*	F	2.86	1.05
15	Pro	257	.	.	.	.	T	T	.	1.46	-1.01	*	*	F	3.40	1.05
	Thr	258	.	.	.	.	T	T	.	1.14	-0.10	*	*	F	2.76	1.48
	Gly	259	.	.	.	.	T	T	.	1.14	-0.31	.	*	F	2.27	0.88
	Asp	260	.	.	.	.	T	.	.	1.11	-0.31	.	*	F	1.73	0.95
	Trp	261	.	.	.	.	T	.	.	1.08	-0.06	.	*	F	1.39	0.46
20	Gly	262	.	.	.	.	.	.	C	0.94	-0.04	.	*	F	0.85	0.63
	Asp	263	.	.	.	.	T	.	.	1.26	-0.04	.	*	F	1.05	0.38
	Ile	264	.	.	.	.	T	.	.	1.29	-0.04	.	*	.	0.90	0.60
	His	265	.	.	.	.	T	T	.	0.62	-0.47	*	.	.	1.10	0.87
	Gly	266	.	.	.	.	T	T	.	0.91	-0.33	*	*	F	1.25	0.28
25	Asp	267	.	.	.	.	T	T	.	0.59	-0.33	.	*	F	1.56	0.69
	Thr	268	.	.	.	.	T	T	.	0.59	-0.44	.	*	F	1.87	0.27
	Cys	269	.	.	.	.	T	T	.	1.48	-0.94	*	*	.	2.33	0.46
	Glu	270	.	.	.	.	T	T	.	1.62	-1.37	.	.	.	2.64	0.48
	Cys	271	.	.	.	.	T	T	.	1.97	-1.37	*	.	F	3.10	0.65
30	Asp	272	.	.	.	.	T	T	.	1.30	-1.86	*	.	F	2.94	2.01
	Glu	273	.	.	.	.	T	.	.	1.72	-1.86	*	*	F	2.28	0.62
	Arg	274	.	.	.	.	T	T	.	1.80	-1.86	*	.	F	2.32	2.28
	Asp	275	.	.	.	.	T	T	.	0.94	-1.93	*	.	F	2.01	1.38
	Cys	276	.	.	.	.	T	T	.	1.37	-1.29	*	.	.	1.40	0.59
35	Arg	277	.	.	.	.	T	T	.	1.37	-0.53	*	.	.	1.40	0.47
	Ala	278	.	.	B	B	.	.	.	1.48	-0.53	*	.	.	0.60	0.47
	Val	279	.	.	B	B	.	.	.	1.12	-0.53	*	.	.	1.09	1.73
	Tyr	280	.	.	.	B	T	.	.	0.82	-0.34	*	*	.	1.53	1.38
	Asp	281	.	.	.	.	T	T	.	1.49	0.04	*	.	.	1.67	1.83
40	Arg	282	.	.	.	.	T	T	.	1.38	-0.46	*	*	F	2.76	4.12
	Tyr	283	.	.	.	.	T	T	.	1.27	-1.10	*	*	F	3.40	4.39

	Ser	284	.	.	.	.	T	T	.	1.46	-1.07	*	*	F	3.06	2.28
	Asp	285	.	.	.	.	T	.	.	1.40	-0.50	*	.	F	2.07	0.62
	Asp	286	.	.	.	.	T	.	.	1.06	-0.11	*	.	F	1.73	0.53
	Phe	287	.	.	.	.	T	.	.	0.91	-0.44	*	*	.	1.24	0.39
5	Cys	288	.	.	.	.	T	T	.	0.81	-0.33	.	.	.	1.10	0.32
	Ser	289	.	.	.	.	T	T	.	1.11	0.10	.	.	.	0.50	0.19
	Gly	290	.	.	.	.	T	T	.	0.44	0.50	.	*	F	0.35	0.38
	His	291	.	.	.	.	T	T	.	0.44	0.29	.	*	F	0.87	0.38
	Gly	292	.	.	.	.	T	.	.	0.48	0.11	.	*	F	0.89	0.46
10	Gln	293	.	.	.	.	T	.	.	0.80	0.30	*	*	.	0.96	0.25
	Cys	294	.	.	.	.	T	T	.	1.21	0.30	*	*	.	1.38	0.18
	Asn	295	.	.	.	.	T	T	.	0.89	-0.20	.	*	.	2.20	0.36
	Cys	296	.	.	.	.	T	T	.	0.92	-0.06	.	*	.	1.98	0.11
	Gly	297	.	.	.	.	T	T	.	0.60	-0.46	*	*	.	2.04	0.34
15	Arg	298	.	.	.	.	T	.	.	0.64	-0.46	*	*	.	1.90	0.11
	Cys	299	.	.	.	.	T	T	.	0.72	-0.86	*	*	.	2.46	0.43
	Asp	300	.	.	.	.	T	T	.	0.38	-0.93	*	*	.	2.52	0.44
	Cys	301	.	.	.	.	T	T	.	0.76	-0.93	*	*	.	2.80	0.22
	Lys	302	.	.	.	.	T	T	.	0.86	-0.01	*	*	.	2.22	0.43
20	Ala	303	.	.	.	.	T	.	.	0.40	0.17	*	*	.	1.14	0.40
	Gly	304	.	.	.	.	T	.	.	1.11	0.60	.	*	.	0.56	0.75
	Trp	305	.	.	.	.	T	.	.	1.16	0.03	.	*	.	0.92	0.75
	Tyr	306	.	.	.	.	T	.	.	1.16	0.03	.	*	.	1.13	1.48
	Gly	307	.	.	.	.	T	T	.	1.11	0.10	*	.	F	1.67	0.80
25	Lys	308	.	.	.	.	T	T	.	1.67	-0.33	*	.	F	2.76	1.32
	Lys	309	.	.	.	.	T	T	.	1.80	-0.74	.	.	F	3.40	1.15
	Cys	310	.	.	.	.	T	T	.	2.09	-1.07	.	.	F	3.06	1.79
	Glu	311	.	.	.	.	T	.	.	2.03	-1.10	.	.	F	2.52	1.55
	His	312	.	.	.	.	.	T	C	1.71	-0.71	.	.	F	2.18	1.04
30	Pro	313	.	.	.	.	T	T	.	1.36	-0.14	.	.	F	1.74	1.04
	Gln	314	.	.	.	.	T	T	.	0.50	-0.23	.	.	F	1.25	0.87
	Ser	315	.	.	.	.	T	T	.	0.87	0.46	.	.	F	0.35	0.52
	Cys	316	.	.	.	B	T	.	.	0.28	0.34	.	.	F	0.25	0.45
	Thr	317	.	.	.	B	.	.	C	0.31	0.41	.	.	.	-0.40	0.27
35	Leu	318	.	.	.	B	.	.	C	0.52	0.01	.	.	.	-0.10	0.34
	Ser	319	.	.	.	B	.	.	C	0.22	-0.37	.	*	.	0.65	1.11
	Ala	320	A	A	.	.	.	.	.	-0.37	-0.56	*	*	F	0.90	1.03
	Glu	321	A	A	.	.	.	.	.	0.41	-0.36	*	*	F	0.45	0.87
	Glu	322	A	A	.	.	.	.	.	0.77	-1.04	*	*	F	0.90	1.28
40	Ser	323	.	A	.	.	T	.	.	0.91	-1.43	*	*	F	1.64	2.53
	Ile	324	.	A	.	.	T	.	.	1.21	-1.36	*	*	F	1.83	0.78



	Arg	325	.	A	.	.	T	.	.	1.46	-0.96	*	.	F	2.17	0.78
	Lys	326	.	A	.	.	T	.	.	1.16	-0.53	*	.	F	2.51	0.58
	Cys	327	.	.	.	.	T	T	.	0.86	-0.53	*	.	F	3.40	1.11
	Gln	328	.	.	.	.	T	T	.	1.16	-0.83	*	*	F	2.91	0.76
5	Gly	329	.	.	.	.	T	T	.	1.23	-0.83	*	*	F	2.57	0.63
	Ser	330	.	.	.	.	T	T	.	0.91	-0.14	*	*	F	1.93	0.97
	Ser	331	.	.	.	.	T	.	.	0.20	-0.29	.	*	F	1.39	0.87
	Asp	332	.	.	.	.	T	.	.	0.57	-0.11	*	*	F	1.05	0.47
	Leu	333	.	.	.	.	.	.	C	0.22	-0.16	*	*	F	1.16	0.47
10	Pro	334	.	.	.	.	T	.	.	0.68	-0.11	*	*	F	1.67	0.35
	Cys	335	.	.	.	.	T	T	.	0.63	-0.50	.	*	F	2.18	0.41
	Ser	336	.	.	.	.	T	T	.	0.98	-0.07	.	*	F	2.49	0.49
	Gly	337	.	.	.	.	T	T	.	0.31	-0.76	.	*	F	3.10	0.63
	Arg	338	.	.	.	.	T	T	.	1.12	-0.61	.	*	F	2.79	0.63
15	Gly	339	.	.	.	.	T	.	.	0.67	-1.19	.	*	F	2.56	0.82
	Lys	340	.	.	.	.	T	.	.	0.99	-1.00	*	*	F	2.53	0.44
	Cys	341	.	.	.	.	T	T	.	1.33	-1.00	*	*	F	2.70	0.22
	Glu	342	.	.	.	.	T	T	.	1.01	-1.00	*	*	.	2.52	0.45
	Cys	343	.	.	.	.	T	T	.	0.59	-0.86	*	*	.	2.80	0.12
20	Gly	344	.	.	.	.	T	T	.	0.27	-0.37	.	.	.	2.22	0.33
	Lys	345	.	.	.	.	T	.	.	-0.02	-0.37	.	.	.	1.74	0.10
	Cys	346	.	.	.	.	T	.	.	0.43	0.39	.	.	.	0.86	0.29
	Thr	347	.	.	.	.	T	.	.	0.22	0.24	.	.	.	0.58	0.46
	Cys	348	.	.	.	.	T	.	.	0.54	0.24	.	*	.	0.64	0.36
25	Tyr	349	.	.	B	.	.	.	.	0.89	0.67	.	*	.	0.28	0.66
	Pro	350	.	.	.	.	.	T	C	0.96	0.10	.	.	F	1.47	0.76
	Pro	351	.	.	.	.	T	T	.	1.73	-0.39	*	.	F	2.76	2.78
	Gly	352	.	.	.	.	T	T	.	1.19	-0.96	*	.	F	3.40	3.47
	Asp	353	.	.	.	.	T	T	.	1.61	-1.07	*	.	F	3.06	1.67
30	Arg	354	.	.	.	.	T	.	.	1.51	-0.74	*	*	F	2.52	1.69
	Arg	355	.	.	.	.	T	.	.	1.77	-0.74	*	*	F	2.18	1.69
	Val	356	.	.	.	.	T	.	.	1.67	-1.17	*	*	.	1.69	2.02
	Tyr	357	.	.	.	.	T	.	.	1.34	-0.69	*	*	.	1.35	1.49
	Gly	358	.	.	.	.	T	T	.	1.34	-0.11	*	*	F	1.25	0.41
35	Lys	359	.	.	.	.	T	T	.	0.57	-0.11	*	.	F	1.25	0.95
	Thr	360	.	.	.	.	T	T	.	0.46	-0.19	*	*	F	1.59	0.33
	Cys	361	.	.	.	.	T	T	.	1.31	-0.94	*	*	F	2.23	0.55
	Glu	362	.	.	.	.	T	.	.	1.67	-1.37	*	.	.	2.22	0.46
	Cys	363	.	.	.	.	T	T	.	2.12	-1.37	*	.	.	2.76	0.62
40	Asp	364	.	.	.	.	T	T	.	1.41	-1.86	*	.	F	3.40	2.28
	Asp	365	.	.	.	.	T	T	.	1.72	-1.86	*	.	F	2.91	0.70

	Arg	366	.	.	.	.	T	T	.	2.39	-1.86	*	.	F	3.03	2.28
	Arg	367	.	.	.	.	T	.	.	1.58	-2.43	*	.	F	2.80	2.28
	Cys	368	.	.	.	.	T	.	.	2.24	-1.74	.	.	F	2.77	1.12
	Glu	369	.	.	.	.	T	.	.	1.90	-1.74	.	.	F	2.59	0.96
5	Asp	370	.	.	.	.	T	T	.	1.04	-1.31	*	.	F	3.10	0.48
	Leu	371	.	.	.	.	T	T	.	0.08	-0.67	*	.	F	2.79	0.67
	Asp	372	.	.	.	.	T	T	.	-0.70	-0.60	.	.	F	2.48	0.29
	Gly	373	.	.	.	.	T	T	.	-0.38	-0.03	*	.	.	1.72	0.09
	Val	374	.	.	B	.	.	.	.	-0.72	0.40	*	.	.	0.21	0.11
10	Val	375	.	.	B	.	.	.	.	-0.76	0.14	.	*	.	-0.10	0.07
	Cys	376	.	.	.	.	T	T	.	-0.29	0.64	.	.	.	0.20	0.09
	Gly	377	.	.	.	.	T	T	.	-0.60	0.64	.	.	.	0.20	0.12
	Gly	378	.	.	.	.	T	T	.	-0.92	0.49	.	.	F	0.35	0.23
	His	379	.	.	.	.	T	T	.	-0.37	0.41	.	.	F	0.35	0.23
15	Gly	380	.	.	.	.	T	.	.	-0.18	0.23	.	.	F	0.45	0.32
	Thr	381	.	.	.	.	T	.	.	0.14	0.37	*	.	F	0.45	0.17
	Cys	382	.	.	.	.	T	T	.	0.60	0.37	*	.	.	0.50	0.12
	Ser	383	.	.	.	.	T	T	.	0.28	-0.13	*	.	.	1.28	0.25
	Cys	384	.	.	.	.	T	T	.	-0.54	0.01	*	.	.	0.86	0.09
20	Gly	385	.	.	.	.	T	T	.	-0.87	0.17	*	.	.	1.04	0.13
	Arg	386	.	.	.	.	T	.	.	-0.56	0.17	*	.	.	1.02	0.05
	Cys	387	.	.	B	.	T	.	.	0.22	-0.21	*	.	.	1.80	0.16
	Val	388	.	.	B	.	.	.	.	0.18	-0.79	*	.	.	1.52	0.32
	Cys	389	.	.	B	.	.	.	.	0.56	-0.79	*	*	.	1.34	0.16
25	Glu	390	.	.	.	.	T	T	.	0.20	0.13	*	.	.	0.86	0.32
	Arg	391	.	.	.	.	T	T	.	-0.26	0.34	.	.	.	0.68	0.38
	Gly	392	.	.	.	.	T	T	.	0.46	0.13	.	.	.	0.50	0.69
	Trp	393	.	.	.	.	T	T	.	0.50	-0.44	.	.	.	1.10	0.80
	Phe	394	.	.	.	.	T	.	.	0.50	0.24	*	.	.	0.30	0.34
30	Gly	395	.	.	.	.	T	.	.	0.50	0.81	*	.	.	0.00	0.18
	Lys	396	.	.	.	.	T	.	.	0.36	0.79	*	.	.	0.00	0.30
	Leu	397	.	.	.	.	T	.	.	0.49	0.37	*	*	.	0.64	0.47
	Cys	398	.	.	.	.	T	.	.	0.89	0.01	*	*	.	0.98	0.74
	Gln	399	.	.	.	.	T	.	.	1.63	-0.41	*	.	.	1.92	0.72
35	His	400	.	.	.	.	.	T	C	1.31	-0.41	*	*	.	2.41	1.75
	Pro	401	.	.	.	.	T	T	.	1.27	-0.53	*	*	F	3.40	1.75
	Arg	402	.	.	.	.	T	T	.	1.48	-0.70	*	.	F	3.06	1.63
	Lys	403	.	.	.	.	T	T	.	1.83	-0.49	.	.	F	2.42	1.18
	Cys	404	.	.	.	.	T	.	.	1.83	-0.50	*	.	.	2.03	1.11
40	Asn	405	.	A	.	.	.	.	C	1.87	-0.93	.	.	.	1.14	0.98
	Met	406	.	A	.	.	.	.	C	2.08	-0.93	*	.	F	0.95	0.85

5	Thr	407	.	A	.	.	.	.	C	1.67	-0.53	*	.	F	1.44	2.73
	Glu	408	A	A	.	.	.	.	.	1.67	-0.71	.	*	F	1.58	2.28
	Glu	409	A	A	.	.	.	.	.	2.33	-1.11	*	.	F	1.92	4.61
	Gln	410	.	A	.	.	T	.	.	1.52	-1.33	*	.	F	2.66	5.13
	Ser	411	.	.	.	.	T	T	.	1.46	-1.13	*	.	F	3.40	2.44
	Lys	412	.	.	.	.	T	T	.	1.77	-0.56	*	.	F	2.91	0.76
	Asn	413	.	.	.	.	.	T	C	1.47	-0.56	*	.	F	2.62	0.76
10	Leu	414	.	.	.	.	.	T	C	0.88	-0.57	*	.	.	2.38	0.76
	Cys	415	.	.	.	.	T	.	.	0.88	-0.46	*	.	.	1.99	0.38
	Glu	416	.	.	.	.	T	.	.	0.83	-0.46	*	.	F	2.05	0.40
	Ser	417	.	.	.	.	T	T	.	-0.10	-0.43	*	.	F	2.50	0.48
	Ala	418	.	.	.	.	T	T	.	-0.91	-0.43	*	.	F	2.25	0.62
15	Asp	419	.	.	.	.	T	T	.	-0.77	-0.31	*	.	F	2.00	0.30
	Gly	420	.	.	.	.	T	T	.	-0.40	0.26	*	.	.	1.00	0.12
	Ile	421	.	.	B	.	.	.	.	-0.74	0.26	*	.	.	0.15	0.16
	Leu	422	.	.	B	.	.	.	.	-0.40	0.19	*	*	.	0.15	0.09
	Cys	423	.	.	.	.	T	T	.	-0.16	0.19	*	*	.	1.00	0.19
20	Ser	424	.	.	.	.	T	T	.	-0.46	0.19	*	*	F	1.40	0.27
	Gly	425	.	.	.	.	T	T	.	-0.78	-0.11	.	*	F	2.25	0.43
	Lys	426	.	.	.	.	T	T	.	0.08	-0.23	.	*	F	2.50	0.43
	Gly	427	.	.	.	.	T	.	.	0.22	-0.30	.	*	F	2.05	0.44
	Ser	428	.	.	.	.	T	.	.	0.54	-0.11	*	*	F	1.80	0.24
25	Cys	429	.	.	.	.	T	.	.	0.89	-0.11	*	*	.	1.40	0.12
	His	430	.	.	.	.	T	T	.	0.57	-0.11	*	.	.	1.35	0.24
	Cys	431	.	.	.	.	T	T	.	-0.37	0.03	*	.	.	0.50	0.10
	Gly	432	.	.	.	.	T	T	.	-0.69	0.33	*	.	.	0.50	0.12
	Lys	433	.	.	.	.	T	T	.	-0.69	0.33	*	.	.	0.50	0.05
30	Cys	434	.	.	.	.	T	.	.	-0.61	0.21	*	.	.	0.30	0.12
	Ile	435	.	A	.	.	T	.	.	-0.58	0.14	*	.	.	0.10	0.13
	Cys	436	.	A	B	.	.	.	.	0.09	-0.29	*	.	.	0.30	0.11
	Ser	437	.	A	.	.	.	.	C	0.14	-0.29	*	.	.	0.50	0.35
	Ala	438	.	A	.	.	.	.	C	-0.14	0.06	*	.	.	-0.10	0.52
35	Glu	439	.	A	.	.	T	.	.	-0.37	0.13	.	.	.	0.25	1.53
	Glu	440	.	A	.	B	T	.	.	0.22	0.24	.	.	.	0.10	0.80
	Trp	441	.	A	.	B	T	.	.	0.54	0.24	.	*	.	0.25	1.06
	Tyr	442	.	A	.	B	T	.	.	0.84	0.17	.	*	.	0.10	0.61
	Ile	443	.	.	.	B	T	.	.	0.73	0.17	.	*	.	0.10	0.61
40	Ser	444	.	.	.	B	T	.	.	0.07	0.96	.	*	.	-0.20	0.50
	Gly	445	.	.	.	.	T	.	.	0.07	0.61	.	*	F	0.15	0.17
	Glu	446	.	.	.	.	T	.	.	-0.31	-0.14	.	*	.	0.90	0.41
	Phe	447	.	.	.	.	T	.	.	-0.07	-0.26	*	.	.	1.24	0.16

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	Cys	448	.	.	.	.	T	T	.	0.82	-0.64	*	*	.	2.08	0.28
	Asp	449	.	.	.	.	T	T	.	1.23	-1.07	*	.	.	2.42	0.27
	Cys	450	.	.	.	.	T	T	.	1.58	-1.07	*	.	.	2.76	0.60
	Asp	451	.	.	.	.	T	T	.	0.91	-1.86	*	.	F	3.40	1.87
5	Asp	452	.	.	.	.	T	T	.	1.61	-1.86	*	.	F	2.91	0.60
	Arg	453	.	.	.	.	T	T	.	2.32	-1.86	*	*	F	2.72	1.87
	Asp	454	.	.	.	.	T	T	.	2.29	-2.43	*	*	F	2.72	2.24
	Cys	455	.	.	.	.	T	T	.	2.96	-1.93	.	.	F	2.72	1.83
	Asp	456	.	.	.	.	T	.	.	2.61	-1.93	.	.	F	2.52	1.56
10	Lys	457	.	.	.	.	T	.	.	1.80	-1.50	*	.	F	2.71	0.92
	His	458	.	.	.	.	T	T	.	0.80	-0.81	*	.	F	3.40	1.42
	Asp	459	.	.	.	.	T	T	.	0.13	-0.70	.	.	F	2.91	0.60
	Gly	460	.	.	.	.	T	T	.	0.49	-0.13	.	.	.	2.12	0.16
	Leu	461	.	.	B	.	.	T	.	0.14	0.36	.	.	.	0.78	0.17
15	Ile	462	.	.	B	.	.	.	.	0.10	0.29	.	.	.	0.24	0.10
	Cys	463	.	.	.	.	T	T	.	-0.21	0.69	*	.	.	0.20	0.16
	Thr	464	.	.	.	.	T	T	.	-1.10	0.69	*	.	F	0.35	0.20
	Gly	465	.	.	.	.	T	T	.	-1.42	0.69	*	.	F	0.35	0.20
	Asn	466	.	.	.	.	T	T	.	-0.91	0.57	*	.	F	0.35	0.20
20	Gly	467	.	.	.	.	T	.	.	-0.69	0.39	.	.	F	0.45	0.18
	Ile	468	.	.	.	.	T	.	.	-0.37	0.47	*	.	.	0.00	0.10
	Cys	469	.	.	.	.	T	T	.	-0.06	0.47	*	.	.	0.42	0.06
	Ser	470	.	.	.	.	T	T	.	-0.38	0.47	*	.	.	0.64	0.10
	Cys	471	.	.	.	.	T	T	.	-0.38	0.61	.	.	.	0.86	0.08
25	Gly	472	.	.	.	.	T	T	.	-0.70	-0.07	.	.	.	1.98	0.24
	Asn	473	.	.	.	.	T	T	.	-0.10	-0.07	.	.	.	2.20	0.10
	Cys	474	.	.	.	.	T	T	.	0.57	0.46	.	.	.	1.08	0.19
	Glu	475	.	.	.	.	T	T	.	0.52	-0.11	.	.	.	1.76	0.32
	Cys	476	.	.	.	.	T	T	.	0.90	-0.11	.	.	.	1.54	0.20
30	Trp	477	.	.	.	.	T	T	.	1.24	0.40	.	.	.	0.42	0.39
	Asp	478	.	.	.	.	T	T	.	0.90	0.23	.	.	.	0.50	0.36
	Gly	479	.	.	.	.	T	T	.	1.57	0.66	.	.	F	0.35	0.67
	Trp	480	.	.	.	.	T	T	.	0.98	0.49	.	.	F	0.50	1.02
	Asn	481	.	.	.	.	.	T	C	0.98	0.07	.	.	F	0.45	0.62
35	Gly	482	.	.	.	.	.	T	C	1.27	0.64	*	.	F	0.15	0.33
	Asn	483	.	.	.	.	.	T	C	0.38	0.21	*	.	.	0.30	0.55
	Ala	484	.	.	.	.	.	T	C	0.43	-0.01	.	.	.	0.90	0.24
	Cys	485	.	A	.	.	T	.	.	-0.09	0.50	.	.	.	-0.20	0.25
	Glu	486	.	A	B	.	.	.	.	-0.43	0.76	.	.	.	-0.60	0.13
40	Ile	487	.	A	.	.	T	.	.	-0.39	0.79	.	.	.	-0.20	0.13
	Trp	488	.	A	.	.	T	.	.	-0.39	0.67	.	.	.	-0.20	0.32

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5	Leu	489	.	A	.	.	.	C	-0.04	0.10	.	.	.	-0.10	0.32
	Gly	490	.	.	.	.	T	T	.	0.41	0.86	.	*	F	0.56 0.72
	Ser	491	.	.	.	.	.	T	C	0.02	0.60	.	.	F	0.72 1.05
	Glu	492	.	.	.	.	.	T	C	0.52	0.11	.	.	F	1.23 1.63
	Tyr	493	.	.	.	.	.	T	C	0.42	-0.14	.	.	.	1.89 2.11
	Pro	494	.	.	.	.	T	.	.	0.84	-0.14	.	.	.	2.10 2.01
	Ter	495	.	.	.	.	T	.	.	0.80	-0.10	.	.	.	1.89 1.48

Table III

	Res Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
5	Met 1	A	A	.	.	.	.	.	0.10	-0.19	.	.	.	0.30	0.92
	Glu 2	A	A	.	.	.	.	.	-0.32	-0.11	*	*	.	0.30	0.72
	Thr 3	A	A	.	.	.	.	.	0.18	0.14	*	.	.	-0.30	0.47
	Gly 4	A	A	.	.	.	.	.	0.68	-0.29	*	.	.	0.30	0.93
	Ala 5	A	A	.	.	.	.	.	0.86	-0.90	*	.	F	0.90	1.05
10	Leu 6	A	A	.	.	.	.	.	1.46	-0.47	.	.	F	0.60	1.12
	Arg 7	.	A	B	.	.	.	.	0.64	-0.56	.	.	F	0.90	1.96
	Arg 8	.	.	B	.	.	.	.	0.14	-0.30	*	.	F	0.80	1.60
	Pro 9	.	A	B	.	.	.	.	0.28	-0.11	.	.	F	0.60	1.60
	Gln 10	.	A	B	.	.	.	.	0.06	-0.37	.	.	F	0.60	1.26
15	Leu 11	.	A	B	.	.	.	.	0.06	0.31	*	.	.	-0.30	0.53
	Leu 12	.	A	B	.	.	.	.	-0.87	1.00	.	.	.	-0.60	0.28
	Pro 13	.	A	B	.	.	.	.	-1.79	1.26	.	*	.	-0.60	0.14
	Leu 14	.	A	B	.	.	.	.	-2.39	1.54	.	.	.	-0.60	0.14
	Leu 15	.	A	B	.	.	.	.	-3.06	1.54	.	.	.	-0.60	0.14
20	Leu 16	.	A	B	.	.	.	.	-2.59	1.43	.	.	.	-0.60	0.05
	Leu 17	.	A	B	.	.	.	.	-2.12	1.43	.	.	.	-0.60	0.06
	Leu 18	.	A	B	.	.	.	.	-2.58	1.17	.	.	.	-0.60	0.07
	Cys 19	.	.	B	.	.	T	.	-1.98	1.06	*	*	.	-0.20	0.04
	Gly 20	.	.	.	.	T	T	.	-1.06	0.80	*	*	.	0.20	0.08
25	Gly 21	.	.	.	.	T	T	.	-0.83	0.11	.	*	F	0.65	0.20
	Cys 22	.	.	B	.	.	T	.	-0.37	-0.07	.	*	F	0.85	0.37
	Pro 23	.	.	B	.	.	.	.	0.10	-0.21	*	*	F	0.96	0.37
	Arg 24	.	.	.	.	T	T	.	0.10	-0.21	.	*	F	1.87	0.37
	Ala 25	.	.	.	.	T	T	.	0.44	-0.07	.	*	F	2.18	0.37
30	Gly 26	.	.	.	.	T	T	.	0.79	-0.24	.	*	F	2.49	0.38
	Gly 27	.	.	.	.	T	T	.	1.14	-0.67	.	*	F	3.10	0.34
	Cys 28	.	.	.	.	T	.	.	1.01	-0.19	.	*	F	2.29	0.48
	Asn 29	.	.	.	.	.	T	C	0.30	-0.26	.	*	F	1.98	0.48
	Glu 30	.	.	B	.	.	T	.	0.08	-0.07	.	.	F	1.47	0.48
35	Thr 31	.	.	B	.	.	T	.	0.42	0.19	*	.	F	0.56	0.74
	Gly 32	.	.	B	.	.	T	.	0.88	-0.39	*	.	F	0.85	0.80
	Met 33	A	A	.	.	.	.	.	0.73	-0.79	*	.	.	0.60	0.91
	Leu 34	A	A	.	.	.	.	.	0.52	-0.10	*	*	.	0.30	0.52
	Glu 35	A	A	.	.	.	.	.	-0.29	-0.16	.	*	.	0.30	0.81
40	Arg 36	A	A	.	.	.	.	.	-0.64	0.10	*	*	.	-0.30	0.67

5	Leu	37	A	A	.	.	.	.	.	-0.64	0.06	*	*	.	-0.30	0.44
	Pro	38	A	A	.	.	.	.	.	0.00	-0.20	*	*	.	0.30	0.25
	Leu	39	A	A	.	.	.	.	.	0.22	-0.20	*	*	.	0.30	0.26
	Cys	40	A	A	.	.	.	.	.	-0.48	0.30	*	*	.	-0.30	0.31
	Gly	41	A	A	.	.	.	.	.	-1.18	0.40	*	*	.	-0.30	0.18
	Lys	42	A	A	.	.	.	.	.	-0.37	0.47	*	*	.	-0.60	0.21
	Ala	43	A	A	.	.	.	.	.	-0.76	-0.21	*	*	.	0.30	0.67
	Phe	44	A	A	.	.	.	.	.	-0.54	-0.17	*	*	.	0.30	0.67
10	Ala	45	A	A	.	.	.	.	.	-0.22	0.01	*	*	.	-0.30	0.33
	Asp	46	A	A	.	.	.	.	.	0.17	0.44	*	*	.	-0.60	0.32
	Met	47	A	A	.	.	.	.	.	-0.73	-0.06	*	*	.	0.30	0.75
	Met	48	A	A	.	.	.	.	.	-0.14	-0.20	*	*	.	0.30	0.55
15	Gly	49	A	A	.	.	.	.	.	-0.30	-0.70	*	*	.	0.60	0.55
	Lys	50	A	.	.	B	.	.	.	0.00	-0.06	.	*	.	0.30	0.41
	Val	51	A	.	.	B	.	.	.	0.04	0.24	.	*	.	-0.30	0.44
	Asp	52	A	.	.	B	.	.	.	0.36	-0.37	.	*	.	0.30	0.89
	Val	53	A	.	.	B	.	.	.	0.29	0.11	.	*	.	-0.30	0.47
	Trp	54	A	.	.	B	.	.	.	0.63	0.69	.	*	.	-0.60	0.34
	Lys	55	A	.	.	B	.	.	.	-0.22	0.44	.	*	.	-0.60	0.32
	Trp	56	A	.	.	B	.	.	.	0.33	1.13	.	.	.	-0.60	0.36
20	Cys	57	A	.	.	B	.	.	.	0.33	0.87	.	.	.	-0.60	0.46
	Asn	58	.	.	.	B	.	.	C	0.49	-0.04	*	.	.	0.50	0.40
	Leu	59	.	.	.	B	.	.	C	-0.11	0.74	*	.	.	-0.40	0.33
	Ser	60	.	.	.	B	.	.	C	-1.01	0.51	*	.	.	-0.40	0.43
	Glu	61	.	.	B	B	.	.	.	-0.97	0.59	*	.	.	-0.60	0.20
	Phe	62	.	.	B	B	.	.	.	-0.54	0.94	.	.	.	-0.60	0.38
	Ile	63	.	.	B	B	.	.	.	-0.54	1.01	*	.	.	-0.60	0.44
	Val	64	.	.	B	B	.	.	.	-0.03	0.63	*	.	.	-0.60	0.44
30	Tyr	65	.	.	B	B	.	.	.	-0.43	1.01	.	.	.	-0.60	0.68
	Tyr	66	.	.	B	B	.	.	.	-0.74	1.01	*	.	.	-0.60	0.84
	Glu	67	.	.	.	B	T	.	.	-0.04	0.81	*	.	.	-0.05	1.63
	Ser	68	.	.	.	B	T	.	.	0.18	0.57	.	.	.	-0.05	1.68
35	Phe	69	.	.	.	.	T	T	.	0.72	0.39	*	.	.	0.50	0.57
	Thr	70	.	.	.	.	T	T	.	0.97	0.11	*	.	F	0.65	0.48
	Asn	71	.	.	.	.	.	T	C	0.61	0.11	.	.	F	0.45	0.62
	Cys	72	A	.	.	.	.	T	.	0.61	0.34	.	*	F	0.25	0.71
40	Thr	73	A	A	.	.	.	.	.	0.32	-0.44	.	*	F	0.45	0.85
	Glu	74	A	A	.	.	.	.	.	1.02	-0.43	*	*	.	0.30	0.53
	Met	75	A	A	.	.	.	.	.	0.48	-0.43	.	*	.	0.45	1.60
	Glu	76	A	A	.	.	.	.	.	-0.38	-0.36	.	*	.	0.30	0.82
	Ala	77	A	A	.	.	.	.	.	-0.06	-0.20	.	*	.	0.30	0.35

5	Asn	78	A	A	.	.	.	.	.	-0.41	0.23	.	*	.	-0.30	0.35
	Val	79	.	A	B	.	.	.	.	-0.66	0.19	.	*	.	-0.30	0.11
	Val	80	.	A	B	.	.	.	.	-0.34	0.94	.	*	.	-0.60	0.17
	Gly	81	.	A	B	.	.	.	.	-0.56	1.36	.	*	.	-0.60	0.11
	Cys	82	.	.	.	.	T	.	.	0.03	1.39	*	.	.	0.00	0.23
	Tyr	83	.	.	.	.	T	.	.	-0.18	1.14	*	.	.	0.00	0.50
	Trp	84	.	.	B	.	.	T	.	-0.13	0.93	.	.	.	-0.20	0.78
	Pro	85	.	.	.	.	.	T	C	0.13	1.19	*	.	F	0.30	1.20
10	Asn	86	.	.	.	.	.	T	C	0.48	1.11	*	.	F	0.15	0.77
	Pro	87	.	.	.	.	.	T	C	0.80	0.76	*	.	F	0.30	1.27
	Leu	88	.	.	.	.	.	.	C	0.34	0.27	*	.	F	0.25	0.81
	Ala	89	.	.	.	.	.	.	C	-0.26	0.63	*	.	F	-0.05	0.44
15	Gln	90	.	.	B	B	.	.	.	-0.36	0.91	*	.	.	-0.60	0.20
	Gly	91	.	.	B	B	.	.	.	-0.70	0.97	*	.	.	-0.60	0.35
	Phe	92	.	.	B	B	.	.	.	-1.38	0.71	*	.	.	-0.60	0.34
	Ile	93	.	.	B	B	.	.	.	-0.60	0.90	*	.	.	-0.60	0.14
	Thr	94	.	.	B	B	.	.	.	0.10	1.00	*	.	.	-0.60	0.19
20	Gly	95	.	.	B	B	.	.	.	0.10	0.57	*	.	.	-0.60	0.43
	Ile	96	.	.	B	B	.	.	.	-0.26	0.19	*	.	.	-0.15	1.06
	His	97	.	.	B	B	.	.	.	-0.26	0.29	*	.	.	-0.30	0.64
	Arg	98	.	.	.	B	T	.	.	0.33	0.59	*	.	.	-0.20	0.56
	Gln	99	.	.	.	B	T	.	.	0.64	0.54	*	.	.	-0.05	1.06
25	Phe	100	.	.	.	B	T	.	.	0.32	0.26	*	.	.	0.25	1.26
	Phe	101	.	.	.	.	T	T	.	0.90	0.33	*	.	.	0.50	0.34
	Ser	102	.	.	.	.	T	T	.	0.08	0.81	.	*	.	0.20	0.29
	Asn	103	.	.	.	.	T	T	.	-0.03	1.06	.	.	.	0.20	0.25
	Cys	104	.	.	.	.	T	T	.	0.08	0.27	.	*	.	0.50	0.47
30	Thr	105	.	.	.	.	T	.	.	-0.08	-0.51	.	.	.	1.20	0.69
	Val	106	.	A	.	.	T	.	.	0.59	-0.26	.	*	.	0.70	0.32
	Asp	107	.	A	B	.	.	.	.	0.08	-0.16	.	*	.	0.30	0.81
	Arg	108	.	A	B	.	.	.	.	0.08	-0.04	.	*	.	0.30	0.46
	Val	109	.	A	B	.	.	.	.	0.74	-0.53	.	*	.	0.75	1.08
35	His	110	.	A	B	.	.	.	.	0.84	-1.17	.	*	.	0.75	1.08
	Leu	111	.	A	.	.	.	.	C	1.49	-0.74	.	*	.	0.80	0.85
	Glu	112	.	A	.	.	.	.	C	1.49	-0.31	.	*	F	0.80	1.78
	Asp	113	.	A	.	.	.	.	C	1.38	-0.96	*	*	F	1.10	2.18
	Pro	114	.	.	.	.	.	T	C	1.38	-1.46	*	*	F	1.50	4.58
40	Pro	115	.	.	.	.	T	T	.	0.60	-1.50	*	.	F	1.70	1.96
	Asp	116	A	.	.	.	.	T	.	0.52	-0.81	*	.	F	1.15	0.97
	Glu	117	A	.	.	.	.	T	.	0.31	-0.13	*	*	.	0.70	0.44
	Val	118	A	.	.	B	.	.	.	-0.50	-0.13	*	.	.	0.30	0.44



	Leu	119	.	.	B	B	.	.	.	-1.18	0.13	.	.	.	-0.30	0.22
	Ile	120	.	.	B	B	.	.	.	-1.82	0.81	.	.	.	-0.60	0.09
	Pro	121	.	.	B	B	.	.	.	-2.71	1.46	.	.	.	-0.60	0.09
	Leu	122	.	.	B	B	.	.	.	-2.92	1.50	.	*	.	-0.60	0.07
5	Ile	123	.	.	B	B	.	.	.	-2.92	1.24	.	.	.	-0.60	0.16
	Val	124	.	.	B	B	.	.	.	-2.97	1.20	.	.	.	-0.60	0.08
	Ile	125	.	.	B	B	.	.	.	-2.89	1.41	.	.	.	-0.60	0.07
	Pro	126	.	.	B	B	.	.	.	-2.99	1.41	.	*	.	-0.60	0.08
	Val	127	.	.	B	B	.	.	.	-3.03	1.21	.	.	.	-0.60	0.16
10	Val	128	.	.	B	B	.	.	.	-2.73	1.21	.	*	.	-0.60	0.17
	Leu	129	.	.	B	B	.	.	.	-2.48	1.03	.	.	.	-0.60	0.11
	Thr	130	.	.	B	B	.	.	.	-2.18	1.21	.	*	.	-0.60	0.15
	Val	131	.	.	B	B	.	.	.	-2.31	1.07	.	.	.	-0.60	0.20
	Ala	132	A	.	.	B	.	.	.	-2.27	0.86	.	.	.	-0.60	0.25
15	Met	133	A	.	.	B	.	.	.	-2.27	0.86	.	.	.	-0.60	0.14
	Ala	134	A	.	.	B	.	.	.	-2.31	1.01	.	.	.	-0.60	0.14
	Gly	135	A	.	.	B	.	.	.	-2.29	1.01	*	*	.	-0.60	0.10
	Leu	136	A	.	.	B	.	.	.	-1.32	1.43	*	*	.	-0.60	0.11
	Val	137	A	.	.	B	.	.	.	-1.03	0.81	.	*	.	-0.60	0.21
20	Val	138	A	.	.	B	.	.	.	-0.39	0.70	*	.	.	-0.26	0.29
	Trp	139	.	.	B	B	.	.	.	0.31	0.27	*	.	.	0.38	0.70
	Arg	140	.	.	B	B	.	.	.	0.34	-0.41	.	.	F	1.62	1.84
	Ser	141	.	.	B	.	.	T	.	1.16	-0.57	.	.	F	2.66	3.58
	Lys	142	.	.	.	.	T	T	.	1.70	-1.21	.	*	F	3.40	5.68
25	Arg	143	.	.	.	.	T	T	.	1.74	-1.64	*	.	F	3.06	4.19
	Thr	144	.	.	.	.	T	T	.	1.22	-0.96	.	*	F	2.72	2.58
	Asp	145	.	A	.	.	T	.	.	0.72	-0.66	.	.	F	1.98	1.06
	Thr	146	.	A	B	.	.	.	.	0.63	-0.23	*	.	F	0.79	0.69
	Leu	147	.	A	B	.	.	.	.	0.20	0.20	*	.	.	-0.30	0.61
30	Leu	148	.	A	B	.	.	.	.	-0.30	0.14	.	*	.	-0.30	0.47
	Ter	149	.	A	B	.	.	.	.	-0.38	0.57	.	.	.	-0.60	0.42

Table IV

	Res Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
5	Met 1	A	A	.	.	.	.	.	-0.76	0.27	.	*	.	-0.30	0.49
	Arg 2	A	A	.	.	.	.	.	-1.07	0.34	*	*	.	-0.30	0.39
	Leu 3	A	A	.	.	.	.	.	-1.49	0.70	*	*	.	-0.60	0.26
	Leu 4	A	A	.	.	.	.	.	-1.40	0.96	.	*	.	-0.60	0.22
	Ala 5	A	A	.	.	.	.	.	-1.82	0.73	.	*	.	-0.60	0.15
10	Phe 6	A	A	.	.	.	.	.	-2.03	1.41	*	*	.	-0.60	0.15
	Leu 7	A	A	.	.	.	.	.	-2.73	1.41	.	*	.	-0.60	0.15
	Ser 8	A	A	.	.	.	.	.	-2.73	1.23	.	.	.	-0.60	0.15
	Leu 9	A	A	.	.	.	.	.	-2.78	1.41	.	.	.	-0.60	0.14
	Leu 10	A	A	.	.	.	.	.	-3.00	1.27	*	.	.	-0.60	0.13
15	Ala 11	A	A	.	.	.	.	.	-2.30	1.27	*	.	.	-0.60	0.08
	Leu 12	A	A	.	.	.	.	.	-1.49	1.29	.	.	.	-0.60	0.17
	Val 13	A	A	.	.	.	.	.	-1.50	0.60	.	.	.	-0.60	0.35
	Leu 14	A	A	.	.	.	.	.	-1.03	0.40	.	.	.	-0.02	0.50
	Gln 15	A	A	B	.	.	.	.	-0.53	0.33	.	.	F	0.41	0.60
20	Glu 16	A	.	.	.	.	T	.	-0.53	0.13	.	.	F	1.24	1.17
	Thr 17	A	.	.	.	.	T	.	-0.02	-0.01	.	*	F	2.12	1.43
	Gly 18	.	.	.	.	T	T	.	0.02	-0.31	.	.	F	2.80	1.11
	Thr 19	A	.	.	.	.	T	.	0.62	-0.03	*	*	F	1.97	0.53
	Ala 20	A	.	.	.	.	.	.	0.73	0.40	.	.	F	0.89	0.57
25	Ser 21	.	.	.	.	.	.	C	0.78	-0.09	.	.	F	1.56	1.12
	Leu 22	.	A	.	.	.	.	C	1.09	-0.51	*	.	F	1.38	1.55
	Pro 23	A	A	.	.	.	.	.	1.54	-1.00	*	.	F	0.90	2.66
	Arg 24	A	A	.	.	.	.	.	1.90	-1.50	*	*	F	0.90	3.88
	Lys 25	A	A	.	.	.	.	.	2.60	-1.89	.	.	F	0.90	9.42
30	Glu 26	A	A	.	.	.	.	.	3.01	-2.57	.	.	F	0.90	11.93
	Arg 27	A	A	.	.	.	.	.	3.82	-3.00	.	.	F	0.90	11.93
	Lys 28	A	A	.	.	.	.	.	4.03	-3.00	.	.	F	0.90	10.33
	Arg 29	A	A	.	.	.	.	.	3.92	-3.00	.	.	F	0.90	10.33
	Arg 30	A	A	.	.	.	.	.	3.28	-2.60	.	*	F	0.90	9.13
35	Glu 31	A	A	.	.	.	.	.	3.07	-1.99	*	.	F	0.90	4.52
	Glu 32	A	A	.	.	.	.	.	3.07	-1.56	.	.	F	1.24	3.57
	Gln 33	A	A	.	.	.	.	.	3.02	-1.56	*	.	F	1.58	3.57
	Met 34	.	A	.	.	.	.	C	2.57	-1.56	*	.	F	2.12	3.57
	Pro 35	A	.	.	.	.	T	.	2.46	-1.13	*	.	F	2.66	2.04
40	Arg 36	.	.	.	.	T	T	.	2.16	-1.13	*	.	F	3.40	1.97

	Glu	37	A	.	.	.	.	T	.	1.46	-1.14	*	.	F	2.66	2.66
	Gly	38	.	.	.	.	.	T	T	1.46	-0.97	*	*	F	2.72	1.49
	Asp	39	A	.	.	.	.	.	.	1.20	-1.40	*	.	F	1.78	1.32
	Ser	40	A	.	.	.	.	.	.	0.60	-0.76	*	.	F	1.29	0.57
5	Phe	41	.	.	B	.	.	.	.	0.28	-0.07	.	.	.	0.50	0.47
	Glu	42	.	.	B	.	.	.	.	-0.53	-0.07	.	.	.	0.50	0.44
	Val	43	.	.	B	.	.	.	.	-0.08	0.61	.	.	.	-0.40	0.27
	Leu	44	.	.	B	.	.	.	.	-0.08	0.23	.	*	.	-0.10	0.61
	Pro	45	A	.	.	.	.	.	.	0.22	-0.16	.	*	.	0.50	0.56
10	Leu	46	A	.	.	.	.	T	.	0.07	-0.16	.	*	.	0.85	1.27
	Arg	47	A	.	.	.	.	T	.	-0.74	-0.16	.	*	F	1.00	1.14
	Asn	48	.	.	B	.	T	T	.	0.11	-0.16	.	*	F	1.25	0.61
	Asp	49	.	.	B	.	.	T	.	0.71	-0.19	.	*	F	1.00	1.19
	Val	50	.	.	B	.	.	.	.	0.92	-0.44	.	*	F	0.65	0.94
15	Leu	51	.	.	B	.	.	.	.	1.73	-0.44	.	*	F	0.95	0.97
	Asn	52	.	.	B	.	.	T	.	1.38	-0.44	.	.	F	1.45	0.94
	Pro	53	.	.	.	.	.	T	C	1.03	0.31	.	.	F	1.50	1.98
	Asp	54	.	.	.	.	T	T	.	1.03	0.10	.	*	F	2.00	2.37
	Asn	55	.	.	.	.	.	T	C	1.03	-0.59	.	.	F	3.00	2.56
20	Tyr	56	.	.	B	B	.	.	.	0.96	-0.34	.	*	F	1.80	1.23
	Gly	57	.	.	B	B	.	.	.	0.96	-0.09	.	.	.	1.20	0.52
	Glu	58	.	.	B	B	.	.	.	0.36	-0.09	*	.	.	0.90	0.53
	Val	59	.	.	B	B	.	.	.	0.06	0.20	*	.	.	0.00	0.28
	Ile	60	.	.	B	B	.	.	.	0.06	-0.17	.	.	.	0.30	0.38
25	Asp	61	.	.	B	B	.	.	.	0.06	-0.20	.	.	.	0.30	0.35
	Leu	62	.	.	B	.	.	T	.	0.40	0.56	.	.	.	-0.20	0.75
	Ser	63	.	.	.	.	.	T	C	0.40	-0.09	.	.	.	1.05	1.85
	Asn	64	.	.	.	.	.	T	C	0.44	-0.77	.	.	F	1.50	1.91
	Tyr	65	A	.	.	.	.	T	.	1.02	-0.09	.	*	F	1.34	1.91
30	Glu	66	A	.	.	.	.	.	.	1.02	-0.29	.	.	F	1.48	2.06
	Glu	67	A	.	.	.	.	.	.	1.59	-0.67	*	.	F	2.12	2.14
	Leu	68	.	.	B	.	.	.	.	1.54	-0.31	*	.	F	2.16	2.14
	Thr	69	.	.	.	.	T	T	.	1.54	-0.64	*	.	F	3.40	1.22
	Asp	70	.	.	.	.	T	T	.	1.79	-0.64	*	.	F	3.06	1.18
35	Tyr	71	.	.	.	.	T	T	.	0.98	-0.24	*	.	F	2.42	2.48
	Gly	72	.	.	.	.	T	T	.	0.77	-0.24	*	.	F	2.08	1.42
	Asp	73	A	.	.	.	.	.	.	1.58	-0.30	*	.	F	1.23	1.31
	Gln	74	A	.	.	.	.	.	.	1.03	-0.30	*	*	F	0.98	1.45
	Leu	75	.	.	B	.	.	.	.	1.08	-0.41	.	*	F	1.07	1.09
40	Pro	76	.	.	B	.	.	.	.	0.47	-0.84	.	*	F	1.46	1.30
	Glu	77	.	.	B	B	.	.	.	0.50	-0.20	.	*	F	0.90	0.56

	Val	78	.	.	B	B	.	.	.	0.20	-0.11	.	*	F	0.81	0.98
	Lys	79	.	.	B	B	.	.	.	-0.61	-0.41	.	*	F	0.72	0.85
	Val	80	.	.	B	B	.	.	.	-0.39	-0.16	.	*	F	0.63	0.40
	Thr	81	.	.	B	B	.	.	.	-0.39	0.34	.	*	F	-0.06	0.55
5	Ser	82	.	.	B	.	.	.	.	-0.98	0.13	.	*	F	0.05	0.42
	Leu	83	.	.	B	.	.	.	.	-0.43	0.63	.	*	.	-0.40	0.58
	Ala	84	.	.	B	.	.	.	.	-0.78	0.47	.	*	.	-0.40	0.58
	Pro	85	A	.	.	.	.	.	.	-0.81	0.37	.	.	.	-0.10	0.58
	Ala	86	.	.	B	B	.	.	.	-0.80	0.67	.	.	F	-0.45	0.49
10	Thr	87	.	.	B	B	.	.	.	-0.71	0.37	.	.	F	-0.15	0.65
	Ser	88	.	.	B	B	.	.	.	-0.49	0.30	.	.	F	0.13	0.65
	Ile	89	.	.	B	B	.	.	.	0.14	0.37	.	.	F	0.41	0.65
	Ser	90	.	.	B	.	.	T	.	0.06	-0.13	.	.	F	1.69	0.90
	Pro	91	.	.	.	.	.	T	C	0.33	-0.23	.	.	F	2.17	0.90
15	Ala	92	.	.	.	.	T	T	.	0.33	-0.13	.	.	F	2.80	1.86
	Lys	93	.	.	B	.	.	T	.	0.04	-0.33	.	.	F	2.12	2.00
	Ser	94	.	.	B	.	.	.	.	0.72	-0.21	.	.	F	1.64	1.31
	Thr	95	.	.	B	.	.	.	.	0.68	-0.21	.	.	F	1.36	2.00
	Thr	96	.	.	B	.	.	.	.	0.58	-0.29	.	.	F	0.93	0.99
20	Ala	97	.	.	B	.	.	.	.	0.96	0.20	.	.	F	0.20	1.07
	Pro	98	.	.	B	.	.	.	.	0.61	0.24	.	.	F	0.48	1.14
	Gly	99	.	.	.	.	T	.	.	0.61	0.14	.	.	F	1.16	1.06
	Thr	100	.	.	.	.	.	T	C	0.92	0.04	.	.	F	1.44	1.41
	Pro	101	.	.	.	.	.	T	C	1.02	-0.06	.	.	F	2.32	1.46
25	Ser	102	.	.	.	.	T	T	.	1.30	-0.06	.	.	F	2.80	2.28
	Ser	103	.	.	.	.	.	T	C	0.91	0.00	.	.	F	2.32	2.28
	Asn	104	.	.	.	.	.	T	C	0.94	0.13	.	.	F	1.44	1.46
	Pro	105	.	.	.	.	.	T	C	1.37	0.19	.	.	F	1.36	1.57
	Thr	106	.	.	.	.	T	T	.	1.37	-0.20	.	.	F	2.08	2.30
30	Met	107	.	.	B	.	.	T	.	1.36	-0.16	.	.	F	1.60	2.21
	Thr	108	.	.	B	.	.	.	.	1.34	-0.07	.	.	F	1.60	2.07
	Arg	109	.	.	B	.	.	T	.	0.76	-0.01	.	.	F	2.00	2.07
	Pro	110	.	.	B	.	.	T	.	0.62	0.00	*	.	F	1.80	2.11
	Thr	111	.	.	B	.	.	T	.	0.12	-0.19	.	.	F	1.60	1.45
35	Thr	112	.	.	B	.	.	T	.	-0.09	0.01	.	.	F	0.65	0.61
	Ala	113	.	A	B	.	.	.	.	-0.59	0.70	.	.	F	-0.25	0.32
	Gly	114	.	A	B	.	.	.	.	-1.00	0.96	.	.	.	-0.60	0.19
	Leu	115	.	A	B	.	.	.	.	-1.09	0.86	.	.	.	-0.60	0.17
	Leu	116	.	A	B	.	.	.	.	-0.78	0.76	.	.	.	-0.60	0.23
40	Leu	117	.	A	B	.	.	.	.	-0.68	0.66	.	*	F	-0.45	0.40
	Ser	118	.	A	B	.	.	.	.	-0.09	0.66	.	.	F	-0.29	0.75

5	Ser	119	.	.	B	.	.	.	0.22	0.37	.	.	F	0.52	1.46	
	Gln	120	.	.	B	.	.	T	0.69	0.19	.	.	F	0.88	2.41	
	Pro	121	.	.	.	.	T	T	0.69	-0.07	.	.	F	2.04	1.78	
	Asn	122	.	.	.	.	T	T	1.29	0.23	.	*	F	1.60	1.10	
	His	123	.	.	.	.	T	T	1.28	0.27	.	.	F	1.29	0.98	
	Gly	124	.	.	.	.	T	.	0.91	0.36	.	.	.	0.78	0.91	
	Leu	125	.	.	.	.	.	T	C	0.10	0.50	.	.	.	0.32	0.30
	Pro	126	.	.	.	.	T	T	.	-0.54	0.79	.	.	.	0.36	0.18
10	Thr	127	.	.	.	.	T	T	.	-1.21	0.93	.	.	.	0.20	0.14
	Cys	128	.	.	B	.	.	T	.	-2.03	1.07	.	.	.	-0.20	0.09
	Leu	129	.	.	B	B	.	.	.	-2.36	1.03	.	.	.	-0.60	0.04
	Val	130	.	.	B	B	.	.	.	-2.36	1.17	.	.	.	-0.60	0.02
15	Cys	131	.	.	B	B	.	.	.	-2.49	1.37	.	.	.	-0.60	0.02
	Val	132	.	.	B	B	.	.	.	-2.48	1.23	.	.	.	-0.60	0.03
	Cys	133	.	.	B	B	.	.	.	-2.11	0.93	.	.	.	-0.60	0.05
	Leu	134	.	.	B	B	.	.	.	-2.16	0.67	.	.	.	-0.60	0.13
20	Gly	135	.	.	.	.	T	T	.	-1.54	0.74	.	*	F	0.35	0.13
	Ser	136	.	.	.	.	T	T	.	-1.54	0.86	.	*	F	0.35	0.39
	Ser	137	.	.	B	.	.	T	.	-0.69	0.86	.	.	F	-0.05	0.25
	Val	138	.	.	B	.	.	T	.	-0.02	0.17	.	.	.	0.10	0.43
	Tyr	139	.	.	B	.	.	.	.	-0.10	-0.26	.	.	.	0.50	0.53
	Cys	140	.	.	B	.	.	T	.	0.24	0.04	.	*	.	0.10	0.28
	Asp	141	.	.	B	.	.	T	.	-0.27	-0.34	.	*	.	0.70	0.63
	Asp	142	.	.	B	.	.	T	.	0.03	-0.30	.	*	F	0.85	0.33
25	Ile	143	.	.	B	.	.	T	.	0.89	-1.06	.	.	F	1.30	1.07
	Asp	144	.	A	B	.	.	.	.	0.24	-1.63	.	.	F	0.90	1.07
	Leu	145	.	A	B	.	.	.	.	0.70	-0.94	.	.	F	0.75	0.45
	Glu	146	.	A	B	.	.	.	.	0.49	-0.51	.	*	F	0.75	0.99
30	Asp	147	.	A	B	.	.	.	.	-0.32	-0.77	.	*	F	0.99	0.92
	Ile	148	.	A	B	.	.	.	.	0.36	-0.09	*	*	F	0.93	0.92
	Pro	149	.	.	.	.	.	.	C	0.47	-0.34	*	.	F	1.57	0.82
	Pro	150	.	.	.	.	.	.	C	1.39	-0.34	*	.	F	1.81	0.96
35	Leu	151	.	.	.	.	.	T	C	1.08	-0.34	*	.	F	2.40	2.68
	Pro	152	.	.	B	.	.	T	.	0.49	-0.54	*	.	F	2.26	2.50
	Arg	153	.	.	.	.	T	T	.	1.13	-0.47	*	.	F	2.12	1.63
	Arg	154	.	.	B	.	.	T	.	0.53	-0.14	*	.	F	1.48	3.11
40	Thr	155	.	.	B	B	.	.	.	0.50	-0.14	*	.	.	0.69	1.66
	Ala	156	.	.	B	B	.	.	.	0.72	0.19	*	*	.	-0.15	1.33
	Tyr	157	.	.	B	B	.	.	.	1.04	0.69	*	*	.	-0.60	0.68
	Leu	158	.	.	B	B	.	.	.	0.23	0.69	*	*	.	-0.60	0.93
	Tyr	159	.	.	B	B	.	.	.	0.12	0.99	*	*	.	-0.60	0.80

	Ala	160	.	.	B	B	.	.	.	0.54	0.89	*	*	.	-0.60	0.82
	Arg	161	.	.	B	B	.	.	.	0.24	0.13	*	*	.	-0.15	1.94
	Phe	162	.	.	B	B	.	.	.	0.19	0.13	*	*	.	-0.30	0.87
	Asn	163	.	.	B	B	.	.	.	1.11	-0.24	*	*	.	0.45	1.15
5	Arg	164	.	.	B	B	.	.	.	0.47	-0.74	.	*	F	1.08	1.15
	Ile	165	.	.	B	B	.	.	.	1.17	-0.06	.	*	F	0.81	0.93
	Ser	166	.	.	.	B	.	.	C	0.47	-0.84	*	*	F	1.64	1.13
	Arg	167	.	.	B	B	.	.	.	1.17	-0.74	*	*	F	1.47	0.59
	Ile	168	.	.	B	B	.	.	.	1.17	-0.74	*	*	F	1.80	1.45
10	Arg	169	.	.	B	B	.	.	.	0.36	-1.43	*	.	.	1.47	1.80
	Ala	170	A	A	.	.	.	.	.	1.29	-1.03	*	*	F	1.29	0.80
	Glu	171	A	A	.	.	.	.	.	1.24	-1.03	.	*	F	1.26	2.27
	Asp	172	A	A	.	.	.	.	.	0.32	-1.29	.	*	F	1.08	1.15
	Phe	173	A	A	.	.	.	.	.	0.90	-0.60	.	*	F	0.75	0.94
15	Lys	174	A	A	.	.	.	.	.	0.83	-0.61	.	*	F	0.75	0.78
	Gly	175	A	A	.	.	.	.	.	0.61	-0.61	*	*	F	0.75	0.94
	Leu	176	A	A	.	.	.	.	.	0.66	0.07	*	*	F	-0.15	0.89
	Thr	177	A	A	.	.	.	.	.	0.77	-0.71	*	*	F	0.75	0.89
	Lys	178	A	A	.	.	.	.	.	0.58	-0.71	*	*	F	0.90	1.76
20	Leu	179	A	A	.	.	.	.	.	0.53	-0.46	*	*	F	0.60	1.50
	Lys	180	.	A	B	.	.	.	.	0.07	-1.14	*	*	F	0.90	1.73
	Arg	181	.	A	B	.	.	.	.	0.58	-0.94	*	*	F	0.75	0.71
	Ile	182	.	A	B	.	.	.	.	0.89	-0.56	.	*	F	0.90	1.16
	Asp	183	.	A	B	.	.	.	.	0.84	-0.84	.	*	.	0.60	0.93
25	Leu	184	.	.	B	.	.	T	.	0.84	-0.44	*	*	F	0.85	0.77
	Ser	185	.	.	B	.	.	T	.	-0.09	0.24	*	*	F	0.25	0.90
	Asn	186	.	.	.	.	.	T	C	-0.50	0.24	.	*	F	0.45	0.38
	Asn	187	.	.	.	.	.	T	C	0.09	0.63	*	*	F	0.15	0.62
	Leu	188	.	.	B	.	.	.	.	-0.80	0.33	*	*	.	-0.10	0.62
30	Ile	189	.	.	B	.	.	.	.	0.01	0.63	*	.	.	-0.40	0.27
	Ser	190	.	.	B	.	.	.	.	0.31	0.23	*	.	F	0.05	0.28
	Ser	191	.	.	B	.	.	.	.	0.31	0.23	*	*	F	0.05	0.54
	Ile	192	.	.	B	.	.	.	.	-0.28	-0.46	*	.	F	0.80	1.29
	Asp	193	.	.	B	.	.	T	.	-0.17	-0.64	*	.	F	1.15	0.98
35	Asn	194	A	.	.	.	.	T	.	0.83	-0.24	*	*	F	0.85	0.63
	Asp	195	A	.	.	.	.	T	.	0.32	-0.63	*	.	F	1.30	1.76
	Ala	196	A	.	.	.	.	T	.	-0.19	-0.63	*	.	.	1.00	0.87
	Phe	197	A	A	.	.	.	.	.	0.67	0.06	*	.	.	-0.30	0.45
	Arg	198	A	A	.	.	.	.	.	0.08	0.16	*	.	.	-0.30	0.36
40	Leu	199	A	A	.	.	.	.	.	-0.73	0.66	*	*	.	-0.60	0.36
	Leu	200	A	A	.	.	.	.	.	-0.73	0.84	*	.	.	-0.60	0.35

	His	201	A	A	.	.	.	.	-0.14	0.46	*	*	.	-0.60	0.31
	Ala	202	A	A	.	.	.	.	-0.26	0.46	*	*	.	-0.60	0.62
	Leu	203	A	A	.	.	.	.	-1.26	0.46	*	*	.	-0.60	0.62
	Gln	204	A	A	.	.	.	.	-1.26	0.46	*	.	.	-0.60	0.32
5	Asp	205	.	A	B	.	.	.	-0.66	0.64	.	.	.	-0.60	0.26
	Leu	206	.	A	B	.	.	.	-0.62	0.57	.	.	.	-0.60	0.49
	Ile	207	.	A	B	.	.	.	-0.03	-0.11	.	.	.	0.30	0.49
	Leu	208	.	.	B	.	.	T	0.78	-0.11	*	.	F	0.85	0.47
	Pro	209	A	.	.	.	.	T	-0.03	0.29	.	.	F	0.25	0.99
10	Glu	210	A	.	.	.	.	T	-0.03	0.29	.	*	F	0.40	1.16
	Asn	211	A	.	.	.	.	T	0.19	-0.40	.	.	F	1.00	2.44
	Gln	212	A	A	.	.	.	.	0.27	-0.59	.	*	F	0.90	1.60
	Leu	213	A	A	.	.	.	.	0.87	-0.33	.	.	.	0.30	0.76
	Glu	214	A	A	.	.	.	.	0.22	0.10	.	.	.	-0.30	0.73
15	Ala	215	.	A	B	.	.	.	-0.59	0.34	.	.	.	-0.30	0.31
	Leu	216	.	A	B	.	.	.	-0.80	0.63	.	.	.	-0.60	0.31
	Pro	217	.	.	B	.	.	.	-1.10	0.37	.	.	.	-0.10	0.28
	Val	218	.	.	B	.	.	.	-0.63	0.76	*	.	.	-0.40	0.37
	Leu	219	.	.	B	.	.	T	-1.52	0.69	*	.	F	-0.05	0.44
20	Pro	220	.	.	.	.	.	T	-0.93	0.69	*	*	F	0.15	0.20
	Ser	221	.	.	.	.	.	T	-0.82	0.26	*	.	F	0.45	0.47
	Gly	222	.	.	B	.	.	T	-1.42	0.40	*	.	F	0.25	0.49
	Ile	223	.	A	B	.	.	.	-0.57	0.40	*	.	F	-0.15	0.26
	Glu	224	.	A	B	.	.	.	-0.61	-0.03	.	*	.	0.30	0.33
25	Phe	225	.	A	B	.	.	.	-0.29	0.23	.	*	.	-0.30	0.25
	Leu	226	.	A	B	.	.	.	-0.80	-0.20	.	*	.	0.30	0.69
	Asp	227	A	A	.	.	.	.	-0.46	-0.20	*	*	.	0.30	0.33
	Val	228	A	A	.	.	.	.	0.54	0.20	*	.	.	-0.30	0.61
	Arg	229	A	A	.	.	.	.	-0.27	-0.59	.	*	.	0.75	1.45
30	Leu	230	A	A	.	.	.	.	0.43	-0.59	.	*	.	0.88	0.71
	Asn	231	A	A	.	.	.	.	0.94	-0.19	*	*	.	1.01	1.67
	Arg	232	.	A	.	.	T	.	0.64	-0.44	*	*	F	1.84	1.14
	Leu	233	.	A	.	.	T	.	1.16	-0.06	*	.	F	2.12	1.85
	Gln	234	.	.	.	.	T	T	0.16	-0.31	*	.	F	2.80	1.14
35	Ser	235	.	.	.	.	T	T	0.97	-0.03	*	.	F	2.37	0.41
	Ser	236	.	.	.	.	.	T	0.76	0.37	*	*	F	1.29	0.86
	Gly	237	.	.	.	.	T	T	0.06	0.11	*	*	F	1.21	0.76
	Ile	238	.	A	B	.	.	.	0.28	0.21	.	.	F	0.13	0.58
	Gln	239	.	A	B	.	.	.	-0.42	0.33	.	.	F	-0.15	0.43
40	Pro	240	.	A	B	.	.	.	-0.01	0.73	*	*	F	-0.45	0.38
	Ala	241	A	A	.	.	.	.	-0.30	0.30	*	*	.	-0.15	1.06

	Ala	242	A	A	.	.	.	.	.	-0.56	0.11	*	.	.	-0.30	0.62
	Phe	243	A	A	.	.	.	.	.	0.33	0.33	*	*	.	-0.30	0.40
	Arg	244	A	A	.	.	.	.	.	0.38	-0.10	*	*	.	0.30	0.68
	Ala	245	A	A	.	.	.	.	.	-0.22	-0.60	*	*	.	0.75	1.35
5	Met	246	A	A	.	.	.	.	.	0.37	-0.41	*	*	.	0.45	1.28
	Glu	247	A	A	.	.	.	.	.	0.26	-0.80	*	*	.	0.75	1.13
	Lys	248	A	A	.	.	.	.	.	0.14	-0.01	*	*	.	0.30	0.97
	Leu	249	A	A	.	.	.	.	.	-0.21	0.17	*	*	.	-0.30	0.81
	Gln	250	A	A	.	.	.	.	.	-0.43	0.31	.	.	.	-0.30	0.73
10	Phe	251	A	A	.	.	.	.	.	-0.13	1.00	.	.	.	-0.60	0.30
	Leu	252	.	A	B	.	.	.	.	-0.13	1.39	.	*	.	-0.60	0.49
	Tyr	253	.	.	B	.	.	.	.	-0.18	0.70	.	*	.	-0.40	0.47
	Leu	254	.	.	B	.	.	.	.	-0.18	0.70	*	.	.	-0.23	0.88
	Ser	255	.	.	B	.	.	T	.	-0.99	0.60	*	.	.	0.14	0.88
15	Asp	256	.	.	.	.	T	T	.	-0.29	0.60	*	.	.	0.71	0.46
	Asn	257	.	.	.	.	T	T	.	0.22	-0.16	*	.	F	1.93	0.94
	Leu	258	.	.	B	.	.	T	.	-0.42	-0.46	*	.	F	1.70	0.94
	Leu	259	.	.	B	.	.	.	.	0.18	-0.16	*	.	F	1.33	0.39
	Asp	260	.	.	B	.	.	.	.	0.13	0.27	*	.	F	0.56	0.38
20	Ser	261	.	.	B	.	.	.	.	-0.08	0.30	*	.	F	0.39	0.45
	Ile	262	.	.	B	.	.	T	.	-0.89	0.04	*	.	F	0.42	0.85
	Pro	263	.	.	B	.	.	T	.	-0.29	0.04	*	.	F	0.25	0.42
	Gly	264	.	.	.	.	.	T	C	0.31	0.47	*	.	F	0.15	0.48
	Pro	265	.	.	.	.	.	T	C	0.01	0.51	.	*	F	0.30	1.07
25	Leu	266	.	.	.	.	.	.	C	-0.50	0.21	*	*	F	0.42	0.93
	Pro	267	.	.	.	.	.	T	C	0.50	0.47	*	*	F	0.49	0.77
	Pro	268	.	.	.	.	T	T	.	0.41	0.04	*	*	F	1.16	0.98
	Ser	269	.	.	B	.	.	T	.	-0.10	0.00	*	*	F	1.68	1.59
	Leu	270	.	.	B	.	.	T	.	0.08	-0.04	*	*	F	1.70	0.76
30	Arg	271	.	.	B	.	.	.	.	0.08	0.03	*	*	F	0.73	0.67
	Ser	272	.	.	B	.	.	.	.	0.29	0.29	.	.	.	0.41	0.41
	Val	273	.	.	B	.	.	.	.	0.50	0.30	.	*	.	0.24	0.87
	His	274	.	.	B	.	.	.	.	0.80	0.01	.	*	.	0.07	0.71
	Leu	275	.	.	B	.	.	T	.	0.80	0.41	*	.	.	-0.20	0.86
35	Gln	276	.	.	.	.	.	T	C	-0.20	0.71	*	.	F	0.15	0.95
	Asn	277	.	.	.	.	.	T	C	0.10	0.76	.	*	F	0.15	0.49
	Asn	278	.	.	.	.	.	T	C	0.64	0.26	*	*	F	0.60	1.03
	Leu	279	A	A	.	.	.	.	.	0.08	0.06	*	.	.	-0.30	0.86
	Ile	280	A	A	.	.	.	.	.	0.89	0.27	*	*	.	-0.30	0.53
40	Glu	281	.	A	B	.	.	.	.	1.00	0.27	*	.	.	-0.30	0.57
	Thr	282	A	A	.	.	.	.	.	1.00	-0.13	*	.	.	0.45	1.35



	Met	283	.	A	B	.	.	.	.	0.14	-0.81	*	.	F	0.90	3.21
	Gln	284	.	A	B	.	.	.	.	0.26	-0.86	*	.	F	0.90	1.38
	Arg	285	.	A	B	.	.	.	.	0.48	-0.07	*	.	F	0.45	0.83
	Asp	286	.	A	.	.	T	.	.	0.48	0.01	*	.	.	0.10	0.45
5	Val	287	.	A	B	.	.	.	.	0.58	-0.60	*	.	.	0.60	0.43
	Phe	288	A	A	.	.	.	.	.	1.18	-0.57	*	.	.	0.60	0.34
	Cys	289	A	A	.	.	.	.	.	1.18	-0.57	*	.	.	0.60	0.35
	Asp	290	A	A	.	.	.	.	.	1.03	-0.57	*	.	F	0.75	0.82
	Pro	291	A	A	.	.	.	.	.	1.08	-0.71	.	.	F	0.90	1.30
10	Glu	292	A	A	.	.	.	.	.	1.90	-1.50	.	.	F	0.90	4.83
	Glu	293	A	A	.	.	.	.	.	2.29	-1.57	.	.	F	0.90	3.94
	His	294	A	A	.	.	.	.	.	3.07	-1.09	*	.	F	0.90	3.67
	Lys	295	A	A	.	.	.	.	.	3.18	-1.51	.	.	F	0.90	4.16
	His	296	A	A	.	.	.	.	.	3.39	-1.51	*	.	F	0.90	4.70
15	Thr	297	A	A	.	.	.	.	.	2.58	-1.11	*	.	F	0.90	5.98
	Arg	298	A	A	.	.	.	.	.	2.58	-0.93	*	.	F	0.90	2.47
	Arg	299	A	A	.	.	.	.	.	2.61	-0.93	*	.	F	0.90	3.14
	Gln	300	A	A	.	.	.	.	.	1.68	-1.43	*	*	F	0.90	3.63
	Leu	301	A	A	.	.	.	.	.	1.82	-1.23	*	*	F	0.90	1.30
20	Glu	302	.	A	B	.	.	.	.	1.32	-1.23	*	*	F	0.90	1.30
	Asp	303	.	A	B	.	.	.	.	1.21	-0.54	*	*	F	0.75	0.62
	Ile	304	.	A	B	.	.	.	.	0.76	-0.94	*	*	F	1.11	1.25
	Arg	305	.	A	B	.	.	.	.	0.76	-1.20	.	*	F	1.17	0.72
	Leu	306	.	A	B	.	.	.	.	1.36	-0.80	*	*	F	1.38	0.69
25	Asp	307	.	.	.	.	T	T	.	0.47	-0.37	*	*	F	2.24	1.52
	Gly	308	.	.	.	.	.	T	C	0.47	-0.37	.	*	F	2.10	0.54
	Asn	309	.	.	.	.	.	T	C	0.54	0.03	*	*	F	1.44	1.06
	Pro	310	.	.	.	.	.	T	C	0.13	0.03	*	*	F	1.08	0.52
	Ile	311	.	.	B	.	.	.	.	0.13	0.41	.	.	F	0.17	0.71
30	Asn	312	.	.	B	.	.	.	.	-0.57	0.67	.	.	.	-0.19	0.36
	Leu	313	.	.	B	.	.	.	.	-0.43	1.06	.	*	.	-0.40	0.20
	Ser	314	.	.	B	.	.	.	.	-0.73	1.06	.	*	.	-0.40	0.45
	Leu	315	.	.	B	.	.	.	.	-1.11	0.76	.	*	.	-0.40	0.37
	Phe	316	.	.	B	.	.	T	.	-0.47	0.86	.	*	.	-0.20	0.46
35	Pro	317	.	.	.	.	T	T	.	-1.17	0.93	.	*	.	0.20	0.54
	Ser	318	.	.	.	.	T	T	.	-1.02	1.33	.	*	.	0.20	0.56
	Ala	319	.	.	B	.	.	T	.	-1.53	1.21	.	.	.	-0.20	0.35
	Tyr	320	.	.	B	.	.	.	.	-0.93	1.11	*	.	.	-0.40	0.19
	Phe	321	.	.	B	.	.	.	.	-0.12	1.11	*	.	.	-0.40	0.21
40	Cys	322	.	.	B	.	.	.	.	-0.72	0.73	*	.	.	-0.40	0.42
	Leu	323	.	.	B	.	.	.	.	-0.63	0.91	.	*	.	-0.40	0.22

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	Pro	324	.	.	B	.	.	.	-0.93	0.59	.	*	.	-0.40	0.39
	Arg	325	.	.	B	B	.	.	-1.03	0.49	.	.	.	-0.60	0.51
	Leu	326	.	.	B	B	.	.	-0.22	0.34	.	.	.	-0.30	0.61
	Pro	327	.	.	.	B	T	.	-0.26	-0.34	.	*	.	0.70	0.78
5	Ile	328	.	.	.	B	T	.	0.24	0.01	.	.	.	0.10	0.34
	Gly	329	.	.	B	B	.	.	0.07	0.50	.	*	F	-0.60	0.60
	Arg	330	.	.	B	B	.	.	-0.43	0.24	.	*	F	-0.15	0.50
	Phe	331	.	.	B	B	.	.	-0.01	0.24	*	.	.	-0.30	0.91
	Thr	332	.	.	B	B	.	.	-0.19	-0.01	*	*	.	0.45	1.17
10	Ter	333	.	.	B	B	.	.	0.31	-0.01	*	*	.	0.30	0.76

Table V

	Res Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
5	Met 1	.	A	B	.	.	.	.	-1.30	0.70	.	.	.	-0.60	0.39
	Leu 2	.	A	B	.	.	.	.	-1.72	0.96	.	.	.	-0.60	0.25
	Leu 3	.	A	B	.	.	.	.	-2.14	1.21	.	.	.	-0.60	0.16
	Pro 4	.	A	B	.	.	.	.	-2.06	1.47	.	.	.	-0.60	0.14
	Leu 5	.	A	B	.	.	.	.	-1.97	1.24	*	.	.	-0.60	0.22
10	Leu 6	.	A	B	.	.	.	.	-2.18	0.94	.	.	.	-0.60	0.36
	Leu 7	.	A	B	.	.	.	.	-2.18	0.94	.	.	.	-0.60	0.19
	Ser 8	.	A	B	.	.	.	.	-1.71	1.20	*	.	.	-0.60	0.19
	Ser 9	.	.	B	B	.	.	.	-1.84	0.94	.	.	F	-0.45	0.23
	Leu 10	.	.	B	B	.	.	.	-1.33	0.69	.	.	F	-0.45	0.27
15	Leu 11	.	.	.	B	.	.	C	-0.52	0.39	*	.	F	0.05	0.27
	Gly 12	.	.	.	.	.	T	C	-0.30	0.40	.	.	F	0.45	0.35
	Gly 13	.	.	.	.	.	T	C	-0.60	0.51	.	.	F	0.15	0.43
	Ser 14	.	.	B	.	.	T	.	-0.30	0.44	.	.	F	0.12	0.52
	Gln 15	.	.	B	.	.	T	.	0.17	-0.24	.	*	F	1.19	0.88
20	Ala 16	.	.	B	.	.	.	.	1.09	-0.24	.	*	F	1.16	0.88
	Met 17	.	.	B	.	.	T	.	0.73	-0.67	.	*	F	1.98	1.28
	Asp 18	.	.	B	.	.	T	.	0.79	-0.27	.	*	F	1.70	0.64
	Gly 19	.	.	.	.	T	T	.	0.20	0.24	*	*	F	1.33	0.67
	Arg 20	.	.	.	.	T	T	.	0.31	0.43	*	*	.	0.71	0.47
25	Phe 21	.	.	B	B	.	.	.	0.04	-0.19	*	*	.	0.64	0.56
	Trp 22	.	.	B	B	.	.	.	0.64	0.46	*	*	.	-0.43	0.42
	Ile 23	.	.	B	B	.	.	.	0.64	0.43	*	*	.	-0.60	0.37
	Arg 24	.	.	B	B	.	.	.	0.69	0.43	*	*	.	-0.60	0.74
	Val 25	.	.	B	B	.	.	.	-0.28	0.03	*	*	.	-0.30	0.94
30	Gln 26	.	.	.	B	.	.	C	-0.18	-0.24	*	*	F	0.65	0.99
	Glu 27	.	.	.	B	.	.	C	-0.74	-0.31	*	*	F	0.65	0.50
	Ser 28	.	.	.	B	T	.	.	-0.07	0.33	.	*	.	0.10	0.50
	Val 29	.	.	B	B	.	.	.	-0.18	0.11	.	*	.	-0.30	0.45
	Met 30	.	.	B	B	.	.	.	0.09	-0.29	.	.	.	0.30	0.45
35	Val 31	.	.	B	B	.	.	.	-0.58	0.21	.	.	.	-0.30	0.34
	Pro 32	.	.	B	B	.	.	.	-0.58	0.40	.	.	.	-0.30	0.24
	Glu 33	.	.	B	.	.	.	.	-1.17	-0.24	.	.	.	0.50	0.41
	Ala 34	.	.	.	.	T	.	.	-0.61	-0.17	.	.	.	0.90	0.39
	Cys 35	.	.	B	.	.	.	.	-0.87	-0.43	*	.	.	0.50	0.34
40	Asp 36	.	.	.	B	T	.	.	-0.22	-0.21	*	.	.	0.70	0.14

	Ile	37	.	.	B	B	.	.	.	-0.68	0.21	.	.	.	-0.30	0.22
	Ser	38	.	.	B	B	.	.	.	-0.98	0.29	.	*	.	-0.30	0.22
	Val	39	.	.	B	.	.	T	.	-1.09	0.10	.	*	.	0.10	0.18
	Pro	40	.	.	B	.	.	T	.	-0.72	0.89	.	*	.	-0.20	0.22
5	Cys	41	.	.	.	.	T	T	.	-0.97	0.59	.	*	.	0.20	0.22
	Ser	42	.	.	.	.	T	T	.	-0.29	0.96	.	*	.	0.20	0.46
	Phe	43	.	.	.	.	T	.	.	0.12	0.74	*	.	.	0.28	0.46
	Ser	44	.	.	B	.	.	.	.	0.98	0.31	.	.	.	0.61	1.69
	Tyr	45	.	.	B	.	.	T	.	1.19	0.14	.	.	.	1.09	2.19
10	Pro	46	.	.	.	.	T	T	.	1.57	-0.24	.	.	F	2.52	4.22
	Arg	47	.	.	.	.	T	T	.	1.56	-0.11	.	.	F	2.80	3.31
	Gln	48	.	.	.	.	T	T	.	1.91	-0.01	.	.	F	2.52	3.05
	Asp	49	.	.	.	.	T	.	.	1.91	-0.34	.	*	F	2.04	1.95
	Trp	50	.	.	.	.	T	T	.	1.84	-0.39	.	*	F	1.96	1.33
15	Thr	51	.	.	.	.	.	T	C	1.84	0.10	.	*	F	0.88	1.11
	Gly	52	.	.	.	.	T	T	.	1.14	0.13	.	*	F	0.80	1.03
	Ser	53	.	.	.	.	.	T	C	0.90	0.63	.	.	F	0.15	0.99
	Thr	54	.	.	.	.	.	.	C	0.56	0.47	.	.	F	0.10	1.07
	Pro	55	.	.	.	.	.	T	C	0.60	0.41	.	.	F	0.30	1.07
20	Ala	56	.	.	.	.	T	T	.	0.62	0.74	.	.	.	0.35	1.26
	Tyr	57	.	.	.	.	T	T	.	0.27	1.27	.	.	.	0.20	0.91
	Gly	58	.	.	.	.	T	T	.	0.61	1.57	.	.	.	0.20	0.51
	Tyr	59	.	.	B	B	.	.	.	0.33	1.14	*	.	.	-0.45	1.01
	Trp	60	.	.	B	B	.	.	.	-0.31	1.14	*	.	.	-0.60	0.65
25	Phe	61	.	.	B	B	.	.	.	-0.03	1.03	*	.	.	-0.60	0.49
	Lys	62	.	.	B	B	.	.	.	0.21	1.09	*	.	.	-0.60	0.45
	Ala	63	.	.	B	B	.	.	.	0.24	0.33	*	.	.	-0.30	0.74
	Val	64	.	.	B	B	.	.	.	0.18	-0.10	*	.	.	0.79	1.24
	Thr	65	.	.	B	B	.	.	.	0.51	-0.40	*	.	F	1.13	0.89
30	Glu	66	.	.	B	B	.	.	.	0.87	-0.40	*	.	F	1.62	1.77
	Thr	67	.	.	.	B	T	.	.	0.23	-0.47	*	.	F	2.36	2.36
	Thr	68	.	.	.	.	T	T	.	0.61	-0.61	*	.	F	3.40	1.65
	Lys	69	.	.	.	.	T	T	.	0.61	-0.67	*	.	F	3.06	1.48
	Gly	70	.	.	.	.	.	T	C	0.33	-0.03	.	.	F	2.07	0.76
35	Ala	71	.	.	.	.	.	T	C	0.02	-0.01	*	.	F	1.73	0.53
	Pro	72	.	.	B	.	.	.	.	0.33	-0.01	*	.	.	0.84	0.38
	Val	73	.	.	B	.	.	.	.	0.61	0.39	.	.	.	-0.10	0.62
	Ala	74	.	.	B	.	.	.	.	0.57	0.46	.	.	.	-0.10	0.84
	Thr	75	.	.	B	.	.	.	.	0.61	0.36	*	*	.	0.50	0.94
40	Asn	76	.	.	.	.	.	.	C	1.31	0.31	.	.	F	1.30	1.70
	His	77	.	.	.	.	.	T	C	1.52	-0.33	*	.	F	2.40	3.29

	Gln	78	.	.	.	.	.	T	C	1.52	-0.83	*	.	F	3.00	3.95
	Ser	79	.	.	.	.	.	T	C	2.11	-0.67	*	.	F	2.70	1.82
	Arg	80	.	.	B	.	.	T	.	1.82	-1.07	*	.	F	2.20	2.32
	Glu	81	.	A	B	.	.	.	.	1.52	-0.96	*	.	F	1.50	1.33
5	Val	82	.	A	B	.	.	.	.	1.24	-0.97	*	*	F	1.54	1.33
	Glu	83	.	A	B	.	.	.	.	1.36	-0.87	*	*	.	1.28	0.98
	Met	84	.	A	B	.	.	.	.	1.31	-0.87	*	*	.	1.77	1.10
	Ser	85	.	.	.	.	.	T	C	1.31	-0.44	*	*	F	2.56	1.47
	Thr	86	.	.	.	.	.	T	T	0.61	-1.09	.	*	F	3.40	1.67
10	Arg	87	.	.	.	.	.	T	T	1.47	-0.30	.	*	F	2.76	1.46
	Gly	88	.	.	.	.	.	T	T	0.66	-0.51	.	*	F	2.72	1.88
	Arg	89	.	.	B	B	.	.	.	0.94	-0.21	.	*	F	1.28	1.08
	Phe	90	.	.	B	B	.	.	.	0.90	-0.21	.	*	.	0.64	0.79
	Gln	91	.	.	B	B	.	.	.	1.21	0.21	.	*	.	-0.30	0.79
15	Leu	92	.	.	B	B	.	.	.	0.89	-0.21	.	*	.	0.30	0.68
	Thr	93	.	.	B	B	.	.	.	0.64	0.21	.	*	F	0.34	1.21
	Gly	94	.	.	.	B	.	.	C	0.58	-0.07	.	*	F	1.33	0.70
	Asp	95	.	.	.	.	.	T	C	0.93	-0.47	*	*	F	2.22	1.71
	Pro	96	.	.	.	.	.	T	C	0.93	-0.73	.	*	F	2.86	1.17
20	Ala	97	.	.	.	.	.	T	T	1.08	-0.81	.	.	F	3.40	1.90
	Lys	98	.	.	.	.	.	T	T	1.09	-0.67	.	*	F	2.91	0.61
	Gly	99	.	.	.	.	.	T	T	0.62	-0.29	*	.	F	2.27	0.53
	Asn	100	.	.	B	.	.	T	T	-0.23	-0.03	.	*	F	1.93	0.43
	Cys	101	.	.	B	.	.	T	.	-0.91	0.11	*	*	.	0.44	0.16
25	Ser	102	.	.	B	.	.	T	.	-0.21	0.80	*	*	.	-0.20	0.11
	Leu	103	.	A	B	B	.	.	.	-0.26	0.37	*	*	.	-0.30	0.14
	Val	104	.	A	B	B	.	.	.	-0.50	-0.03	*	*	.	0.30	0.43
	Ile	105	.	A	B	B	.	.	.	-0.50	-0.10	*	.	.	0.30	0.33
	Arg	106	.	A	B	B	.	.	.	-0.43	-0.09	*	.	.	0.30	0.68
30	Asp	107	.	A	B	B	.	.	.	-0.13	-0.16	*	.	.	0.30	0.91
	Ala	108	.	A	B	.	.	.	.	0.68	-0.40	*	.	.	0.45	2.25
	Gln	109	.	A	B	.	.	.	.	1.53	-1.09	*	.	.	1.03	1.92
	Met	110	.	A	.	.	.	.	C	2.12	-1.09	.	.	.	1.51	1.99
	Gln	111	.	A	B	.	.	.	.	2.01	-0.70	.	.	F	1.74	2.64
35	Asp	112	.	.	.	.	.	T	T	1.77	-0.80	.	*	F	2.82	2.64
	Glu	113	.	.	.	.	.	T	T	1.66	-0.44	*	.	F	2.80	4.18
	Ser	114	.	.	.	.	.	T	T	0.96	-0.27	*	*	F	2.52	2.09
	Gln	115	.	.	.	.	.	T	T	1.67	0.11	*	*	F	1.64	1.08
	Tyr	116	.	.	B	B	.	.	.	0.81	0.11	*	*	.	0.41	1.22
40	Phe	117	.	.	B	B	.	.	.	0.81	0.76	*	.	.	-0.32	0.68
	Phe	118	.	.	B	B	.	.	.	0.92	0.37	*	*	.	0.04	0.68

5	Arg	119	.	.	B	B	.	.	0.88	-0.03	*	.	0.98	0.85	
	Val	120	.	.	B	B	.	.	0.58	-0.36	*	.	1.32	0.97	
	Glu	121	.	.	.	.	T	T	0.58	-0.76	*	.	F	3.06 1.50	
	Arg	122	.	.	.	.	T	T	0.42	-0.79	*	.	F	3.40 1.20	
	Gly	123	.	.	.	.	T	T	1.23	-0.14	*	*	F	2.76 1.20	
10	Ser	124	.	.	.	.	T	T	0.88	-0.79	*	*	F	2.72 1.36	
	Tyr	125	.	.	B	.	.	.	1.73	-0.03	.	*	.	1.33 1.09	
	Val	126	.	.	B	.	.	.	1.03	0.37	.	*	.	0.39 1.76	
	Arg	127	.	.	B	.	.	.	0.32	0.73	.	.	.	-0.25 1.14	
	Tyr	128	.	.	B	.	.	.	0.67	0.96	.	*	.	-0.40 0.72	
15	Asn	129	.	.	B	.	.	.	0.97	0.60	.	*	.	-0.25 1.56	
	Phe	130	.	.	B	.	.	.	0.87	-0.04	.	*	.	0.65 1.33	
	Met	131	.	.	B	.	.	.	1.02	0.39	.	*	.	-0.10 0.84	
	Asn	132	.	.	.	.	T	T	0.21	0.41	.	*	.	0.20 0.45	
	Asp	133	.	.	.	.	T	T	-0.36	0.80	.	.	.	0.20 0.45	
20	Gly	134	.	.	.	.	T	T	-0.31	0.70	.	*	.	0.20 0.38	
	Phe	135	.	.	B	.	.	T	-0.47	0.09	.	.	.	0.10 0.47	
	Phe	136	.	.	B	B	.	.	-0.18	0.33	.	*	.	-0.30 0.21	
	Leu	137	.	.	B	B	.	.	-1.03	0.81	.	.	.	-0.60 0.30	
	Lys	138	.	.	B	B	.	.	-1.84	1.03	.	.	.	-0.60 0.26	
25	Val	139	.	.	B	B	.	.	-1.80	0.93	.	.	.	-0.60 0.25	
	Thr	140	.	.	B	B	.	.	-1.80	0.53	.	*	.	-0.60 0.40	
	Val	141	.	.	B	B	.	.	-1.41	0.63	.	.	.	-0.60 0.17	
	Leu	142	.	.	B	B	.	.	-0.81	1.11	.	*	.	-0.60 0.34	
	Ser	143	.	.	B	B	.	.	-0.74	0.90	.	*	.	-0.60 0.36	
30	Phe	144	.	.	B	B	.	.	-0.10	0.41	*	*	.	-0.26 0.96	
	Thr	145	.	.	.	.	.	T	C	0.21	0.20	*	*	F	1.28 1.80
	Pro	146	.	.	.	.	.	T	C	1.07	-0.09	*	*	F	2.22 2.32
	Arg	147	.	.	.	.	.	T	C	1.84	-0.47	.	*	F	2.56 4.48
	Pro	148	.	.	.	.	T	T	2.14	-0.76	.	*	F	3.40 4.22	
35	Gln	149	.	.	.	.	T	.	2.53	-0.84	*	*	F	2.86 4.39	
	Asp	150	.	.	.	.	T	.	2.84	-0.79	*	.	F	2.52 3.24	
	His	151	.	.	.	.	T	.	2.24	-0.79	*	.	F	2.18 3.50	
	Asn	152	.	.	.	.	T	T	1.82	-0.53	*	*	F	2.04 1.67	
	Thr	153	.	.	.	.	T	T	1.37	-0.44	.	.	F	1.40 1.44	
40	Asp	154	.	.	.	.	T	T	1.33	0.13	.	*	F	0.65 0.57	
	Leu	155	.	.	B	.	.	T	0.48	0.13	*	*	.	0.10 0.48	
	Thr	156	.	.	B	B	.	.	0.51	0.37	.	*	.	-0.30 0.25	
	Cys	157	.	.	B	B	.	.	-0.19	-0.11	.	*	.	0.49 0.25	
	His	158	.	.	B	B	.	.	-0.18	0.67	*	*	.	-0.22 0.26	
	Val	159	.	.	B	B	.	.	-0.07	0.37	*	*	.	0.27 0.24	

5	Asp	160	.	.	B	B	.	.	.	0.79	-0.11	*	*	.	1.06	0.88
	Phe	161	.	.	B	.	.	.	.	0.76	-0.69	*	.	.	1.90	1.29
	Ser	162	.	.	.	.	T	T	.	0.57	-0.76	*	.	F	2.46	1.72
	Arg	163	.	.	.	.	T	T	.	0.30	-0.76	*	.	F	2.12	0.77
	Lys	164	.	.	.	.	T	T	.	0.57	-0.37	*	.	F	1.78	1.18
10	Gly	165	.	.	.	.	T	T	.	0.57	-0.66	*	.	F	1.74	0.89
	Val	166	.	.	.	B	.	.	C	1.38	-0.64	*	.	F	0.95	0.79
	Ser	167	.	.	.	B	.	.	C	1.37	-0.64	*	.	F	0.95	0.77
	Ala	168	.	.	B	B	.	.	.	0.40	-0.16	*	.	F	0.60	1.13
	Gln	169	.	.	B	B	.	.	.	0.47	0.06	*	*	F	0.00	1.13
15	Arg	170	.	.	B	B	.	.	.	0.00	-0.59	.	*	F	0.90	1.65
	Thr	171	.	.	B	B	.	.	.	0.97	-0.29	.	*	F	0.60	1.35
	Val	172	.	.	B	B	.	.	.	0.41	-0.79	*	*	.	0.75	1.52
	Arg	173	.	.	B	B	.	.	.	0.41	-0.54	*	*	.	0.60	0.58
	Leu	174	.	.	B	B	.	.	.	0.17	-0.04	*	*	.	0.30	0.40
20	Arg	175	.	.	B	B	.	.	.	-0.53	0.23	*	*	.	-0.30	0.85
	Val	176	.	.	B	B	.	.	.	-0.43	0.09	*	*	.	-0.30	0.44
	Ala	177	.	.	B	B	.	.	.	0.53	0.51	*	*	.	-0.60	0.82
	Tyr	178	.	.	B	B	.	.	.	0.42	-0.17	*	*	.	0.30	0.82
	Ala	179	.	.	B	.	.	T	.	0.42	-0.17	*	*	.	0.85	1.85
25	Pro	180	.	.	B	.	.	T	.	-0.54	-0.13	*	*	.	0.85	1.51
	Arg	181	.	.	B	.	.	T	.	-0.58	0.01	*	.	F	0.25	0.72
	Asp	182	.	.	B	.	.	T	.	-0.29	-0.06	*	.	F	0.85	0.50
	Leu	183	.	.	B	B	.	.	.	-0.93	-0.17	*	.	.	0.30	0.43
	Val	184	.	.	B	B	.	.	.	-0.64	0.09	*	.	.	-0.30	0.15
30	Ile	185	.	.	B	B	.	.	.	-0.32	0.47	*	.	.	-0.26	0.12
	Ser	186	.	.	B	B	.	.	.	-0.43	0.47	*	.	.	0.08	0.29
	Ile	187	.	.	B	B	.	.	.	-0.43	-0.21	*	.	.	1.32	0.66
	Ser	188	.	.	B	.	.	T	.	0.07	-0.46	*	.	F	2.36	1.52
	Arg	189	.	.	.	.	T	T	.	0.71	-0.66	*	.	F	3.40	1.63
35	Asp	190	.	.	.	.	T	T	.	1.01	-0.61	*	.	F	3.06	3.61
	Asn	191	.	.	.	.	.	T	C	0.50	-0.80	*	.	F	2.52	2.72
	Thr	192	.	.	.	.	.	.	C	1.39	-0.50	*	.	F	1.98	1.14
	Pro	193	.	.	.	.	.	.	C	1.48	-0.50	.	.	F	1.64	1.19
	Ala	194	.	.	.	.	T	.	.	1.37	-0.07	*	.	F	1.20	1.14
40	Leu	195	.	.	B	.	.	.	.	1.16	-0.07	.	.	F	1.14	1.37
	Glu	196	.	.	B	.	.	.	.	1.16	-0.13	.	*	F	1.48	1.37
	Pro	197	.	.	B	.	.	.	.	1.12	-0.16	.	*	F	1.82	2.35
	Gln	198	.	.	.	.	.	.	C	1.33	-0.23	.	*	F	2.36	2.82
	Pro	199	.	.	.	.	T	T	.	1.07	-0.51	.	*	F	3.40	2.62
	Gln	200	.	.	.	.	T	T	.	1.67	0.13	.	*	F	2.16	1.26

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	Gly	201	.	.	.	.	T	T	.	1.42	0.13	.	*	F	1.82	1.12
	Asn	202	.	.	.	.	.	T	C	0.82	0.49	.	*	F	0.98	1.14
	Val	203	.	.	B	.	.	.	.	0.82	0.74	.	*	F	0.09	0.54
5	Pro	204	.	A	B	.	.	.	.	0.44	0.34	.	.	.	-0.30	0.95
	Tyr	205	.	A	B	.	.	.	.	0.44	0.41	.	.	.	-0.60	0.59
	Leu	206	.	A	B	.	.	.	.	0.83	0.41	.	.	.	-0.17	1.39
	Glu	207	.	A	B	.	.	.	.	0.49	-0.23	.	.	.	1.01	1.79
	Ala	208	.	A	B	.	.	.	.	1.34	-0.23	.	.	F	1.44	1.13
10	Gln	209	.	.	B	.	.	T	.	0.86	-0.59	.	.	F	2.42	2.38
	Lys	210	.	.	.	.	T	T	.	0.29	-0.49	*	.	F	2.80	1.19
	Gly	211	.	.	.	.	T	T	.	1.21	0.20	*	.	F	1.77	0.97
	Gln	212	.	.	B	.	.	T	.	0.40	-0.30	*	.	F	1.84	1.10
	Phe	213	.	A	B	.	.	.	.	0.18	-0.01	*	.	.	0.86	0.45
	Leu	214	.	A	B	.	.	.	.	-0.49	0.67	*	.	.	-0.32	0.38
15	Arg	215	.	A	B	.	.	.	.	-1.12	0.81	*	.	.	-0.60	0.12
	Leu	216	.	A	B	.	.	.	.	-1.37	0.91	*	.	.	-0.60	0.14
	Leu	217	.	A	B	.	.	.	.	-1.37	0.63	*	.	.	-0.60	0.17
	Cys	218	.	A	B	.	.	.	.	-0.97	-0.06	*	*	.	0.54	0.14
	Ala	219	.	A	.	.	T	.	.	-0.16	0.33	*	*	.	0.58	0.23
20	Ala	220	.	.	.	.	T	T	.	-0.48	0.04	*	*	F	1.37	0.49
	Asp	221	.	.	.	.	T	T	.	0.12	-0.21	.	.	F	2.36	1.40
	Ser	222	.	.	.	.	.	T	C	0.34	-0.36	.	.	F	2.40	2.15
	Gln	223	.	.	.	.	.	T	C	0.70	-0.36	.	.	F	2.16	2.15
25	Pro	224	.	.	.	.	.	T	C	0.48	-0.37	.	.	F	1.92	1.85
	Pro	225	.	.	.	.	T	T	.	0.77	0.31	.	*	F	1.28	1.14
	Ala	226	.	.	.	.	T	T	.	0.48	0.31	.	.	F	0.89	0.88
	Thr	227	.	.	B	.	.	T	.	-0.08	0.83	.	.	.	-0.20	0.60
	Leu	228	.	.	B	B	.	.	.	-0.89	1.04	*	*	.	-0.60	0.29
	Ser	229	.	.	B	B	.	.	.	-0.68	1.30	.	.	.	-0.60	0.24
30	Trp	230	.	.	B	B	.	.	.	-0.47	1.20	.	*	.	-0.60	0.28
	Val	231	.	.	B	B	.	.	.	0.23	1.11	.	*	.	-0.60	0.55
	Leu	232	.	.	B	B	.	.	.	-0.31	0.43	.	*	.	-0.60	0.80
	Gln	233	.	.	B	B	.	.	.	-0.31	0.69	.	*	F	-0.45	0.57
	Asn	234	.	.	B	B	.	.	.	-0.31	0.46	.	*	F	-0.45	0.63
35	Arg	235	.	.	B	B	.	.	.	-0.32	0.20	.	.	F	0.00	1.03
	Val	236	.	.	B	B	.	.	.	0.23	-0.10	.	.	F	0.45	0.79
	Leu	237	.	.	B	.	.	T	.	1.01	-0.11	*	*	F	0.85	0.66
	Ser	238	.	.	B	.	.	T	.	0.80	-0.01	*	.	F	0.85	0.46
	Ser	239	.	.	.	.	T	T	.	0.51	0.41	*	.	F	0.35	0.96
40	Ser	240	.	.	.	.	.	T	C	0.06	0.69	*	.	F	0.30	1.22
	His	241	.	.	.	.	.	T	C	0.70	0.43	*	.	F	0.15	0.90



251

5	Pro	242	.	.	.	.	T	T	.	1.62	0.47	*	.	.	0.35	1.04
	Trp	243	.	.	.	.	T	T	.	1.71	0.09	*	.	.	0.65	1.52
	Gly	244	.	.	.	.	.	T	C	1.20	0.13	*	.	F	0.60	1.73
	Pro	245	.	.	.	.	.	.	C	1.16	0.31	.	.	F	0.25	0.92
	Arg	246	.	.	.	.	.	T	C	0.38	0.31	.	.	F	0.45	0.87
10	Pro	247	.	.	.	.	.	T	C	0.59	0.09	*	.	F	0.45	0.72
	Leu	248	.	.	B	.	.	T	.	0.07	-0.34	*	.	.	0.70	0.81
	Gly	249	.	.	B	.	.	T	.	0.20	-0.09	*	.	.	0.70	0.34
	Leu	250	.	.	B	.	.	.	.	0.07	0.34	*	.	.	-0.10	0.34
	Glu	251	.	.	B	.	.	.	.	-0.90	0.34	*	.	.	-0.10	0.41
15	Leu	252	.	.	B	.	.	.	.	-0.64	0.30	.	.	.	-0.10	0.31
	Pro	253	.	.	B	.	.	.	.	-0.42	-0.13	.	.	F	0.65	0.74
	Gly	254	.	.	B	.	.	.	.	-0.42	-0.31	.	.	F	0.65	0.43
	Val	255	.	.	B	.	.	.	.	0.39	0.11	*	.	F	0.05	0.52
	Lys	256	.	.	B	.	.	.	.	0.09	-0.57	.	.	F	1.29	0.56
20	Ala	257	.	.	B	.	.	.	.	0.56	-0.61	*	*	F	1.63	0.76
	Gly	258	.	.	.	.	T	.	.	0.88	-0.61	*	*	F	2.52	1.02
	Asp	259	.	.	.	.	T	T	.	0.98	-1.26	*	*	F	2.91	0.99
	Ser	260	.	.	.	.	T	T	.	1.52	-0.50	*	*	F	3.40	1.54
	Gly	261	.	.	.	.	T	T	.	0.81	-0.51	*	*	F	3.06	2.25
25	Arg	262	.	.	B	.	.	T	.	1.51	-0.37	*	*	F	1.87	0.72
	Tyr	263	.	.	B	B	.	.	.	1.27	-0.37	*	*	F	1.28	1.05
	Thr	264	.	.	B	B	.	.	.	1.27	-0.26	*	*	.	0.79	1.08
	Cys	265	.	.	B	B	.	.	.	1.57	-0.69	*	*	.	0.94	0.95
	Arg	266	.	.	B	B	.	.	.	2.02	-0.29	*	*	.	0.98	0.98
30	Ala	267	.	.	B	.	.	.	.	1.10	-1.04	*	*	F	2.12	1.33
	Glu	268	.	.	B	.	.	.	.	1.00	-0.84	*	*	F	2.46	2.04
	Asn	269	.	.	.	.	T	T	.	1.01	-0.99	*	*	F	3.40	1.03
	Arg	270	.	.	.	.	T	T	.	1.68	-0.60	*	*	F	3.06	1.37
	Leu	271	.	.	.	.	T	T	.	1.57	-0.70	*	*	F	2.72	1.37
35	Gly	272	.	.	.	.	T	T	.	2.27	-0.30	*	*	F	2.08	1.47
	Ser	273	.	.	.	.	.	.	C	1.68	-0.70	*	*	F	1.64	1.47
	Gln	274	.	A	B	.	.	.	.	0.87	-0.20	*	*	F	0.60	1.80
	Gln	275	.	A	B	.	.	.	.	0.76	-0.20	.	*	F	0.60	1.50
	Arg	276	.	A	B	.	.	.	.	0.76	-0.63	*	.	F	0.90	1.87
40	Ala	277	.	A	B	.	.	.	.	0.80	-0.33	*	.	F	0.45	0.89
	Leu	278	.	A	B	.	.	.	.	0.24	-0.34	*	*	.	0.30	0.69
	Asp	279	.	A	B	.	.	.	.	0.24	-0.10	*	*	.	0.30	0.26
	Leu	280	.	A	B	.	.	.	.	0.00	0.30	*	*	.	-0.30	0.45
	Ser	281	.	.	B	.	.	.	.	-0.32	0.56	*	*	.	-0.40	0.85
	Val	282	.	.	B	.	.	.	.	0.06	0.30	*	*	.	-0.10	0.79

	Gln	283	.	.	B	.	.	.	.	0.87	0.73	.	*	.	-0.25	1.48
	Tyr	284	.	.	B	.	.	.	.	0.87	0.04	.	*	.	0.25	1.91
	Pro	285	.	.	.	.	.	T	C	0.87	0.06	*	*	F	1.00	4.14
	Pro	286	.	.	.	.	.	T	C	1.28	0.10	*	*	F	1.20	1.97
5	Glu	287	.	.	.	.	T	T	.	1.28	-0.30	*	*	F	2.20	2.47
	Asn	288	.	.	B	.	.	T	.	0.68	-0.41	*	*	F	2.00	1.18
	Leu	289	.	.	B	B	.	.	.	0.07	-0.23	*	*	.	1.10	0.76
	Arg	290	.	.	B	B	.	.	.	-0.02	-0.01	*	*	.	0.90	0.32
	Val	291	.	.	B	B	.	.	.	0.19	0.37	*	*	.	0.10	0.27
10	Met	292	.	.	B	B	.	.	.	-0.40	0.37	*	*	.	-0.10	0.57
	Val	293	.	.	B	B	.	.	.	-0.40	0.19	*	*	.	-0.30	0.29
	Ser	294	.	.	B	.	.	.	.	0.52	0.59	*	*	.	-0.40	0.63
	Gln	295	.	.	B	.	.	.	.	0.10	-0.06	*	*	F	0.80	1.26
	Ala	296	.	.	B	.	.	.	.	0.10	-0.19	*	.	F	0.80	2.44
15	Asn	297	.	.	B	.	.	.	.	-0.11	-0.19	*	.	F	0.80	1.35
	Arg	298	.	.	B	.	.	.	.	0.74	0.11	*	.	F	0.05	0.64
	Thr	299	.	.	B	.	.	.	.	1.04	-0.29	*	.	F	0.80	1.10
	Val	300	.	.	B	.	.	.	.	0.23	-0.39	*	.	.	0.65	1.10
	Leu	301	.	.	B	.	.	.	.	0.48	-0.10	*	.	.	0.50	0.47
20	Glu	302	.	.	B	.	.	.	.	0.48	0.33	*	.	.	0.03	0.32
	Asn	303	.	.	B	.	.	.	.	0.02	0.24	*	.	F	0.31	0.69
	Leu	304	.	.	.	.	T	T	.	0.02	0.03	*	.	F	1.04	0.83
	Gly	305	.	.	.	.	T	T	.	0.58	-0.17	*	.	F	1.77	0.69
	Asn	306	.	.	.	.	T	T	.	0.58	0.21	*	.	F	1.30	0.58
25	Gly	307	.	.	.	.	.	T	C	0.37	0.50	*	.	F	0.67	0.58
	Thr	308	.	.	.	.	.	.	C	-0.49	0.24	.	.	F	0.64	0.90
	Ser	309	.	.	B	.	.	.	.	-0.49	0.46	.	.	F	0.01	0.42
	Leu	310	.	.	B	.	.	.	.	-0.14	0.74	.	.	.	-0.27	0.35
30	Pro	311	.	.	B	.	.	.	.	-0.49	0.31	.	.	.	-0.10	0.42
	Val	312	.	.	B	.	.	.	.	-0.14	0.26	.	.	.	-0.10	0.31
	Leu	313	.	.	B	.	.	.	.	-0.13	0.27	.	.	F	0.05	0.64
	Glu	314	.	.	B	.	.	.	.	-0.64	-0.03	.	.	F	0.65	0.56
	Gly	315	.	.	.	.	T	T	.	-0.50	0.23	.	.	F	0.65	0.62
	Gln	316	.	.	.	.	T	T	.	-1.10	0.16	.	.	F	0.65	0.40
35	Ser	317	.	.	.	.	T	T	.	-1.10	0.16	.	.	F	0.65	0.19
	Leu	318	.	.	B	.	.	T	.	-0.96	0.80	.	.	.	-0.20	0.14
	Cys	319	.	.	B	B	.	.	.	-1.81	0.94	.	.	.	-0.60	0.04
	Leu	320	.	.	B	B	.	.	.	-1.78	1.19	.	.	.	-0.60	0.02
	Val	321	.	.	B	B	.	.	.	-1.81	1.29	.	.	.	-0.60	0.04
40	Cys	322	.	.	B	B	.	.	.	-1.81	1.10	.	.	.	-0.60	0.11
	Val	323	.	.	B	B	.	.	.	-1.30	0.91	.	.	.	-0.60	0.18

	Thr	324	.	.	B	B	.	.	.	-0.84	0.61	.	.	.	-0.60	0.32
	His	325	.	.	.	.	T	T	.	-0.24	0.40	.	.	F	0.89	0.93
	Ser	326	.	.	.	.	.	T	C	0.02	0.26	*	*	F	1.08	1.93
	Ser	327	.	.	.	.	.	T	C	0.80	0.11	*	*	F	1.32	1.35
5	Pro	328	.	.	.	.	.	T	C	0.84	-0.37	.	*	F	2.16	1.95
	Pro	329	.	.	.	.	T	.	.	0.86	-0.19	.	*	F	2.40	1.20
	Ala	330	.	.	.	.	T	.	.	0.60	-0.19	.	*	F	2.16	1.20
	Arg	331	.	.	B	B	.	.	.	0.59	0.34	.	*	.	0.42	0.82
	Leu	332	.	.	B	B	.	.	.	0.89	0.40	.	*	.	0.18	0.76
10	Ser	333	.	.	B	B	.	.	.	1.21	0.37	.	*	.	0.09	1.30
	Trp	334	.	.	B	B	.	.	.	1.08	-0.13	.	*	.	0.45	1.30
	Thr	335	.	.	B	B	.	.	.	1.67	0.30	.	*	F	0.00	1.56
	Gln	336	.	.	B	.	.	T	.	0.70	0.01	.	*	F	0.40	2.02
	Arg	337	.	.	B	.	.	T	.	0.70	0.27	.	*	F	0.40	1.43
15	Gly	338	.	.	.	.	T	T	.	0.70	0.04	.	*	F	0.65	0.82
	Gln	339	.	.	B	.	.	T	.	0.78	-0.06	.	*	F	0.85	0.63
	Val	340	.	.	B	.	.	.	.	0.79	-0.03	.	.	F	0.65	0.50
	Leu	341	.	.	B	.	.	.	.	0.79	0.36	.	.	F	0.05	0.67
	Ser	342	.	.	B	.	.	T	.	0.47	0.33	.	*	F	0.55	0.67
20	Pro	343	.	.	.	.	T	T	.	0.51	0.36	.	.	F	1.40	1.41
	Ser	344	.	.	.	.	T	T	.	0.51	0.10	.	.	F	1.70	2.28
	Gln	345	.	.	.	.	.	T	C	1.16	-0.59	.	.	F	2.70	2.85
	Pro	346	.	.	.	.	T	.	.	1.62	-0.54	.	.	F	3.00	2.85
	Ser	347	.	.	.	.	.	.	C	1.07	-0.54	.	.	F	2.50	2.10
25	Asp	348	.	.	.	.	.	T	C	0.47	-0.29	.	.	F	1.95	0.90
	Pro	349	.	.	B	.	.	T	.	0.77	0.00	.	.	F	1.45	0.48
	Gly	350	.	.	B	.	.	T	.	-0.04	-0.43	.	.	F	1.15	0.62
	Val	351	.	.	B	.	.	T	.	-0.04	-0.13	*	.	.	0.70	0.31
	Leu	352	.	.	B	.	.	.	.	0.37	0.30	*	.	.	-0.10	0.31
30	Glu	353	.	.	B	.	.	.	.	-0.49	-0.13	*	.	.	0.50	0.61
	Leu	354	.	.	B	B	.	.	.	-0.28	0.09	*	*	.	-0.30	0.61
	Pro	355	.	.	B	B	.	.	.	-0.79	-0.16	*	*	F	0.60	1.27
	Arg	356	.	A	B	B	.	.	.	0.07	-0.20	*	*	.	0.30	0.55
	Val	357	.	A	B	B	.	.	.	0.84	-0.20	.	*	.	0.45	1.15
35	Gln	358	.	A	B	B	.	.	.	0.84	-0.39	.	*	.	0.45	1.01
	Val	359	.	A	B	B	.	.	.	1.31	-0.81	.	*	.	0.60	0.89
	Glu	360	.	A	B	B	.	.	.	1.52	-0.39	.	*	.	0.45	1.19
	His	361	.	A	.	.	.	.	C	0.71	-1.03	.	*	F	1.10	1.19
	Glu	362	.	A	.	.	T	.	.	1.26	-0.64	.	*	F	1.30	1.39
40	Gly	363	.	A	.	.	T	.	.	0.59	-0.80	.	*	F	1.30	1.16
	Glu	364	.	A	.	.	T	.	.	1.41	-0.23	*	*	F	0.85	0.46

5	Phe	365	.	A	.	.	T	.	.	0.82	-0.23	*	*	.	0.70	0.36
	Thr	366	A	A	.	.	.	.	.	0.97	0.27	.	*	.	-0.30	0.37
	Cys	367	.	A	.	.	T	.	.	0.93	-0.16	*	*	.	0.70	0.41
	His	368	.	A	B	.	.	.	.	1.07	0.34	*	*	.	-0.30	0.65
	Ala	369	.	A	.	.	T	.	.	0.26	-0.01	*	*	.	0.95	0.70
	Arg	370	.	A	.	.	.	.	C	0.61	0.19	*	*	.	0.55	1.07
	His	371	.	.	.	.	.	T	C	0.62	0.04	.	*	.	1.05	0.78
10	Pro	372	.	.	.	.	T	T	.	1.29	-0.07	.	*	.	2.25	1.03
	Leu	373	.	.	.	.	T	T	.	1.29	-0.17	.	*	F	2.50	0.91
	Gly	374	.	.	.	.	T	T	.	1.02	0.33	.	*	F	1.65	0.91
	Ser	375	.	.	B	B	.	.	.	0.61	0.47	.	*	F	0.30	0.44
15	Gln	376	.	.	B	B	.	.	.	-0.17	0.43	.	.	F	0.05	0.71
	His	377	.	.	B	B	.	.	.	-0.26	0.43	.	*	.	-0.35	0.59
	Val	378	.	.	B	B	.	.	.	-0.26	0.39	.	*	.	-0.30	0.59
	Ser	379	.	.	B	B	.	.	.	-0.21	0.69	.	*	.	-0.60	0.28
	Leu	380	.	.	B	B	.	.	.	-0.77	0.67	.	*	.	-0.60	0.28
20	Ser	381	.	.	B	B	.	.	.	-0.80	0.81	.	*	.	-0.60	0.28
	Leu	382	.	.	B	B	.	.	.	-1.01	0.67	.	*	.	-0.60	0.28
	Ser	383	.	.	B	B	.	.	.	-0.46	1.04	.	*	.	-0.60	0.54
	Val	384	.	.	B	B	.	.	.	-0.37	0.74	.	*	.	-0.60	0.54
	His	385	.	.	B	B	.	.	.	0.49	0.79	*	*	.	-0.45	1.01
25	Tyr	386	.	.	B	B	.	.	.	-0.02	0.10	*	*	.	-0.15	1.50
	Ser	387	.	.	B	.	.	T	.	-0.02	0.40	.	*	.	0.25	1.67
	Pro	388	.	.	B	.	.	T	.	-0.07	0.44	*	*	F	0.10	1.01
	Lys	389	.	.	.	.	T	T	.	0.58	0.37	*	*	F	0.65	0.64
	Leu	390	.	.	.	.	T	T	.	0.31	0.04	*	.	F	0.65	0.74
30	Leu	391	.	.	B	.	.	.	.	-0.11	0.04	.	.	F	0.05	0.64
	Gly	392	.	.	.	.	.	T	C	-0.11	0.19	.	.	F	0.45	0.17
	Pro	393	.	.	.	.	.	T	C	-0.19	0.57	.	.	F	0.15	0.28
	Ser	394	.	.	.	.	.	T	C	-0.23	0.80	.	.	F	0.15	0.36
	Cys	395	.	.	.	.	.	T	C	-0.01	0.11	.	*	.	0.30	0.62
35	Ser	396	.	A	.	.	.	.	C	0.80	0.19	.	*	.	-0.10	0.41
	Trp	397	.	A	B	.	.	.	.	0.80	-0.24	.	.	.	0.30	0.52
	Glu	398	.	A	B	.	.	.	.	0.20	-0.20	.	.	.	0.30	0.97
	Ala	399	.	A	.	.	T	.	.	0.47	-0.09	.	.	.	0.70	0.60
	Glu	400	.	A	.	.	T	.	.	0.47	0.03	.	.	F	0.10	0.77
40	Gly	401	.	A	.	.	T	.	.	0.47	-0.31	.	.	.	0.70	0.24
	Leu	402	.	A	.	.	T	.	.	0.09	0.07	.	.	.	0.10	0.32
	His	403	.	A	.	.	T	.	.	-0.21	0.14	.	.	.	0.10	0.10
	Cys	404	.	.	.	.	T	T	.	0.08	0.53	.	.	.	0.20	0.13
	Ser	405	.	.	.	.	T	T	.	0.08	0.49	.	.	.	0.20	0.22

255

	Cys	406	.	.	.	.	T	T	.	-0.17	0.20	.	.	.	0.50	0.27
	Ser	407	.	.	.	.	T	T	.	0.34	0.20	.	*	F	0.65	0.52
	Ser	408	.	.	.	.	T	.	.	0.17	0.01	.	.	F	0.45	0.52
	Gln	409	.	.	.	.	T	.	.	0.24	0.06	.	.	F	0.60	1.49
5	Ala	410	.	.	.	.	.	.	C	0.33	-0.01	.	.	F	1.24	1.13
	Ser	411	.	.	.	.	.	.	C	0.70	0.03	.	.	F	0.88	1.30
	Pro	412	.	.	.	.	.	.	C	0.19	0.03	.	*	F	1.12	1.00
	Ala	413	.	.	.	.	.	T	C	0.60	0.31	.	*	F	1.41	0.82
	Pro	414	.	.	.	.	.	T	C	0.31	-0.19	*	*	F	2.40	1.20
10	Ser	415	.	.	.	.	.	T	C	0.61	0.34	*	*	F	1.41	0.82
	Leu	416	.	.	B	.	.	T	.	0.10	0.83	*	*	.	0.52	0.85
	Arg	417	.	.	B	B	.	.	.	-0.03	1.01	*	*	.	-0.12	0.45
	Trp	418	.	.	B	B	.	.	.	0.56	1.01	.	*	.	-0.36	0.33
	Trp	419	.	A	.	B	.	.	C	0.77	0.63	.	*	.	-0.40	0.70
15	Leu	420	.	A	.	B	.	.	C	0.26	-0.06	.	*	.	0.50	0.62
	Gly	421	.	A	.	B	.	.	C	0.26	0.63	.	*	.	-0.40	0.49
	Glu	422	.	A	B	.	.	.	.	0.14	0.40	.	*	F	-0.15	0.38
	Glu	423	.	A	B	.	.	.	.	0.09	-0.51	.	.	F	0.75	0.80
	Leu	424	.	A	.	.	.	.	C	0.38	-0.77	*	.	F	0.95	0.80
20	Leu	425	.	A	.	.	.	.	C	0.89	-0.80	*	.	F	1.25	0.74
	Glu	426	.	A	.	.	T	.	.	0.93	-0.41	.	.	F	1.45	0.58
	Gly	427	.	A	.	.	T	.	.	0.93	-0.03	.	.	F	1.75	0.94
	Asn	428	.	.	.	.	T	T	.	0.93	-0.31	.	.	F	2.60	1.97
	Ser	429	.	.	.	.	.	T	C	1.44	-1.00	.	.	F	3.00	1.89
25	Ser	430	.	.	.	.	.	T	C	1.56	-0.61	.	.	F	2.70	2.57
	Gln	431	.	.	.	.	.	T	C	1.56	-0.26	.	.	F	2.10	1.38
	Asp	432	.	A	.	.	.	.	C	1.04	-0.66	*	.	F	1.70	1.79
	Ser	433	.	A	B	.	.	.	.	0.73	-0.40	*	.	F	0.75	0.99
	Phe	434	.	A	B	.	.	.	.	0.82	-0.30	.	*	.	0.30	0.82
30	Glu	435	.	A	B	.	.	.	.	0.82	-0.27	.	.	.	0.43	0.76
	Val	436	.	A	B	.	.	.	.	0.52	0.11	*	.	F	0.11	0.76
	Thr	437	.	.	B	.	.	T	.	-0.07	0.11	.	.	F	0.79	1.18
	Pro	438	.	.	.	.	.	T	C	-0.11	-0.17	.	.	F	1.57	0.69
	Ser	439	.	.	.	.	T	T	.	0.38	0.26	.	.	F	1.30	0.92
35	Ser	440	.	.	.	.	.	T	C	0.09	0.04	.	.	F	0.97	0.98
	Ala	441	.	.	.	.	.	.	C	0.36	0.47	.	.	F	0.34	0.67
	Gly	442	.	.	.	.	.	T	C	0.67	0.54	.	.	F	0.41	0.50
	Pro	443	.	.	.	.	T	T	.	0.58	0.56	.	.	F	0.48	0.61
	Trp	444	.	.	.	.	.	T	C	0.58	0.56	*	.	F	0.15	0.80
40	Ala	445	.	.	B	.	.	T	.	0.07	0.44	*	.	F	0.10	1.09
	Asn	446	.	.	B	.	.	T	.	0.36	0.70	.	.	F	-0.05	0.58

256

5	Ser	447	.	.	B	.	.	T	.	-0.11	0.66	.	*	F	-0.05	0.74
	Ser	448	.	.	B	.	.	T	.	0.07	0.43	.	*	F	-0.05	0.60
	Leu	449	.	.	B	.	.	T	.	0.01	0.43	.	*	.	-0.20	0.51
	Ser	450	.	.	B	.	.	.	.	0.26	0.46	.	*	.	-0.40	0.38
	Leu	451	.	.	B	.	.	T	.	-0.56	0.50	.	*	.	-0.20	0.28
10	His	452	.	.	B	.	.	T	.	-0.56	0.80	.	*	.	-0.20	0.28
	Gly	453	.	.	.	.	T	T	.	-0.56	0.50	.	*	.	0.20	0.28
	Gly	454	.	.	.	.	.	T	C	-0.09	0.50	.	*	F	0.15	0.45
	Leu	455	.	.	.	.	.	.	C	-0.60	0.24	*	*	F	0.39	0.33
	Ser	456	.	.	.	.	.	T	C	0.32	0.43	*	*	F	0.43	0.27
15	Ser	457	.	.	.	.	T	T	.	-0.46	0.00	.	*	F	1.67	0.54
	Gly	458	.	.	B	.	.	T	.	0.00	0.26	.	*	F	0.81	0.54
	Leu	459	.	.	B	.	.	T	.	-0.32	-0.43	*	*	.	1.40	0.79
	Arg	460	.	A	B	.	.	.	.	0.49	-0.24	*	*	.	0.86	0.32
	Leu	461	.	A	B	.	.	.	.	0.20	-0.63	*	*	.	1.02	0.56
20	Arg	462	.	A	B	.	.	.	.	0.21	-0.56	*	*	.	0.88	0.68
	Cys	463	.	A	B	.	.	.	.	0.56	-0.33	*	*	.	0.44	0.37
	Glu	464	.	A	B	.	.	.	.	0.51	0.07	.	*	.	-0.30	0.71
	Ala	465	.	A	.	.	T	.	.	0.37	0.03	*	*	.	0.10	0.27
	Trp	466	.	A	.	.	T	.	.	0.83	0.53	*	*	.	-0.20	0.68
25	Asn	467	.	.	B	.	.	T	.	0.13	0.39	.	.	.	0.10	0.39
	Val	468	.	.	B	.	.	T	.	0.80	0.89	.	.	.	-0.20	0.39
	His	469	.	.	.	.	.	T	C	0.50	0.79	.	.	.	0.00	0.64
	Gly	470	.	.	.	.	.	T	C	0.74	0.26	.	.	.	0.30	0.54
	Ala	471	.	.	.	.	.	.	C	0.73	0.29	.	.	F	0.25	0.72
30	Gln	472	.	.	.	.	.	T	C	-0.16	0.03	.	.	F	0.45	0.71
	Ser	473	.	.	.	.	.	T	C	-0.11	0.21	.	.	F	0.45	0.50
	Gly	474	.	.	B	.	.	T	.	-0.08	0.47	.	.	F	-0.05	0.41
	Ser	475	.	.	B	.	.	T	.	-0.54	0.37	.	.	F	0.25	0.41
	Ile	476	.	.	B	.	.	.	.	-0.17	0.66	.	.	.	-0.40	0.25
35	Leu	477	.	.	B	.	.	.	.	-0.17	0.70	*	.	.	-0.06	0.39
	Gln	478	.	.	B	.	.	.	.	0.18	0.27	*	.	.	0.58	0.49
	Leu	479	.	.	B	.	.	T	.	0.57	-0.11	*	.	.	1.87	1.39
	Pro	480	.	.	B	.	.	T	.	0.52	-0.80	*	.	F	2.66	3.38
	Asp	481	.	.	.	.	T	T	.	0.60	-1.06	.	.	F	3.40	1.93
40	Lys	482	.	.	.	.	T	T	.	0.52	-0.77	.	.	F	3.06	1.93
	Lys	483	.	.	.	B	T	.	.	0.22	-0.77	.	.	F	2.17	0.88
	Gly	484	.	.	B	B	.	.	.	0.72	-0.81	.	.	F	1.43	0.70
	Leu	485	.	.	B	B	.	.	.	0.34	-0.33	.	.	F	0.79	0.51
	Ile	486	.	.	B	B	.	.	.	-0.36	0.17	.	.	.	-0.30	0.26
	Ser	487	.	.	B	B	.	.	.	-0.70	0.96	.	.	.	-0.60	0.22

5	Thr	488	.	.	B	B	.	.	-0.74	0.91	*	.	.	-0.60	0.36
	Ala	489	.	.	B	B	.	.	-0.74	0.63	*	.	.	-0.60	0.84
	Phe	490	.	.	B	.	.	T	-0.52	0.37	.	.	F	0.25	0.62
	Ser	491	.	.	.	.	.	T	-0.33	0.49	*	.	F	0.15	0.43
	Asn	492	.	.	.	.	.	T	-0.84	0.79	.	.	F	0.15	0.37
10	Gly	493	.	.	.	.	.	T	-0.88	0.97	.	.	F	0.15	0.35
	Ala	494	.	.	.	B	.	.	-1.18	0.61	.	.	.	-0.40	0.26
	Phe	495	.	.	B	B	.	.	-0.82	0.91	.	.	.	-0.60	0.11
	Leu	496	.	.	B	B	.	.	-1.41	0.94	.	.	.	-0.60	0.11
	Gly	497	.	.	B	B	.	.	-1.72	1.20	.	.	.	-0.60	0.08
15	Ile	498	.	.	B	B	.	.	-1.97	1.19	.	.	.	-0.60	0.13
	Gly	499	.	.	B	B	.	.	-2.19	0.90	.	.	.	-0.60	0.16
	Ile	500	.	A	B	.	.	.	-2.30	0.90	.	.	.	-0.60	0.13
	Thr	501	.	A	B	.	.	.	-2.19	1.16	.	.	.	-0.60	0.16
	Ala	502	.	A	B	.	.	.	-2.66	1.26	.	.	.	-0.60	0.14
20	Leu	503	.	A	B	.	.	.	-2.43	1.51	.	.	.	-0.60	0.16
	Leu	504	.	A	B	.	.	.	-2.90	1.40	.	.	.	-0.60	0.06
	Phe	505	.	A	B	.	.	.	-2.60	1.60	.	.	.	-0.60	0.05
	Leu	506	.	A	B	.	.	.	-3.10	1.60	.	.	.	-0.60	0.06
	Cys	507	A	A	.	.	.	.	-3.40	1.60	.	.	.	-0.60	0.06
25	Leu	508	A	A	.	.	.	.	-3.48	1.60	.	.	.	-0.60	0.05
	Ala	509	A	A	.	.	.	.	-3.27	1.50	*	.	.	-0.60	0.04
	Leu	510	A	A	.	.	.	.	-2.52	1.43	*	.	.	-0.60	0.08
	Ile	511	.	A	B	.	.	.	-2.60	0.86	*	.	.	-0.60	0.19
	Ile	512	.	A	B	.	.	.	-2.74	0.86	*	.	.	-0.60	0.13
30	Met	513	.	A	B	.	.	.	-2.14	1.04	*	.	.	-0.60	0.13
	Lys	514	.	A	B	.	.	.	-1.51	0.79	*	.	.	-0.26	0.28
	Ile	515	.	A	B	.	.	.	-0.59	0.10	.	.	.	0.38	0.81
	Leu	516	.	A	B	.	.	.	0.41	-0.59	.	*	.	1.77	1.61
	Pro	517	.	.	.	.	.	T	0.99	-1.20	.	.	F	2.86	1.57
35	Lys	518	.	.	.	.	.	T	1.59	-0.71	.	*	F	3.40	3.24
	Arg	519	.	.	.	.	.	T	1.23	-1.00	.	*	F	3.06	6.80
	Arg	520	.	.	.	.	.	T	2.12	-1.20	.	.	F	2.72	6.34
	Thr	521	.	.	.	.	.	T	2.62	-1.63	.	.	F	2.18	5.49
	Gln	522	.	.	B	.	.	.	2.62	-1.14	*	.	F	1.44	4.05
40	Thr	523	.	.	B	.	.	.	2.69	-0.71	*	.	F	1.10	3.20
	Glu	524	.	.	B	.	.	.	2.37	-0.71	*	*	F	1.10	4.34
	Thr	525	.	.	B	.	.	T	2.37	-0.77	.	*	F	1.30	3.87
	Pro	526	.	.	.	.	.	T	1.98	-1.17	.	*	F	1.50	5.26
	Arg	527	.	.	.	.	.	T	1.68	-0.87	*	*	F	1.84	2.63
	Pro	528	.	.	.	.	.	T	2.10	-0.49	*	*	F	2.08	2.44

	Arg	529	.	.	.	.	T	.	.	2.07	-0.97	*	*	F	2.52	3.09
	Phe	530	.	.	.	.	T	.	.	2.08	-0.90	*	*	F	2.86	2.15
	Ser	531	.	.	.	.	T	T	.	1.98	-0.51	.	*	F	3.40	1.86
5	Arg	532	.	.	B	.	.	T	.	0.98	-0.46	*	*	F	2.36	1.37
	His	533	.	.	B	.	.	T	.	0.38	0.23	*	.	F	1.42	1.11
	Ser	534	.	.	B	.	.	T	.	0.27	0.13	*	.	F	0.93	0.68
	Thr	535	.	.	B	B	.	.	.	0.72	-0.26	*	.	.	0.64	0.58
	Ile	536	.	.	B	B	.	.	.	0.13	0.50	*	.	.	-0.60	0.67
10	Leu	537	.	.	B	B	.	.	.	0.02	0.69	.	*	.	-0.60	0.35
	Asp	538	.	.	B	B	.	.	.	-0.80	0.70	*	.	.	-0.60	0.39
	Tyr	539	.	.	B	B	.	.	.	-1.36	0.86	*	.	.	-0.60	0.41
	Ile	540	.	.	B	B	.	.	.	-1.26	0.81	*	.	.	-0.60	0.37
	Asn	541	.	.	B	B	.	.	.	-0.68	0.56	*	.	.	-0.60	0.34
	Val	542	.	.	B	B	.	.	.	-0.46	1.04	*	.	.	-0.60	0.32
15	Val	543	.	.	B	B	.	.	.	-0.80	0.79	*	.	.	-0.60	0.46
	Pro	544	.	.	B	.	.	.	.	-0.77	0.53	*	.	F	-0.25	0.28
	Thr	545	.	.	B	.	.	T	.	-0.69	0.56	*	.	F	-0.05	0.59
	Ala	546	.	.	B	.	.	T	.	-1.28	0.60	*	.	F	-0.05	0.65
	Gly	547	.	.	B	.	.	T	.	-0.42	0.46	*	.	F	-0.05	0.43
20	Pro	548	.	.	B	.	.	T	.	0.48	0.43	*	.	F	0.21	0.51
	Leu	549	.	.	B	.	.	.	.	0.80	-0.06	.	.	F	1.32	1.01
	Ala	550	.	.	B	.	.	.	.	1.11	-0.56	.	.	F	1.88	2.00
	Gln	551	.	.	B	.	.	.	.	1.70	-0.59	.	.	F	2.14	2.08
	Lys	552	.	.	B	.	.	T	.	2.09	-0.61	*	.	F	2.60	4.38
25	Arg	553	.	.	B	.	.	T	.	1.71	-1.30	.	.	F	2.34	8.66
	Asn	554	.	.	B	.	.	T	.	2.21	-1.30	.	.	F	2.08	5.05
	Gln	555	.	.	B	.	.	T	.	2.59	-1.21	*	.	F	2.10	3.65
	Lys	556	.	.	B	.	.	.	.	2.59	-0.79	*	.	F	1.92	2.88
	Ala	557	.	.	.	.	.	.	C	2.24	-0.39	*	.	F	1.84	2.88
30	Thr	558	.	.	.	.	.	T	C	1.92	-0.40	*	.	F	2.32	2.23
	Pro	559	.	.	.	.	T	T	.	2.03	-0.37	*	.	F	2.80	1.72
	Asn	560	.	.	.	.	T	T	.	1.72	-0.37	*	.	F	2.52	3.34
	Ser	561	.	.	.	.	.	T	C	1.47	-0.39	*	*	F	2.04	3.34
	Pro	562	.	.	.	.	T	.	.	1.24	-0.44	*	.	F	1.76	3.34
35	Arg	563	.	.	.	.	T	.	.	1.34	-0.19	*	.	F	1.48	1.71
	Thr	564	.	.	B	.	.	.	.	1.34	-0.16	*	.	F	0.80	1.98
	Pro	565	.	.	B	.	.	.	.	1.00	-0.11	*	.	F	0.80	1.98
	Leu	566	.	.	B	.	.	.	.	0.71	-0.11	.	*	F	0.65	1.00
	Pro	567	.	.	B	.	.	T	.	0.71	0.39	.	*	F	0.25	0.70
40	Pro	568	.	.	.	.	T	T	.	0.30	0.33	.	.	F	0.65	0.70
	Gly	569	.	.	.	.	.	T	C	0.40	0.29	.	.	F	0.60	1.14



	Ala	570	.	.	.	.	.	T	C	0.61	0.03	.	.	F	0.94	1.14
	Pro	571	.	.	.	.	.	.	C	1.12	-0.40	.	.	F	1.68	1.27
	Ser	572	.	.	.	.	.	T	C	1.38	-0.44	.	.	F	2.22	1.72
	Pro	573	.	.	.	.	.	T	C	1.63	-0.87	.	.	F	2.86	3.41
5	Glu	574	.	.	.	.	T	T	.	1.98	-1.37	.	.	F	3.40	4.41
	Ser	575	.	.	.	.	T	T	.	2.57	-1.40	.	.	F	3.06	5.29
	Lys	576	.	.	.	.	T	T	.	2.82	-1.39	.	.	F	2.94	5.93
	Lys	577	.	.	.	.	T	T	.	3.17	-1.81	.	.	F	2.82	6.84
	Asn	578	.	.	.	.	T	T	.	3.38	-1.81	.	.	F	2.70	10.21
10	Gln	579	.	.	.	.	T	T	.	3.13	-1.80	*	.	F	2.58	8.84
	Lys	580	.	.	B	.	.	.	.	3.43	-1.04	*	.	F	2.20	6.93
	Lys	581	.	.	B	.	.	.	.	2.58	-0.64	*	.	F	1.98	7.46
	Gln	582	.	.	B	.	.	.	.	2.32	-0.36	*	.	F	1.46	3.55
	Tyr	583	.	.	B	.	.	.	.	2.02	-0.33	.	.	.	1.09	2.75
15	Gln	584	.	.	B	.	.	.	.	1.32	0.06	.	.	.	0.27	1.84
	Leu	585	.	.	B	.	.	T	.	1.07	0.84	.	.	.	-0.20	0.92
	Pro	586	.	.	B	.	.	T	.	1.02	0.87	.	.	F	-0.05	0.91
	Ser	587	.	.	B	.	.	T	.	0.81	0.11	.	.	F	0.59	0.91
	Phe	588	.	.	B	.	.	T	.	1.10	0.14	.	.	F	1.08	1.70
20	Pro	589	.	.	.	.	.	.	C	0.80	-0.54	.	.	F	2.32	2.20
	Glu	590	.	.	.	.	.	.	C	1.31	-0.59	.	.	F	2.66	2.20
	Pro	591	.	.	.	.	T	T	.	1.21	-0.59	.	.	F	3.40	3.41
	Lys	592	.	.	.	.	T	T	.	1.51	-0.89	.	.	F	3.06	3.18
	Ser	593	.	.	.	.	.	T	C	1.62	-0.91	.	.	F	2.52	3.18
25	Ser	594	.	.	.	.	.	T	C	1.62	-0.41	*	.	F	1.88	2.08
	Thr	595	.	.	.	.	.	.	C	1.62	-0.41	*	.	F	1.64	1.61
	Gln	596	.	.	.	.	.	.	C	1.53	-0.41	*	.	F	1.60	2.08
	Ala	597	.	.	.	.	.	T	C	1.49	-0.41	*	.	F	2.10	2.08
	Pro	598	.	.	.	.	.	T	C	1.79	-0.40	.	.	F	2.40	2.49
30	Glu	599	.	.	.	.	.	T	C	1.79	-0.89	.	.	F	3.00	2.49
	Ser	600	.	.	.	.	.	T	C	2.10	-0.90	.	.	F	2.70	3.31
	Gln	601	.	A	.	.	.	.	C	2.10	-1.00	.	.	F	2.00	3.70
	Glu	602	.	A	.	.	.	.	C	2.69	-1.43	.	.	F	1.70	3.70
	Ser	603	.	A	.	.	.	.	C	2.09	-1.43	.	.	F	1.40	4.79
35	Gln	604	A	A	.	.	.	.	.	2.06	-1.13	.	.	F	0.90	2.28
	Glu	605	A	A	.	.	.	.	.	2.11	-1.03	*	.	F	0.90	1.79
	Glu	606	A	A	.	.	.	.	.	1.52	-0.27	*	.	F	0.60	2.09
	Leu	607	.	A	B	.	.	.	.	1.21	-0.16	.	.	.	0.45	1.22
	His	608	.	A	B	.	.	.	.	0.70	-0.07	.	.	.	0.45	1.02
40	Tyr	609	.	A	B	.	.	.	.	0.70	0.61	.	.	.	-0.60	0.48
	Ala	610	.	A	B	.	.	.	.	0.00	1.01	*	.	.	-0.60	0.95

	Thr	611	.	A	B	.	.	.	-0.21	1.11	.	*	.	-0.60	0.60
	Leu	612	.	A	.	.	T	.	0.26	1.04	.	.	.	-0.20	0.59
	Asn	613	.	A	B	.	.	.	-0.57	0.71	*	.	.	-0.60	0.58
	Phe	614	.	.	B	B	.	.	-0.21	0.86	.	.	.	-0.60	0.30
5	Pro	615	.	.	.	B	T	.	0.17	0.37	.	*	F	0.25	0.71
	Gly	616	.	.	.	B	T	.	0.59	0.11	.	*	F	0.25	0.68
	Val	617	.	.	.	B	.	C	1.19	-0.29	.	*	F	0.80	1.54
	Arg	618	.	.	.	.	T	C	1.19	-0.64	.	*	F	1.50	1.54
	Pro	619	.	.	.	.	T	C	1.30	-1.07	.	*	F	1.50	2.70
10	Arg	620	.	.	.	.	T	C	1.62	-1.00	.	*	F	1.50	3.68
	Pro	621	.	.	B	.	T	.	1.37	-1.64	.	*	F	1.30	3.68
	Glu	622	.	.	.	.	T	.	2.01	-1.03	*	*	F	1.84	2.35
	Ala	623	.	.	B	.	.	.	1.94	-1.03	*	*	F	1.78	1.86
	Arg	624	.	.	B	.	.	.	1.81	-1.03	*	*	.	1.97	2.40
15	Met	625	.	.	B	.	T	.	1.39	-1.03	*	*	F	2.66	1.37
	Pro	626	.	.	.	.	T	T	1.60	-0.54	.	*	F	3.40	1.96
	Lys	627	.	.	.	.	T	T	1.01	-0.64	.	*	F	3.06	1.74
	Gly	628	.	.	.	.	T	C	1.60	-0.14	*	.	F	2.22	1.77
	Thr	629	.	A	.	.	.	C	1.24	-0.76	*	.	F	1.78	1.91
20	Gln	630	.	A	B	.	.	.	1.26	-0.43	.	.	F	0.94	1.50
	Ala	631	.	A	B	.	.	.	1.47	0.07	.	.	F	0.00	1.53
	Asp	632	.	A	B	.	.	.	0.57	-0.36	.	.	.	0.45	1.84
	Tyr	633	.	A	B	.	.	.	0.96	-0.20	.	*	.	0.30	0.79
	Ala	634	.	A	B	.	.	.	0.57	-0.60	.	*	.	0.75	1.56
25	Glu	635	.	A	B	.	.	.	0.57	-0.31	.	*	.	0.30	0.81
	Val	636	.	A	B	.	.	.	0.77	0.09	.	*	.	-0.30	0.89
	Lys	637	.	A	B	.	.	.	0.38	-0.24	.	*	.	0.45	1.13
	Phe	638	.	A	B	.	.	.	0.23	-0.31	.	*	.	0.30	0.83
	Gln	639	.	A	B	.	.	.	0.43	0.11	.	*	.	-0.15	1.44
30	Ter	640	.	A	B	.	.	.	0.04	-0.10	.	*	.	0.30	0.92

Table VI

	Res Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
5	Met 1	.	A	B	.	.	.	.	-1.90	0.96	.	.	.	-0.60	0.21
	Leu 2	.	A	B	.	.	.	.	-2.32	1.21	.	.	.	-0.60	0.13
	Leu 3	.	A	B	.	.	.	.	-2.74	1.47	.	.	.	-0.60	0.09
	Leu 4	.	A	B	.	.	.	.	-2.57	1.73	.	.	.	-0.60	0.07
	Leu 5	.	A	B	.	.	.	.	-2.99	1.54	.	.	.	-0.60	0.14
10	Leu 6	.	A	B	.	.	.	.	-3.20	1.54	.	.	.	-0.60	0.14
	Leu 7	.	A	B	.	.	.	.	-2.68	1.54	.	.	.	-0.60	0.14
	Pro 8	.	A	B	.	.	.	.	-2.21	1.77	*	.	.	-0.60	0.17
	Leu 9	.	A	B	.	.	.	.	-1.29	1.51	.	.	.	-0.60	0.21
	Leu 10	.	A	B	.	.	.	.	-0.48	0.83	.	*	.	-0.60	0.49
15	Trp 11	.	A	.	.	.	.	C	0.44	0.14	.	*	.	-0.10	0.55
	Gly 12	.	A	.	.	.	.	C	0.40	-0.29	.	*	F	0.80	1.31
	Arg 13	.	A	.	.	.	.	C	0.61	-0.33	.	*	F	0.80	1.18
	Glu 14	.	A	B	.	.	.	.	1.08	-1.01	.	*	F	0.90	1.94
	Arg 15	.	A	B	.	.	.	.	1.89	-1.50	.	*	F	1.24	1.94
20	Val 16	.	A	B	.	.	.	.	2.22	-1.53	.	*	F	1.58	1.71
	Glu 17	.	A	.	.	T	.	.	2.27	-1.53	.	*	F	2.32	1.98
	Gly 18	.	.	.	.	T	.	.	2.16	-1.14	*	*	F	2.86	1.35
	Gln 19	.	.	.	.	T	T	.	2.27	-0.74	.	*	F	3.40	2.93
	Lys 20	.	.	.	.	.	T	C	2.20	-1.39	.	*	F	2.86	3.32
25	Ser 21	.	.	.	.	.	T	C	3.06	-1.39	.	.	F	2.86	6.70
	Asn 22	.	.	.	.	T	T	.	2.81	-1.81	*	.	F	3.06	6.46
	Arg 23	.	.	.	.	T	T	.	2.86	-1.46	*	.	F	3.06	5.06
	Lys 24	.	.	.	.	T	T	.	2.04	-1.07	*	.	F	3.06	5.06
	Asp 25	.	.	.	.	T	T	.	1.69	-0.77	*	.	F	3.40	2.60
30	Tyr 26	.	.	B	.	.	T	.	1.39	-0.69	.	*	.	2.51	1.91
	Ser 27	.	.	B	B	.	.	.	1.39	-0.07	.	*	.	1.32	0.95
	Leu 28	.	.	B	B	.	.	.	0.98	0.33	.	*	.	0.38	0.98
	Thr 29	.	.	B	B	.	.	.	0.63	0.71	.	*	.	-0.26	0.84
	Met 30	.	.	B	.	.	T	.	-0.22	0.34	.	*	.	0.10	0.84
35	Gln 31	.	.	B	.	.	T	.	-0.29	0.60	.	*	F	-0.05	0.76
	Ser 32	.	.	B	.	.	T	.	-0.84	0.40	.	*	F	0.25	0.76
	Ser 33	.	.	B	.	.	T	.	-0.03	0.56	.	*	F	-0.05	0.57
	Val 34	.	.	B	B	.	.	.	0.28	0.34	.	*	F	-0.15	0.57
	Thr 35	.	.	B	B	.	.	.	0.53	-0.06	.	*	F	0.45	0.73
40	Val 36	.	.	B	B	.	.	.	-0.07	-0.01	.	.	F	0.45	0.54

5	Gln	37	.	.	B	B	.	.	.	-0.43	0.21	.	.	F	-0.15	0.72
	Glu	38	.	.	B	B	.	.	.	-0.99	0.14	.	.	F	-0.15	0.27
	Gly	39	.	.	.	B	T	.	.	-0.17	0.30	.	*	.	0.10	0.27
	Met	40	.	.	B	B	.	.	.	-0.71	0.16	*	*	.	-0.30	0.21
	Cys	41	.	.	B	B	.	.	.	0.26	0.40	*	*	.	-0.30	0.09
	Val	42	.	.	B	B	.	.	.	-0.41	0.40	*	*	.	-0.30	0.18
	His	43	.	.	B	B	.	.	.	-0.71	0.54	*	*	.	-0.60	0.10
10	Val	44	.	.	B	B	.	.	.	-1.07	0.31	.	*	.	-0.30	0.24
	Arg	45	.	.	B	B	.	.	.	-0.77	0.53	.	*	.	-0.60	0.28
	Cys	46	.	.	B	.	.	T	.	-0.34	0.27	.	*	.	0.10	0.28
	Ser	47	.	.	.	.	T	T	.	0.30	0.53	.	*	.	0.20	0.59
15	Phe	48	.	.	.	.	T	T	.	-0.52	0.31	*	*	.	0.50	0.46
	Ser	49	.	.	B	.	.	T	.	0.33	0.96	*	*	.	-0.20	0.64
	Tyr	50	.	.	B	.	.	.	.	-0.08	0.39	.	*	.	-0.10	0.80
	Pro	51	.	.	B	.	.	T	.	0.59	0.39	.	*	.	0.25	1.24
	Val	52	.	.	.	.	T	T	.	0.58	0.00	*	*	F	1.40	1.60
20	Asp	53	.	.	B	.	.	T	.	1.28	0.10	*	*	F	0.74	1.47
	Ser	54	.	.	B	.	.	T	.	1.28	-0.66	.	*	F	1.98	1.59
	Gln	55	.	.	B	.	.	.	.	1.52	-0.70	.	*	F	2.12	2.87
	Thr	56	.	.	.	.	T	.	.	1.52	-1.34	.	*	F	2.86	2.87
	Asp	57	.	.	.	.	T	T	.	1.52	-0.91	.	*	F	3.40	3.31
25	Ser	58	.	.	.	.	.	T	C	1.49	-0.66	.	.	F	2.86	1.42
	Asp	59	.	.	B	.	.	T	.	1.44	-0.56	.	.	F	2.32	1.34
	Pro	60	.	.	B	.	.	T	.	1.20	-0.61	.	.	F	1.83	0.79
	Val	61	.	.	.	.	T	.	.	1.22	0.14	.	.	.	0.64	0.93
	His	62	.	.	B	.	.	T	.	0.52	0.67	*	.	.	-0.20	0.58
30	Gly	63	.	.	B	.	.	T	.	0.93	1.46	*	.	.	-0.20	0.33
	Tyr	64	.	.	B	.	.	T	.	0.34	1.03	*	.	.	-0.20	0.86
	Trp	65	.	.	B	.	.	T	.	0.21	0.89	*	.	.	-0.20	0.64
	Phe	66	.	.	B	.	.	.	.	1.07	0.81	*	.	.	-0.09	0.64
	Arg	67	.	.	B	.	.	T	.	1.10	0.79	*	*	.	0.42	0.66
35	Ala	68	.	.	.	.	T	T	.	0.56	0.03	*	*	.	1.58	1.04
	Gly	69	.	.	.	.	T	T	.	0.50	-0.20	*	*	F	2.49	0.85
	Asn	70	.	.	.	.	T	T	.	0.50	-0.60	*	*	F	3.10	0.58
	Asp	71	.	.	.	.	.	.	C	1.24	0.31	*	*	F	1.49	0.60
	Ile	72	.	.	.	.	.	.	C	0.54	-0.19	*	*	F	1.93	1.22
40	Ser	73	.	A	.	.	T	.	.	0.92	-0.11	.	*	.	1.32	0.76
	Trp	74	.	A	B	.	.	.	.	0.41	-0.09	.	*	.	0.61	0.71
	Lys	75	.	A	B	.	.	.	.	-0.18	0.56	.	*	.	-0.60	0.75
	Ala	76	.	A	B	.	.	.	.	-0.49	0.37	.	*	.	-0.30	0.56
	Pro	77	.	.	B	.	.	.	.	0.40	0.47	.	*	.	-0.40	0.77

5	Val	78	.	.	B	.	.	.	0.70	-0.04	.	*	.	0.50 0.62
	Ala	79	.	.	B	.	.	.	0.78	0.36	.	*	.	-0.10 0.99
	Thr	80	.	.	.	.	.	C	0.14	0.29	.	.	F	0.25 0.99
	Asn	81	.	.	.	.	.	C	0.44	0.36	.	.	F	0.40 1.35
	Asn	82	.	.	.	.	T	C	0.07	0.63	.	.	F	0.30 1.41
10	Pro	83	.	.	.	.	T	C	0.07	0.63	.	.	F	0.15 0.98
	Ala	84	.	.	.	.	T	T	0.66	0.79	*	.	.	0.20 0.45
	Trp	85	.	.	.	.	T	C	0.97	0.79	.	.	.	0.00 0.49
	Ala	86	.	A	B	.	.	.	0.97	0.39	.	.	.	-0.30 0.55
	Val	87	.	A	B	.	.	.	0.66	-0.04	*	*	.	0.30 0.94
15	Gln	88	.	A	B	.	.	.	0.98	-0.06	*	.	F	0.94 1.29
	Glu	89	.	A	B	.	.	.	1.57	-0.97	.	*	F	1.58 2.50
	Glu	90	.	A	B	.	.	.	1.97	-1.47	.	*	F	1.92 5.62
	Thr	91	.	.	.	.	T	T	1.86	-2.11	.	*	F	3.06 6.36
	Arg	92	.	.	.	.	T	T	2.68	-1.73	.	*	F	3.40 3.18
20	Asp	93	.	.	.	.	T	T	1.87	-1.23	.	*	F	3.06 2.50
	Arg	94	.	.	B	.	.	T	1.06	-0.54	*	*	.	2.17 1.43
	Phe	95	.	A	B	.	.	.	0.71	-0.34	*	*	.	0.98 0.60
	His	96	.	A	B	.	.	.	1.02	0.09	*	*	.	0.04 0.36
	Leu	97	.	A	.	.	.	C	0.70	0.09	.	*	.	-0.10 0.30
25	Leu	98	.	A	.	.	T	.	0.70	0.51	.	*	.	-0.20 0.54
	Gly	99	.	A	.	.	T	.	0.28	0.13	*	*	F	0.59 0.69
	Asp	100	.	.	.	.	.	C	1.02	0.11	*	*	F	1.08 1.21
	Pro	101	.	.	.	.	T	.	1.06	-0.57	.	.	F	2.52 2.93
	Gln	102	.	.	.	.	T	.	1.20	-0.86	.	.	F	2.86 4.76
30	Thr	103	.	.	.	.	T	T	1.70	-0.71	.	.	F	3.40 1.53
	Lys	104	.	.	B	.	.	T	1.23	-0.23	.	.	F	2.36 1.43
	Asn	105	.	.	B	.	.	T	0.93	0.03	.	.	F	1.27 0.68
	Cys	106	.	.	B	.	.	T	0.26	0.01	*	*	.	0.78 0.63
	Thr	107	.	.	B	B	.	.	0.37	0.21	*	*	.	0.04 0.22
35	Leu	108	.	.	B	B	.	.	0.68	0.21	*	*	.	-0.30 0.27
	Ser	109	.	.	B	B	.	.	0.04	-0.19	*	.	.	0.30 0.84
	Ile	110	.	.	B	B	.	.	0.16	-0.26	*	*	.	0.30 0.59
	Arg	111	.	.	B	B	.	.	0.22	-0.74	*	*	F	0.90 1.39
	Asp	112	.	A	B	.	.	.	0.23	-0.81	*	.	F	0.90 1.03
40	Ala	113	.	A	B	.	.	.	1.04	-0.81	*	.	F	0.90 1.97
	Arg	114	.	A	B	.	.	.	0.76	-1.50	*	.	.	1.03 1.68
	Met	115	.	A	B	.	.	.	1.30	-1.00	.	*	F	1.46 1.01
	Ser	116	.	A	.	.	.	C	1.30	-0.57	.	*	F	1.79 0.99
	Asp	117	.	.	.	.	T	T	1.06	-1.07	*	*	F	2.67 0.99
	Ala	118	.	.	.	.	T	T	0.94	-0.31	*	*	F	2.80 1.57

	Gly	119	.	.	.	.	T	T	.	0.13	-0.14	*	*	F	2.52	1.02
	Arg	120	.	.	B	.	.	T	.	0.84	0.26	*	*	.	0.94	0.53
	Tyr	121	.	.	B	B	.	.	.	0.54	0.26	*	*	.	0.41	1.02
	Phe	122	.	.	B	B	.	.	.	0.54	0.37	*	*	.	0.13	1.02
5	Phe	123	.	.	B	B	.	.	.	1.18	-0.06	*	*	.	0.30	0.90
	Arg	124	.	.	B	B	.	.	.	1.18	-0.06	*	*	.	0.79	1.15
	Met	125	.	.	B	.	.	.	.	1.07	-0.39	*	*	.	1.33	1.32
	Glu	126	.	.	.	.	T	T	.	0.42	-0.77	*	*	F	2.72	2.45
	Lys	127	.	.	.	.	T	T	.	1.17	-0.87	*	*	F	2.91	0.88
10	Gly	128	.	.	.	.	T	T	.	1.58	-0.87	*	*	F	3.40	1.77
	Asn	129	.	.	.	.	T	T	.	1.47	-0.57	*	*	F	3.06	1.08
	Ile	130	.	.	.	.	.	.	C	1.82	-0.17	.	*	F	1.87	0.86
	Lys	131	.	.	.	.	T	.	.	1.87	0.59	.	*	.	0.83	1.37
	Trp	132	.	.	.	.	T	.	.	1.58	0.16	.	*	.	0.79	1.70
15	Asn	133	.	.	B	.	.	T	.	1.92	0.51	.	*	.	0.19	3.81
	Tyr	134	.	.	B	.	.	T	.	1.92	-0.17	.	*	.	1.33	3.18
	Lys	135	.	.	B	.	.	T	.	2.00	0.23	*	*	.	0.97	5.23
	Tyr	136	.	.	.	.	T	T	.	1.66	0.00	.	*	F	2.36	2.68
	Asp	137	.	.	.	.	T	.	.	1.09	-0.01	.	*	F	2.40	2.30
20	Gln	138	.	.	B	B	.	.	.	1.09	-0.13	.	*	F	1.41	0.85
	Leu	139	.	.	B	B	.	.	.	0.48	0.27	.	*	.	0.42	0.87
	Ser	140	.	.	B	B	.	.	.	0.12	0.16	.	*	.	0.18	0.39
	Val	141	.	.	B	B	.	.	.	-0.22	0.64	*	*	.	-0.36	0.32
	Asn	142	.	.	B	B	.	.	.	-1.03	0.74	.	*	.	-0.60	0.40
25	Val	143	.	.	B	B	.	.	.	-1.34	0.74	.	*	.	-0.60	0.24
	Thr	144	.	.	B	B	.	.	.	-0.57	0.84	*	*	.	-0.60	0.47
	Ala	145	.	.	B	B	.	.	.	-0.16	0.70	.	*	.	-0.60	0.40
	Leu	146	.	.	B	B	.	.	.	0.49	0.30	.	*	.	-0.15	1.06
	Thr	147	.	.	B	B	.	.	.	0.49	0.09	.	*	.	-0.15	1.14
30	His	148	.	.	B	B	.	.	.	0.46	0.00	.	*	.	0.45	1.81
	Arg	149	.	.	B	.	.	T	.	-0.04	0.19	.	*	.	0.25	1.54
	Pro	150	.	.	B	.	.	T	.	-0.34	0.19	.	*	.	0.10	0.88
	Asn	151	.	.	.	.	T	T	.	0.26	0.39	.	*	.	0.50	0.45
	Ile	152	.	.	B	.	.	T	.	0.22	0.31	.	*	.	0.10	0.36
35	Leu	153	.	.	B	.	.	.	.	-0.06	0.74	.	*	.	-0.40	0.23
	Ile	154	.	.	B	.	.	T	.	-0.98	0.80	*	*	.	-0.20	0.21
	Pro	155	.	.	B	.	.	T	.	-0.77	1.09	.	*	F	-0.05	0.24
	Gly	156	.	.	B	.	.	T	.	-1.07	0.40	.	*	F	0.25	0.51
	Thr	157	.	.	B	.	.	T	.	-0.52	0.10	.	.	F	0.25	0.97
40	Leu	158	.	.	B	.	.	.	.	-0.38	-0.16	.	.	F	0.65	0.62
	Glu	159	.	.	B	.	.	T	.	-0.19	-0.01	.	.	F	0.85	0.34

	Ser	160	.	.	.	.	T	T	.	0.02	0.34	.	.	F	0.65	0.20
	Gly	161	.	.	.	.	T	T	.	0.37	0.26	.	.	F	0.61	0.42
	Cys	162	.	.	.	.	T	T	.	-0.13	-0.03	.	.	.	1.02	0.39
5	Phe	163	.	.	B	B	.	.	.	0.37	0.66	.	.	.	-0.72	0.24
	Gln	164	.	.	B	B	.	.	.	-0.30	0.76	.	.	.	-0.76	0.35
	Asn	165	.	.	.	B	T	.	.	-0.30	0.90	*	.	.	-0.40	0.35
	Leu	166	.	.	B	B	.	.	.	-0.81	0.71	*	.	.	-0.76	0.55
	Thr	167	.	.	.	B	T	.	.	-0.36	0.57	*	.	.	-0.32	0.23
10	Cys	168	.	.	.	B	T	.	.	0.06	0.60	*	.	.	-0.28	0.22
	Ser	169	.	.	.	B	T	.	.	-0.53	1.11	*	.	.	-0.24	0.29
	Val	170	.	.	.	B	.	.	C	-1.20	0.93	*	*	.	-0.40	0.20
	Pro	171	.	.	.	.	T	.	.	-0.39	1.01	*	.	.	0.00	0.20
	Trp	172	.	.	.	.	T	.	.	-0.08	0.44	.	.	.	0.00	0.26
15	Ala	173	.	.	B	.	.	.	.	0.24	0.46	.	.	.	-0.12	0.61
	Cys	174	.	.	B	.	.	.	.	0.23	0.24	.	.	.	0.46	0.39
	Glu	175	.	.	.	.	T	T	.	0.88	0.30	.	.	F	1.49	0.53
	Gln	176	.	.	.	.	T	T	.	0.88	-0.19	.	.	F	2.37	0.81
	Gly	177	.	.	.	.	T	T	.	0.57	-0.26	.	.	F	2.80	2.35
20	Thr	178	.	.	.	.	.	T	C	0.27	-0.21	.	.	F	2.32	1.34
	Pro	179	.	.	.	.	.	.	C	0.63	0.47	*	.	F	0.79	0.54
	Pro	180	.	.	.	B	.	.	C	0.34	0.46	*	.	F	0.31	0.74
	Met	181	.	.	B	B	.	.	.	-0.26	0.94	*	.	.	-0.32	0.54
	Ile	182	.	.	B	B	.	.	.	-0.26	1.07	.	.	.	-0.60	0.34
25	Ser	183	.	.	B	B	.	.	.	-0.26	1.07	.	.	.	-0.60	0.22
	Trp	184	.	.	B	B	.	.	.	-0.34	1.13	*	.	.	-0.60	0.32
	Met	185	.	.	B	B	.	.	.	-0.99	0.90	*	.	.	-0.60	0.61
	Gly	186	.	.	.	B	T	.	.	-0.69	0.86	*	.	.	-0.20	0.34
	Thr	187	.	.	.	B	.	.	C	-0.01	0.86	*	.	F	-0.25	0.43
30	Ser	188	.	.	.	B	.	.	C	-0.52	0.37	*	.	F	0.05	0.67
	Val	189	.	.	B	B	.	.	.	-0.27	0.44	.	.	F	-0.45	0.56
	Ser	190	.	.	.	.	.	.	C	0.12	0.51	.	.	F	-0.05	0.53
	Pro	191	.	.	.	.	.	.	C	0.17	0.46	.	.	F	-0.05	0.61
	Leu	192	.	.	.	.	.	.	C	0.17	0.46	.	.	F	0.34	1.10
35	His	193	.	.	B	.	.	T	.	0.16	0.30	*	.	F	0.88	1.19
	Pro	194	.	.	B	.	.	T	.	1.12	0.40	*	.	F	0.82	1.11
	Ser	195	.	.	.	.	T	T	.	1.12	-0.03	*	.	F	2.36	2.64
	Thr	196	.	.	.	.	.	T	C	1.03	-0.33	.	.	F	2.40	2.60
	Thr	197	.	.	B	.	.	T	.	0.99	-0.44	.	.	F	1.96	2.25
40	Arg	198	.	.	B	.	.	T	.	0.21	-0.23	.	.	F	1.72	1.25
	Ser	199	.	.	B	.	.	T	.	0.11	0.07	.	.	F	0.73	0.71
	Ser	200	.	.	B	.	.	T	.	-0.40	0.07	.	.	F	0.49	0.71

	Val	201	.	.	B	B	.	.	.	-0.98	0.27	.	.	.	-0.30	0.30
	Leu	202	.	.	B	B	.	.	.	-0.88	0.96	.	.	.	-0.60	0.16
	Thr	203	.	.	B	B	.	.	.	-0.99	1.00	.	.	.	-0.60	0.18
	Leu	204	.	.	B	B	.	.	.	-0.90	1.01	*	.	.	-0.60	0.42
5	Ile	205	.	.	B	B	.	.	.	-0.60	0.80	*	.	.	-0.60	0.79
	Pro	206	.	.	B	B	.	.	.	0.22	0.51	*	.	F	-0.45	0.95
	Gln	207	.	.	B	.	.	.	.	1.00	0.53	*	.	F	-0.10	1.57
	Pro	208	.	.	B	.	.	.	.	0.97	0.34	*	.	F	0.20	3.04
	Gln	209	.	.	.	.	T	.	.	1.47	0.09	*	.	F	0.60	1.95
10	His	210	.	.	.	.	T	T	.	2.06	0.14	*	.	F	0.80	1.62
	His	211	.	.	.	.	T	T	.	1.46	0.13	.	.	F	0.80	1.41
	Gly	212	.	.	.	.	T	T	.	1.14	0.39	.	.	F	0.65	0.67
	Thr	213	.	.	.	.	T	T	.	0.69	0.47	.	.	F	0.35	0.71
	Ser	214	.	.	.	B	T	.	.	0.69	0.54	*	.	F	-0.05	0.28
15	Leu	215	.	.	B	B	.	.	.	-0.13	0.44	*	.	.	-0.60	0.49
	Thr	216	.	.	B	B	.	.	.	-0.41	0.66	.	*	.	-0.60	0.25
	Cys	217	.	.	B	B	.	.	.	-0.88	0.66	.	*	.	-0.60	0.27
	Gln	218	.	.	B	B	.	.	.	-0.78	0.96	.	*	.	-0.60	0.27
	Val	219	.	.	B	B	.	.	.	-0.82	0.70	.	*	.	-0.60	0.29
20	Thr	220	.	.	B	B	.	.	.	-0.60	0.64	.	*	.	-0.60	0.54
	Leu	221	.	.	B	.	.	T	.	-0.63	0.57	.	.	.	-0.20	0.31
	Pro	222	.	.	B	.	.	T	.	-0.82	0.60	.	.	F	-0.05	0.42
	Gly	223	.	.	.	.	T	T	.	-1.13	0.60	.	.	F	0.35	0.21
	Ala	224	.	.	.	.	.	T	C	-0.59	0.60	.	.	F	0.35	0.38
25	Gly	225	.	.	B	.	.	.	.	-0.28	0.40	*	.	F	0.15	0.35
	Val	226	.	.	B	.	.	.	.	0.64	0.37	*	.	F	0.65	0.57
	Thr	227	.	.	B	.	.	T	.	0.54	-0.06	*	.	F	1.80	1.10
	Thr	228	.	.	B	.	.	T	.	0.00	-0.07	*	.	F	2.00	1.61
	Asn	229	.	.	B	.	.	T	.	0.59	0.19	*	.	F	1.20	1.52
30	Arg	230	.	.	B	.	.	T	.	0.12	-0.06	.	.	F	1.60	1.83
	Thr	231	.	.	B	B	.	.	.	0.98	0.14	.	*	F	0.40	1.04
	Ile	232	.	.	B	B	.	.	.	0.43	0.06	*	*	.	0.05	1.04
	Gln	233	.	.	B	B	.	.	.	0.44	0.30	*	*	.	-0.30	0.40
	Leu	234	.	.	B	B	.	.	.	0.20	0.69	*	*	.	-0.60	0.37
35	Asn	235	.	.	B	.	.	T	.	-0.12	0.96	*	*	.	-0.20	0.82
	Val	236	.	.	B	.	.	T	.	-0.02	0.70	.	*	.	-0.20	0.73
	Ser	237	.	.	.	.	.	T	C	0.87	0.73	.	*	.	0.15	1.37
	Tyr	238	.	.	.	.	.	T	C	0.87	0.44	.	*	F	0.30	1.48
	Pro	239	.	.	.	.	.	.	C	0.87	0.44	.	*	F	0.10	3.21
40	Pro	240	.	.	.	.	T	T	.	0.56	0.49	.	.	F	0.50	1.97
	Gln	241	.	.	.	.	T	T	.	0.56	0.59	.	.	F	0.50	1.82



	Asn	242	.	.	B	.	.	T	.	0.54	0.47	.	.	F	-0.05	0.87
	Leu	243	.	.	B	.	.	T	.	-0.07	0.53	.	.	.	-0.20	0.81
	Thr	244	.	.	B	B	.	.	.	-0.56	0.74	*	.	.	-0.60	0.35
	Val	245	.	.	B	B	.	.	.	-0.34	1.13	*	.	.	-0.60	0.19
5	Thr	246	.	.	B	B	.	.	.	-0.69	1.13	.	.	.	-0.60	0.39
	Val	247	.	.	B	B	.	.	.	-0.69	0.87	.	*	.	-0.60	0.27
	Phe	248	.	.	B	B	.	.	.	-0.22	0.39	.	.	.	-0.30	0.63
	Gln	249	.	.	B	B	.	.	.	-0.22	0.17	.	.	F	0.09	0.43
	Gly	250	.	.	.	.	.	T	C	0.04	0.17	.	.	F	0.93	0.84
10	Glu	251	.	.	.	.	.	T	C	0.06	0.03	.	*	F	1.17	0.98
	Gly	252	.	.	.	.	.	T	C	0.60	-0.37	.	.	F	2.01	0.76
	Thr	253	.	.	.	.	.	T	C	0.71	-0.29	.	*	F	2.40	1.11
	Ala	254	.	.	B	.	.	.	.	-0.10	-0.21	.	.	F	1.61	0.65
	Ser	255	.	.	B	.	.	.	.	-0.10	0.47	.	.	F	0.47	0.54
15	Thr	256	.	.	B	.	.	.	.	-0.10	0.47	.	.	F	0.23	0.37
	Ala	257	.	.	B	.	.	.	.	-0.06	0.39	.	.	F	0.29	0.59
	Leu	258	.	.	B	.	.	.	.	-0.04	0.27	.	.	F	0.05	0.59
	Gly	259	.	.	.	.	T	.	.	0.24	0.27	.	.	F	0.45	0.55
	Asn	260	.	.	.	.	.	T	C	-0.27	0.17	.	.	F	0.45	0.72
20	Ser	261	.	.	.	.	.	T	C	-0.26	0.36	.	.	F	0.45	0.72
	Ser	262	.	.	.	.	.	T	C	-0.52	0.06	.	.	F	0.45	0.98
	Ser	263	.	.	.	.	.	T	C	-0.52	0.27	.	.	F	0.45	0.45
	Leu	264	.	A	B	.	.	.	.	-0.18	0.56	.	.	F	-0.45	0.28
	Ser	265	.	A	B	.	.	.	.	-0.52	0.17	.	.	.	-0.30	0.36
25	Val	266	.	A	B	.	.	.	.	-0.22	0.21	.	.	.	-0.30	0.27
	Leu	267	.	A	B	.	.	.	.	-0.22	0.23	.	.	.	-0.13	0.56
	Glu	268	.	A	B	.	.	.	.	-0.73	-0.07	*	.	F	0.79	0.56
	Gly	269	.	.	.	.	T	T	.	0.19	0.23	*	.	F	1.16	0.62
	Gln	270	.	.	.	.	T	T	.	-0.32	-0.41	*	.	F	2.08	1.47
30	Ser	271	.	.	B	.	.	T	.	-0.32	-0.41	*	.	F	1.70	0.70
	Leu	272	.	.	B	.	.	T	.	-0.18	0.23	*	.	F	0.93	0.53
	Arg	273	.	.	B	B	.	.	.	-0.77	0.37	*	.	.	0.21	0.16
	Leu	274	.	.	B	B	.	.	.	-1.28	0.47	*	*	.	-0.26	0.12
	Val	275	.	.	B	B	.	.	.	-1.28	0.73	*	*	.	-0.43	0.11
35	Cys	276	.	.	B	B	.	.	.	-1.28	0.04	*	*	.	-0.30	0.09
	Ala	277	.	.	B	B	.	.	.	-0.47	0.43	*	*	.	-0.60	0.15
	Val	278	.	.	B	B	.	.	.	-0.79	0.14	*	*	.	0.00	0.33
	Asp	279	.	.	.	.	T	T	.	-0.19	-0.07	.	.	F	1.85	0.96
	Ser	280	.	.	.	.	.	T	C	0.08	-0.21	.	*	F	2.10	1.46
40	Asn	281	.	.	.	.	.	T	C	0.86	-0.21	.	*	F	2.40	1.99
	Pro	282	.	.	.	.	.	T	C	0.63	-0.86	.	*	F	3.00	2.34

	Pro	283	.	.	.	.	T	.	.	1.19	-0.17	.	*	F	2.40	1.44
	Ala	284	.	.	.	.	T	.	.	0.90	-0.17	.	*	F	2.10	1.20
	Arg	285	.	.	B	B	.	.	.	0.89	0.34	*	*	.	0.30	0.82
	Leu	286	.	.	B	B	.	.	.	0.60	0.40	*	*	.	-0.30	0.76
5	Ser	287	.	.	B	B	.	.	.	0.92	0.89	*	*	.	-0.60	0.79
	Trp	288	.	.	B	B	.	.	.	0.83	0.39	*	*	.	-0.30	0.79
	Thr	289	.	.	B	B	.	.	.	0.61	0.77	*	*	.	-0.45	1.29
	Trp	290	.	.	B	B	.	.	.	0.19	0.77	*	*	.	-0.60	0.79
	Arg	291	.	.	B	B	.	.	.	0.19	0.87	*	*	.	-0.45	1.09
10	Ser	292	.	.	B	B	.	.	.	0.24	0.64	*	.	.	-0.60	0.62
	Leu	293	.	.	.	B	T	.	.	0.32	0.91	*	.	.	-0.20	0.93
	Thr	294	.	.	.	B	T	.	.	0.33	0.43	*	.	.	-0.20	0.73
	Leu	295	.	.	.	B	.	.	C	0.62	0.81	*	.	.	-0.40	0.73
	Tyr	296	.	.	B	.	.	T	.	0.30	0.83	*	.	F	0.10	1.53
15	Pro	297	.	.	.	.	T	T	.	0.30	0.57	.	.	F	0.62	1.64
	Ser	298	.	.	.	.	T	T	.	1.11	0.47	.	.	F	0.74	2.67
	Gln	299	.	.	.	.	.	T	C	1.21	0.19	.	.	F	0.96	2.74
	Pro	300	.	.	.	.	T	T	.	1.21	-0.14	.	.	F	1.88	2.74
	Ser	301	.	.	.	.	.	T	C	0.60	0.11	.	.	F	1.20	1.69
20	Asn	302	.	.	.	.	.	T	C	0.00	0.37	.	.	F	0.93	0.72
	Pro	303	.	.	B	.	.	T	.	0.30	0.66	*	.	F	0.31	0.39
	Leu	304	.	A	B	.	.	.	.	-0.51	0.23	*	*	F	0.09	0.50
	Val	305	.	A	B	.	.	.	.	-0.30	0.53	.	*	.	-0.48	0.26
	Leu	306	.	A	B	.	.	.	.	-0.86	0.53	.	*	.	-0.60	0.29
25	Glu	307	.	A	B	.	.	.	.	-0.89	0.74	.	*	.	-0.60	0.26
	Leu	308	.	A	B	.	.	.	.	-1.49	0.56	.	*	.	-0.60	0.47
	Gln	309	.	A	B	.	.	.	.	-1.02	0.60	*	*	.	-0.60	0.47
	Val	310	.	A	B	.	.	.	.	-0.17	0.34	*	*	.	-0.30	0.27
	His	311	.	A	B	.	.	.	.	0.64	0.34	*	*	.	-0.30	0.55
30	Leu	312	.	A	.	.	.	.	C	0.30	-0.34	*	*	.	0.84	0.55
	Gly	313	.	.	.	.	.	T	C	1.11	-0.31	.	*	F	1.73	0.73
	Asp	314	.	.	.	.	T	T	.	0.41	-0.96	.	*	F	2.57	0.93
	Glu	315	.	.	.	.	T	T	.	0.96	-0.67	.	*	F	2.91	0.97
	Gly	316	.	.	.	.	T	T	.	0.32	-0.87	*	*	F	3.40	1.42
35	Glu	317	.	A	.	.	T	.	.	1.24	-0.73	*	*	F	2.51	0.46
	Phe	318	.	A	B	.	.	.	.	1.00	-0.73	*	*	.	1.62	0.52
	Thr	319	.	A	B	.	.	.	.	1.00	-0.23	*	*	.	0.98	0.53
	Cys	320	.	A	B	.	.	.	.	1.00	-0.26	*	*	.	0.89	0.53
	Arg	321	.	A	.	.	T	.	.	1.04	0.14	*	*	.	0.60	0.98
40	Ala	322	.	A	.	.	T	.	.	0.23	-0.26	*	*	F	1.60	0.91
	Gln	323	.	A	.	.	T	.	.	0.59	-0.06	*	*	F	2.00	1.40

	Asn	324	.	.	.	.	T	T	.	0.60	-0.20	*	*	F	2.50	0.71
	Ser	325	.	.	.	.	.	T	C	1.27	0.19	*	*	F	1.45	0.94
	Leu	326	.	.	.	.	.	T	C	1.12	0.09	*	*	F	1.20	0.94
	Gly	327	.	.	.	.	T	T	.	0.86	0.19	.	.	F	1.15	0.79
5	Ser	328	.	.	B	B	.	.	.	0.56	0.43	.	.	F	-0.20	0.44
	Gln	329	.	.	B	B	.	.	.	-0.26	0.43	.	.	F	-0.45	0.71
	His	330	.	.	B	B	.	.	.	0.04	0.43	.	*	.	-0.60	0.59
	Val	331	.	.	B	B	.	.	.	0.04	0.40	.	*	.	-0.60	0.71
	Ser	332	.	A	B	.	.	.	.	0.09	0.70	.	*	.	-0.60	0.34
10	Leu	333	.	A	B	.	.	.	.	-0.42	0.69	.	*	.	-0.60	0.33
	Asn	334	.	A	B	.	.	.	.	-0.42	0.87	.	*	.	-0.60	0.37
	Leu	335	.	A	.	.	.	.	C	-0.39	0.63	.	*	.	-0.40	0.48
	Ser	336	.	A	.	.	.	.	C	0.47	0.64	.	*	.	-0.25	1.01
	Leu	337	.	A	B	.	.	.	.	0.52	-0.04	.	*	.	0.45	1.09
15	Gln	338	.	A	B	.	.	.	.	1.02	0.31	.	*	F	0.00	2.06
	Gln	339	.	A	B	.	.	.	.	0.68	0.11	.	*	F	0.34	2.22
	Glu	340	.	A	B	.	.	.	.	1.53	0.16	.	*	F	0.68	2.66
	Tyr	341	.	.	B	.	.	T	.	1.23	-0.53	*	*	F	2.32	3.08
	Thr	342	.	.	.	.	T	T	.	2.16	-0.31	*	*	F	2.76	1.76
20	Gly	343	.	.	.	.	T	T	.	1.94	-0.71	*	*	F	3.40	1.99
	Lys	344	.	.	.	.	T	T	.	1.09	-0.29	*	*	F	2.76	1.96
	Met	345	.	.	B	.	.	.	.	0.79	-0.40	.	*	F	1.82	1.01
	Arg	346	.	.	B	.	.	.	.	0.69	-0.50	*	*	F	1.48	1.37
	Pro	347	.	.	B	.	.	T	.	0.14	-0.50	*	*	F	1.19	0.68
25	Val	348	.	.	B	.	.	T	.	-0.32	0.14	.	*	F	0.25	0.51
	Ser	349	.	.	B	.	.	T	.	-1.18	0.21	*	*	F	0.25	0.21
	Gly	350	.	.	B	.	.	T	.	-0.92	0.90	*	.	.	-0.20	0.11
	Val	351	.	.	B	B	.	.	.	-1.62	0.90	*	.	.	-0.60	0.15
	Leu	352	.	.	B	B	.	.	.	-2.27	0.76	.	.	.	-0.60	0.11
30	Leu	353	.	.	B	B	.	.	.	-1.76	1.01	.	.	.	-0.60	0.09
	Gly	354	.	.	B	B	.	.	.	-1.80	1.01	.	.	.	-0.60	0.11
	Ala	355	.	.	B	B	.	.	.	-2.04	0.80	.	.	.	-0.60	0.14
	Val	356	.	.	B	B	.	.	.	-1.53	0.61	.	.	.	-0.60	0.17
	Gly	357	.	.	B	.	.	.	.	-1.31	0.36	.	.	.	-0.10	0.17
35	Gly	358	.	.	.	.	.	T	C	-0.81	0.43	.	.	F	0.15	0.17
	Ala	359	.	.	B	.	.	T	.	-1.06	0.41	.	.	F	-0.05	0.33
	Gly	360	.	.	B	.	.	T	.	-1.28	0.27	.	.	.	0.10	0.33
	Ala	361	.	.	B	.	.	T	.	-1.28	0.53	.	.	.	-0.20	0.28
	Thr	362	.	.	B	B	.	.	.	-1.63	0.74	.	.	.	-0.60	0.20
40	Ala	363	.	.	B	B	.	.	.	-2.10	1.03	.	.	.	-0.60	0.18
	Leu	364	.	.	B	B	.	.	.	-1.81	1.29	.	.	.	-0.60	0.15

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	Val	365	.	.	B	B	.	.	.	-2.17	1.17	.	.	.	-0.60	0.14
	Phe	366	.	.	B	B	.	.	.	-2.24	1.47	.	.	.	-0.60	0.12
	Leu	367	.	.	B	B	.	.	.	-2.79	1.54	.	.	.	-0.60	0.08
	Ser	368	.	.	B	B	.	.	.	-3.09	1.50	.	.	.	-0.60	0.08
5	Phe	369	.	.	B	B	.	.	.	-2.98	1.54	.	.	.	-0.60	0.06
	Cys	370	.	.	B	B	.	.	.	-3.01	1.54	.	.	.	-0.60	0.06
	Val	371	.	.	B	B	.	.	.	-3.17	1.54	.	.	.	-0.60	0.03
	Ile	372	.	.	B	B	.	.	.	-3.21	1.80	*	*	.	-0.60	0.03
	Phe	373	.	.	B	B	.	.	.	-2.80	1.66	*	.	.	-0.60	0.04
10	Ile	374	.	.	B	B	.	.	.	-2.40	1.09	*	.	.	-0.60	0.11
	Val	375	.	.	B	B	.	.	.	-2.40	0.83	*	.	.	-0.26	0.20
	Val	376	.	.	B	B	.	.	.	-1.43	0.71	*	.	.	0.08	0.12
	Arg	377	.	.	B	.	.	T	.	-0.50	-0.07	*	.	.	1.72	0.35
	Ser	378	.	.	.	.	T	T	.	0.24	-0.76	*	.	F	2.91	0.94
15	Cys	379	.	.	.	.	T	T	.	0.83	-1.40	*	.	F	3.40	2.53
	Arg	380	.	.	.	.	T	T	.	1.10	-1.66	*	.	F	3.06	1.73
	Lys	381	.	A	.	.	T	.	.	2.07	-1.16	*	.	F	2.32	1.30
	Lys	382	.	A	.	.	T	.	.	1.74	-1.54	*	.	F	1.98	4.76
	Ser	383	.	A	.	.	.	.	C	1.46	-1.69	*	.	F	1.44	3.76
20	Ala	384	.	A	B	.	.	.	.	1.53	-1.19	*	*	F	0.90	1.90
	Arg	385	.	A	B	.	.	.	.	1.42	-0.69	*	*	F	0.75	0.96
	Pro	386	.	A	B	.	.	.	.	0.52	-0.69	*	*	F	0.90	1.20
	Ala	387	.	A	B	.	.	.	.	0.13	-0.43	*	.	.	0.30	0.88
	Ala	388	.	A	B	.	.	.	.	0.43	-0.50	*	*	.	0.30	0.44
25	Asp	389	.	.	B	.	.	T	.	0.13	-0.50	*	*	.	0.70	0.48
	Val	390	.	.	B	.	.	T	.	-0.32	-0.24	*	*	.	0.70	0.33
	Gly	391	.	.	B	.	.	T	.	-0.71	-0.31	*	.	F	0.85	0.33
	Asp	392	.	.	B	.	.	T	.	-0.08	-0.20	*	.	F	0.85	0.19
	Ile	393	.	A	B	.	.	.	.	0.51	-0.20	*	.	F	0.45	0.52
30	Gly	394	.	A	B	.	.	.	.	-0.08	-0.84	*	.	F	0.75	0.88
	Met	395	.	A	B	.	.	.	.	0.78	-0.77	*	.	F	1.01	0.53
	Lys	396	.	A	B	.	.	.	.	0.81	-0.37	*	.	F	1.12	1.22
	Asp	397	.	.	B	.	.	T	.	-0.08	-0.57	*	*	F	2.08	1.78
	Ala	398	.	.	B	.	.	T	.	0.92	-0.31	*	*	F	2.04	1.26
35	Asn	399	.	.	B	.	.	T	.	0.92	-0.93	*	*	F	2.60	1.23
	Thr	400	.	.	B	.	.	T	.	1.22	-0.50	*	*	F	1.89	0.73
	Ile	401	.	.	B	.	.	T	.	0.59	-0.11	*	*	F	1.63	0.97
	Arg	402	.	.	B	.	.	T	.	0.29	-0.11	*	.	F	1.61	0.61
	Gly	403	.	.	B	.	.	T	.	0.88	-0.13	*	*	F	1.59	0.57
40	Ser	404	.	.	.	.	.	T	C	0.53	-0.21	*	*	F	1.92	1.40
	Ala	405	.	.	.	.	.	.	C	0.84	-0.47	*	*	F	1.81	0.71

	Ser	406	.	.	.	.	.	T	C	0.92	-0.07	*	*	F	2.40	1.15
	Gln	407	.	.	.	.	.	T	C	0.50	0.19	*	.	F	1.41	0.71
	Gly	408	.	.	.	.	.	T	C	0.84	0.29	.	.	F	1.32	1.01
	Asn	409	.	.	.	.	.	T	C	0.84	-0.21	.	.	F	1.68	1.30
5	Leu	410	.	.	.	.	.	.	C	1.14	-0.21	.	.	F	1.58	1.01
	Thr	411	.	.	B	.	.	T	.	0.86	0.30	*	.	F	1.08	1.07
	Glu	412	.	.	B	.	.	T	.	0.86	0.37	*	.	F	1.27	0.67
	Ser	413	.	.	B	.	.	T	.	1.20	-0.03	*	.	F	2.36	1.36
	Trp	414	.	.	.	.	T	T	.	1.20	-0.71	*	.	F	3.40	1.58
10	Ala	415	.	.	.	.	.	.	C	1.80	-0.80	*	*	F	2.66	1.46
	Asp	416	.	.	.	.	T	.	.	2.22	-0.37	*	.	F	2.56	1.69
	Asp	417	.	.	.	.	.	.	C	2.19	-0.76	*	*	F	2.66	3.15
	Asn	418	.	.	.	.	.	T	C	2.46	-1.17	*	*	F	2.86	4.24
	Pro	419	.	.	.	.	.	T	C	2.40	-1.17	.	.	F	2.86	3.45
15	Arg	420	.	.	.	.	T	T	.	2.18	-0.74	.	*	F	3.40	2.05
	His	421	.	.	.	.	.	T	C	1.59	-0.06	.	.	.	2.41	1.05
	His	422	.	A	.	.	.	.	C	1.00	0.04	.	.	.	0.92	0.69
	Gly	423	.	A	B	.	.	.	.	0.97	0.11	.	.	.	0.38	0.35
	Leu	424	.	A	B	.	.	.	.	0.88	0.61	.	.	.	-0.26	0.35
20	Ala	425	.	A	B	.	.	.	.	0.47	0.50	.	.	.	-0.30	0.35
	Ala	426	.	A	.	.	.	.	C	0.16	0.39	.	.	.	0.50	0.47
	His	427	.	.	.	.	.	T	C	0.19	0.39	.	.	.	1.20	0.57
	Ser	428	.	.	.	.	.	T	C	0.53	-0.30	.	*	F	2.25	0.97
	Ser	429	.	.	.	.	.	T	C	1.46	-0.80	.	.	F	3.00	1.66
25	Gly	430	.	.	.	.	.	T	C	2.04	-1.30	.	.	F	2.70	2.39
	Glu	431	.	A	.	.	.	.	C	1.74	-1.80	.	.	F	2.00	3.09
	Glu	432	.	A	.	.	.	.	C	1.78	-1.50	*	.	F	1.70	1.62
	Arg	433	.	A	B	.	.	.	.	1.83	-1.49	*	.	F	1.20	2.83
	Glu	434	.	A	B	.	.	.	.	1.54	-1.16	*	.	F	0.90	2.56
30	Ile	435	.	A	B	.	.	.	.	1.68	-0.66	.	.	.	0.75	1.49
	Gln	436	.	A	B	.	.	.	.	0.87	-0.23	*	.	.	0.45	1.18
	Tyr	437	.	A	B	.	.	.	.	0.57	0.46	*	.	.	-0.60	0.56
	Ala	438	.	.	.	.	.	.	C	-0.24	0.84	*	.	.	-0.05	1.07
	Pro	439	.	.	B	.	.	.	.	-0.28	0.94	*	.	.	-0.40	0.54
35	Leu	440	.	.	B	.	.	.	.	0.66	1.04	*	.	.	-0.40	0.47
	Ser	441	.	.	.	.	.	.	C	0.31	0.29	*	.	.	0.10	0.92
	Phe	442	.	.	.	.	.	.	C	0.56	0.21	.	.	.	0.10	0.59
	His	443	.	.	.	.	T	.	.	0.93	-0.21	.	.	.	1.05	1.24
	Lys	444	.	.	.	.	T	.	.	1.14	-0.47	.	.	F	1.50	1.43
40	Gly	445	.	.	.	.	.	.	C	1.96	-0.46	.	.	F	1.60	2.86
	Glu	446	.	.	.	.	.	.	C	1.44	-1.24	*	.	F	2.20	3.51

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	Pro	447	.	.	.	.	.	C	1.84	-1.06	*	.	F	2.50	1.45
	Gln	448	.	.	.	.	T	.	1.53	-0.67	.	.	F	3.00	1.96
	Asp	449	.	.	.	.	.	C	1.49	-0.67	.	.	F	2.50	1.12
	Leu	450	.	.	.	.	.	T	1.83	-0.27	.	.	F	2.10	1.26
5	Ser	451	.	.	.	.	.	T	1.24	-0.70	.	.	F	2.10	1.26
	Gly	452	.	.	B	.	.	T	1.14	-0.60	.	.	F	1.45	0.76
	Gln	453	.	.	.	.	.	T	1.14	-0.11	.	.	F	1.20	1.33
	Glu	454	.	.	.	.	.	C	1.14	-0.40	.	.	F	1.00	1.60
	Ala	455	.	.	.	.	.	C	1.96	-0.39	.	.	F	1.30	2.59
10	Thr	456	.	.	.	.	.	C	2.01	-0.81	.	.	F	1.90	2.59
	Asn	457	.	.	.	.	.	T	2.06	-0.46	.	.	F	2.10	2.35
	Asn	458	.	.	.	.	.	T	2.06	-0.07	*	.	F	2.40	3.11
	Glu	459	.	.	.	.	.	T	1.17	-0.57	*	.	F	3.00	3.73
	Tyr	460	.	.	.	.	T	T	1.80	-0.37	.	*	F	2.60	1.63
15	Ser	461	.	.	.	.	T	.	1.22	-0.77	.	*	F	2.40	2.02
	Glu	462	.	.	B	.	.	.	1.01	-0.49	.	.	F	1.25	0.82
	Ile	463	.	.	B	.	.	.	1.06	-0.06	.	.	F	1.22	0.81
	Lys	464	.	.	B	.	.	.	0.67	-0.81	.	.	F	1.64	1.21
	Ile	465	.	.	B	.	.	.	0.52	-0.77	.	*	F	1.76	0.89
20	Pro	466	.	.	B	.	.	.	0.43	-0.34	.	*	.	1.73	1.62
	Lys	467	.	.	.	.	T	.	0.04	-0.60	.	*	.	2.70	1.04
	Ter	468	.	.	B	.	.	.	0.54	-0.17	*	.	.	1.73	1.89

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Table VII

	Res	Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
5	Met	1	.	.	B	.	.	.	.	0.43	0.01	*	.	.	-0.10	0.79
	Asp	2	.	.	B	.	.	.	.	0.48	-0.41	*	.	.	0.65	1.21
	Leu	3	.	.	B	.	.	T	.	0.06	-0.41	*	.	.	0.70	0.94
	Pro	4	A	.	.	.	.	T	.	-0.41	-0.16	*	.	.	0.70	0.78
	Arg	5	.	.	B	.	.	T	.	-0.88	-0.13	*	.	F	0.85	0.35
10	Gly	6	.	.	B	.	.	T	.	-0.87	0.51	*	.	F	-0.05	0.31
	Leu	7	.	.	B	B	.	.	.	-1.16	0.33	*	.	.	-0.30	0.20
	Val	8	.	.	B	B	.	.	.	-0.93	0.81	*	.	.	-0.60	0.11
	Val	9	.	.	B	B	.	.	.	-1.53	1.31	.	.	.	-0.60	0.11
	Ala	10	.	.	B	B	.	.	.	-1.94	1.57	.	*	.	-0.60	0.11
15	Trp	11	.	.	B	B	.	.	.	-2.41	1.27	.	.	.	-0.60	0.20
	Ala	12	.	.	B	B	.	.	.	-1.89	1.31	.	.	.	-0.60	0.22
	Leu	13	.	.	B	B	.	.	.	-1.24	1.59	.	.	.	-0.60	0.23
	Ser	14	.	.	.	.	.	.	C	-0.73	1.51	.	.	.	-0.20	0.34
	Leu	15	.	.	.	.	.	.	C	-0.84	1.03	.	.	.	-0.20	0.34
20	Trp	16	.	.	.	.	.	T	C	-0.87	1.31	*	.	.	0.00	0.35
	Pro	17	.	.	.	.	.	T	C	-0.28	1.11	*	.	.	0.00	0.38
	Gly	18	.	.	.	.	T	T	.	0.22	0.73	*	.	F	0.35	0.77
	Phe	19	.	.	.	.	T	T	.	-0.18	0.53	*	.	F	0.50	1.06
	Thr	20	.	.	.	.	.	.	C	0.63	0.40	*	.	F	0.25	0.59
25	Asp	21	.	.	.	.	.	.	C	0.32	0.37	.	*	F	0.25	0.96
	Thr	22	.	.	.	.	.	.	C	0.53	0.56	.	*	.	0.29	1.10
	Phe	23	.	.	B	.	.	.	.	0.57	-0.23	*	*	.	1.33	1.27
	Asn	24	.	.	B	.	.	T	.	1.38	-0.23	*	*	.	1.87	1.10
	Met	25	.	.	.	.	T	T	.	1.73	-0.23	*	*	.	2.61	1.49
30	Asp	26	.	.	.	.	T	T	.	1.52	-0.71	*	.	F	3.40	3.44
	Thr	27	.	.	.	.	T	T	.	1.94	-1.07	*	*	F	3.06	3.31
	Arg	28	.	.	.	.	T	.	.	1.79	-1.47	*	*	F	2.52	6.55
	Lys	29	.	.	B	.	.	.	.	0.90	-1.44	*	.	F	1.78	2.91
	Pro	30	.	.	B	B	.	.	.	1.29	-0.76	*	.	F	1.24	1.41
35	Arg	31	.	.	B	B	.	.	.	0.94	-0.81	.	.	F	0.90	1.12
	Val	32	.	.	B	B	.	.	.	0.96	-0.39	.	*	.	0.30	0.55
	Ile	33	.	.	B	.	.	T	.	0.96	0.00	.	*	F	0.22	0.48
	Pro	34	.	.	B	.	.	T	.	0.60	-0.43	.	*	F	0.79	0.48
	Gly	35	.	.	.	.	T	T	.	0.22	0.06	*	*	F	0.56	0.93
40	Ser	36	.	.	B	.	.	T	.	-0.59	-0.09	*	*	F	0.88	1.34

	Arg	37	.	.	B	B	.	.	.	-0.43	0.01	.	.	F	-0.30	0.75
	Thr	38	.	.	B	B	.	.	.	0.11	0.37	.	.	F	-0.27	0.66
	Ala	39	.	.	B	B	.	.	.	0.08	0.37	.	.	.	-0.39	0.49
	Phe	40	.	.	B	B	.	.	.	0.11	0.74	.	.	.	-0.66	0.39
5	Phe	41	.	.	B	B	.	.	.	-0.44	1.23	.	.	.	-0.63	0.39
	Gly	42	.	.	B	B	.	.	.	-0.56	1.39	.	.	.	-0.60	0.29
	Tyr	43	.	.	B	B	.	.	.	-0.24	1.29	.	.	.	-0.60	0.57
	Thr	44	.	.	B	B	.	.	.	0.31	0.90	.	.	.	-0.45	1.14
	Val	45	.	.	B	B	.	.	.	1.01	0.61	.	.	.	-0.45	1.57
10	Gln	46	.	.	B	B	.	.	.	0.82	0.19	.	.	.	-0.15	1.67
	Gln	47	.	.	B	B	.	.	.	0.87	0.11	.	.	.	-0.30	0.81
	His	48	.	.	B	B	.	.	.	0.77	0.01	.	.	.	0.10	1.47
	Asp	49	.	.	B	B	.	.	.	1.08	-0.20	.	.	F	0.95	0.84
	Ile	50	.	.	.	B	T	.	.	1.98	-0.20	.	.	F	1.60	0.78
15	Ser	51	.	.	.	.	T	T	.	1.69	-0.60	.	.	F	2.70	1.14
	Gly	52	.	.	.	.	T	T	.	0.88	-0.19	.	.	F	2.50	0.72
	Asn	53	.	.	.	.	T	T	.	0.06	0.50	.	.	F	1.35	0.85
	Lys	54	.	.	.	.	T	T	.	-0.80	0.46	.	.	F	1.10	0.47
	Trp	55	.	.	B	B	.	.	.	-0.26	0.71	.	.	.	-0.10	0.35
20	Leu	56	.	.	B	B	.	.	.	-0.54	0.71	.	.	.	-0.35	0.22
	Val	57	.	.	B	B	.	.	.	-0.41	0.81	.	.	.	-0.60	0.11
	Val	58	.	.	B	B	.	.	.	-1.22	1.24	.	.	.	-0.60	0.16
	Gly	59	.	.	B	B	.	.	.	-1.27	1.01	.	.	.	-0.60	0.16
	Ala	60	.	.	B	.	.	.	.	-1.29	0.33	.	.	.	-0.10	0.38
25	Pro	61	.	.	.	.	.	.	C	-0.48	0.17	.	*	.	0.10	0.73
	Leu	62	.	.	.	.	.	.	C	0.03	-0.07	.	.	F	1.34	1.19
	Glu	63	A	.	.	.	.	T	.	0.64	-0.07	.	*	F	1.68	1.16
	Thr	64	.	.	B	.	.	T	.	0.99	0.19	.	*	F	1.42	1.18
	Asn	65	.	.	.	.	T	T	.	1.62	0.16	.	*	F	2.16	2.47
30	Gly	66	.	.	.	.	T	T	.	1.52	-0.53	.	.	F	3.40	2.86
	Tyr	67	.	.	.	.	T	.	.	1.99	-0.04	.	.	F	2.56	2.86
	Gln	68	.	.	.	.	T	.	.	1.99	-0.10	.	.	F	2.48	1.76
	Lys	69	.	.	B	.	T	T	.	1.44	-0.50	*	.	F	2.60	2.97
	Thr	70	.	.	B	.	.	T	.	1.20	-0.29	*	.	F	2.12	1.41
35	Gly	71	.	.	B	.	.	T	.	1.59	-0.29	*	.	F	2.04	1.27
	Asp	72	.	.	B	.	.	T	.	1.17	-0.69	*	.	F	2.60	1.27
	Val	73	.	.	B	.	.	.	.	0.96	-0.11	*	.	F	1.69	0.47
	Tyr	74	.	.	B	.	.	T	.	0.06	-0.17	.	.	.	1.48	0.74
	Lys	75	.	.	B	.	.	T	.	-0.52	0.04	.	.	.	0.62	0.33
40	Cys	76	.	.	B	.	.	T	.	-0.21	0.73	.	.	.	0.06	0.31
	Pro	77	.	.	B	.	.	T	.	-0.56	0.59	.	.	.	-0.20	0.27



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	Val	78	.	.	B	.	.	.	.	0.30	0.26	.	.	.	-0.10	0.13
	Ile	79	.	.	B	.	.	.	.	-0.12	0.66	.	.	.	-0.40	0.40
	His	80	.	.	B	.	.	T	.	-0.48	0.66	.	.	.	-0.20	0.14
	Gly	81	.	.	B	.	.	T	.	0.23	0.71	.	.	.	-0.20	0.27
5	Asn	82	.	.	.	.	T	T	.	-0.37	0.07	.	.	.	0.50	0.77
	Cys	83	.	.	B	.	.	T	.	0.49	0.07	.	*	F	0.25	0.47
	Thr	84	.	.	B	.	.	.	.	0.57	-0.03	.	*	F	0.65	0.76
	Lys	85	.	.	B	.	.	.	.	0.26	0.23	.	.	F	0.05	0.39
	Leu	86	.	.	B	.	.	.	.	0.71	0.26	.	.	.	-0.10	0.72
10	Asn	87	.	.	B	.	.	.	.	-0.14	-0.31	.	.	.	0.50	0.97
	Leu	88	.	.	B	B	.	.	.	0.21	-0.16	.	*	.	0.30	0.36
	Gly	89	.	.	B	B	.	.	.	-0.29	0.33	.	*	.	-0.30	0.63
	Arg	90	.	.	B	B	.	.	.	-0.63	0.33	.	.	.	-0.30	0.32
	Val	91	.	.	B	B	.	.	.	0.18	0.31	*	.	.	-0.30	0.53
15	Thr	92	.	.	B	B	.	.	.	-0.68	0.03	*	.	.	-0.30	0.85
	Leu	93	.	.	B	B	.	.	.	-0.17	0.24	*	*	.	-0.30	0.32
	Ser	94	.	.	B	B	.	.	.	0.18	0.63	.	*	.	-0.60	0.58
	Asn	95	.	.	B	B	.	.	.	0.18	-0.01	.	*	F	0.45	0.70
	Val	96	.	.	B	B	.	.	.	1.08	-0.50	.	.	F	0.60	1.67
20	Ser	97	A	.	.	.	.	.	.	1.39	-1.19	*	.	F	1.10	2.49
	Glu	98	A	.	.	.	.	.	.	2.20	-1.57	*	.	F	1.10	2.58
	Arg	99	A	.	.	.	.	T	.	1.90	-1.57	.	*	F	1.30	5.60
	Lys	100	A	.	.	.	.	T	.	2.01	-1.60	.	*	F	1.30	4.13
	Asp	101	A	.	.	.	.	T	.	2.06	-1.99	.	*	F	1.30	4.67
25	Asn	102	A	.	.	.	.	T	.	2.01	-1.30	.	*	.	1.15	1.97
	Met	103	A	.	.	.	.	.	.	1.20	-0.87	.	*	.	0.80	0.97
	Arg	104	A	.	.	.	.	.	.	0.79	-0.19	.	*	.	0.50	0.48
	Leu	105	.	.	B	.	.	.	.	-0.07	0.20	*	*	.	-0.10	0.40
	Gly	106	.	.	B	.	.	.	.	-0.66	0.49	*	*	.	-0.40	0.33
30	Leu	107	.	.	B	.	.	.	.	-0.97	0.37	*	*	.	-0.10	0.17
	Ser	108	.	.	B	.	.	.	.	-0.37	0.86	*	*	.	-0.40	0.30
	Leu	109	.	.	B	.	.	.	.	-0.69	0.57	*	*	.	-0.06	0.49
	Ala	110	.	.	B	.	.	.	.	0.17	0.57	.	*	.	0.28	0.92
	Thr	111	.	.	B	.	.	.	.	0.51	-0.11	.	.	F	1.82	1.37
35	Asn	112	.	.	.	.	.	T	C	1.32	-0.50	.	*	F	2.56	2.78
	Pro	113	.	.	.	.	T	T	.	1.32	-0.79	.	.	F	3.40	4.42
	Lys	114	.	.	.	.	T	T	.	1.43	-0.90	.	.	F	3.06	4.10
	Asp	115	.	.	.	.	T	T	.	1.21	-0.60	.	.	F	2.72	2.21
	Asn	116	.	.	.	.	T	T	.	0.93	-0.31	.	.	F	2.08	1.18
40	Ser	117	.	.	B	.	.	T	.	0.27	-0.24	.	.	F	1.19	0.60
	Phe	118	.	.	B	.	.	T	.	0.18	0.33	.	.	.	0.10	0.19

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	Leu	119	.	.	B	.	.	T	.	-0.08	0.71	.	.	.	-0.20	0.16
	Ala	120	.	.	B	.	.	.	.	-0.89	0.74	.	.	.	-0.40	0.18
	Cys	121	.	.	B	.	.	.	.	-1.18	1.04	.	.	.	-0.40	0.17
	Ser	122	.	.	.	.	.	T	C	-1.18	1.17	.	.	.	0.00	0.22
5	Pro	123	.	.	.	.	T	T	.	-0.51	0.87	.	.	.	0.20	0.30
	Leu	124	.	.	.	.	T	T	.	0.30	0.87	.	.	.	0.20	0.75
	Trp	125	.	.	.	.	T	T	.	0.22	0.30	.	.	.	0.50	0.97
	Ser	126	.	.	B	.	.	.	.	0.54	0.49	.	.	.	-0.27	0.34
	His	127	.	.	B	.	.	T	.	0.54	0.49	.	.	.	0.06	0.40
10	Glu	128	.	.	.	.	T	T	.	0.46	0.19	.	.	.	0.89	0.51
	Cys	129	.	.	.	.	T	T	.	1.02	-0.34	.	.	F	1.77	0.51
	Gly	130	.	.	.	.	T	T	.	1.07	0.03	.	.	F	1.30	0.59
	Ser	131	.	.	.	.	T	T	.	1.06	0.29	.	.	F	1.17	0.54
	Ser	132	.	.	.	.	T	T	.	0.78	0.77	.	.	F	0.89	1.44
15	Tyr	133	.	.	.	.	T	T	.	0.43	0.69	.	.	F	0.76	2.11
	Tyr	134	.	.	B	.	.	T	.	0.50	0.69	.	.	F	0.23	1.55
	Thr	135	.	.	B	.	.	.	.	0.18	0.91	.	.	F	-0.10	1.15
	Thr	136	.	.	B	.	.	.	.	0.18	1.10	.	.	.	-0.40	0.39
	Gly	137	.	.	B	.	.	T	.	0.59	0.73	.	*	.	-0.20	0.34
20	Met	138	.	.	B	.	.	T	.	-0.02	-0.03	.	*	.	0.70	0.46
	Cys	139	.	.	B	.	.	T	.	0.22	0.13	.	*	.	0.10	0.23
	Ser	140	.	.	B	.	.	T	.	0.23	0.04	.	*	.	0.10	0.38
	Arg	141	.	.	B	.	.	.	.	0.54	0.00	*	*	F	0.05	0.52
	Val	142	.	.	B	.	.	.	.	0.19	-0.21	*	*	F	0.80	1.55
25	Asn	143	.	.	B	.	.	T	.	0.90	0.00	*	*	F	0.61	1.00
	Ser	144	.	.	.	.	.	T	C	0.87	-0.39	*	*	F	1.62	1.00
	Asn	145	.	.	.	.	T	T	.	0.87	0.40	*	*	F	1.13	1.17
	Phe	146	.	.	.	.	T	T	.	0.80	0.14	*	*	.	1.34	0.97
	Arg	147	.	.	.	.	T	.	.	1.34	-0.26	*	*	.	2.10	1.45
30	Phe	148	.	.	.	B	T	.	.	0.49	-0.16	*	*	.	1.69	1.30
	Ser	149	.	.	B	B	.	.	.	0.20	0.09	*	*	F	0.63	1.12
	Lys	150	.	.	.	B	.	.	C	-0.01	-0.20	*	*	F	1.07	0.58
	Thr	151	.	.	.	B	T	.	.	0.10	0.23	*	*	F	0.61	1.03
	Val	152	.	.	.	B	.	.	C	-0.82	-0.06	*	.	.	0.50	0.77
35	Ala	153	.	.	B	B	.	.	C	-0.12	0.24	*	.	.	-0.10	0.32
	Pro	154	A	A	.	.	.	.	.	0.29	0.64	*	.	.	-0.60	0.38
	Ala	155	A	A	.	.	.	.	.	-0.42	0.16	*	.	.	-0.15	1.01
	Leu	156	A	A	.	B	.	.	.	-0.11	0.09	*	.	.	-0.30	0.54
	Gln	157	A	A	.	B	.	.	.	0.43	-0.01	*	.	.	0.30	0.60
40	Arg	158	.	A	B	B	.	.	.	0.78	0.04	*	.	F	-0.15	0.86
	Cys	159	.	A	B	B	.	.	.	0.39	0.30	*	*	F	0.00	1.63

	Gln	160	.	.	B	B	.	.	.	0.98	0.23	*	*	.	-0.30	0.93
	Thr	161	.	.	B	B	.	.	.	0.90	-0.17	*	*	.	0.30	0.80
	Tyr	162	.	.	B	B	.	.	.	0.04	0.51	*	*	.	-0.45	1.04
	Met	163	.	.	B	B	.	.	.	-0.96	0.59	.	*	.	-0.60	0.45
5	Asp	164	.	.	B	B	.	.	.	-1.14	0.87	.	*	.	-0.60	0.22
	Ile	165	.	.	B	B	.	.	.	-1.96	1.03	.	*	.	-0.60	0.10
	Val	166	.	.	B	B	.	.	.	-1.64	0.96	.	*	.	-0.60	0.09
	Ile	167	.	.	B	B	.	.	.	-1.74	0.34	.	*	.	-0.30	0.09
	Val	168	.	.	B	B	.	.	.	-1.44	0.77	.	*	.	-0.35	0.12
10	Leu	169	.	.	B	B	.	.	.	-1.44	-0.47	.	*	.	-0.10	0.22
	Asp	170	.	.	.	B	T	.	.	-0.86	0.23	*	*	F	1.00	0.50
	Gly	171	.	.	.	.	T	T	.	-0.89	-0.07	.	.	F	2.25	0.90
	Ser	172	.	.	.	.	T	T	.	-0.24	-0.03	*	*	F	2.50	0.77
	Asn	173	.	.	.	.	.	T	C	0.40	0.04	*	.	F	1.45	0.72
15	Ser	174	.	.	.	.	.	T	C	0.92	0.47	*	.	F	1.05	1.12
	Ile	175	.	.	.	B	.	.	C	0.07	0.96	*	.	.	0.10	0.88
	Tyr	176	.	.	.	B	.	.	C	0.41	1.21	*	.	.	-0.15	0.41
	Pro	177	.	.	B	B	.	.	.	-0.14	0.81	.	*	.	-0.60	0.53
	Trp	178	.	.	B	B	.	.	.	-0.14	1.07	.	*	.	-0.60	0.56
20	Val	179	.	.	B	B	.	.	.	0.12	0.79	.	.	.	-0.60	0.62
	Glu	180	.	.	B	B	.	.	.	0.31	0.53	.	*	.	-0.60	0.54
	Val	181	A	.	.	B	.	.	.	-0.26	0.89	.	.	.	-0.60	0.45
	Gln	182	A	.	.	B	.	.	.	-0.93	0.66	.	.	.	-0.60	0.50
	His	183	A	.	.	B	.	.	.	-0.64	0.70	*	*	.	-0.60	0.20
25	Phe	184	A	.	.	B	.	.	.	-0.68	1.10	*	.	.	-0.60	0.43
	Leu	185	A	.	.	B	.	.	.	-1.49	1.14	*	.	.	-0.60	0.18
	Ile	186	A	.	.	B	.	.	.	-0.59	1.43	*	.	.	-0.60	0.11
	Asn	187	A	.	.	B	.	.	.	-0.54	0.93	*	.	.	-0.60	0.25
	Ile	188	A	.	.	B	.	.	.	-1.21	0.14	*	*	.	-0.30	0.60
30	Leu	189	A	.	.	B	.	.	.	-0.76	0.24	*	*	.	-0.30	0.74
	Lys	190	.	.	B	B	.	.	.	-0.83	0.31	*	.	.	-0.30	0.72
	Lys	191	.	.	B	B	.	.	.	-0.29	0.60	*	*	.	-0.60	0.72
	Phe	192	.	.	B	B	.	.	.	-0.50	0.34	*	.	.	-0.30	0.86
	Tyr	193	.	.	B	B	.	.	.	0.04	0.09	*	.	.	-0.30	0.67
35	Ile	194	.	.	B	B	.	.	.	0.86	0.51	*	.	.	-0.60	0.33
	Gly	195	.	.	.	.	T	C	.	-0.08	0.91	*	.	.	0.00	0.66
	Pro	196	.	.	.	.	T	T	.	-0.12	0.81	.	*	F	0.35	0.30
	Gly	197	.	.	.	.	T	T	.	-0.28	0.46	.	*	F	0.35	0.73
	Gln	198	.	.	B	.	.	T	.	-0.38	0.41	.	*	F	-0.05	0.55
40	Ile	199	.	.	B	B	.	.	.	-0.34	0.41	.	*	.	-0.60	0.35
	Gln	200	.	.	B	B	.	.	.	-0.86	0.63	.	*	.	-0.60	0.26

5	Val	201	.	.	B	B	.	.	.	-0.64	0.84	.	*	.	-0.60	0.11
	Gly	202	.	.	B	B	.	.	.	-0.54	0.84	.	*	.	-0.60	0.28
	Val	203	.	.	B	B	.	.	.	-0.89	0.91	.	*	.	-0.60	0.25
	Val	204	.	.	B	B	.	.	.	0.00	0.94	.	.	.	-0.60	0.34
	Gln	205	.	.	B	B	.	.	.	0.00	0.30	.	.	.	-0.30	0.59
10	Tyr	206	.	.	B	B	.	.	.	0.00	-0.13	*	.	.	0.45	1.32
	Gly	207	.	A	B	B	.	.	.	-0.51	-0.13	*	.	F	0.60	1.32
	Glu	208	A	A	.	B	.	.	.	0.31	-0.13	*	.	F	0.45	0.57
	Asp	209	A	A	.	B	.	.	.	1.17	-0.03	*	.	F	0.45	0.49
	Val	210	A	A	.	B	.	.	.	0.47	-0.79	*	.	.	0.60	0.86
15	Val	211	A	A	.	B	.	.	.	0.68	-0.43	*	.	.	0.30	0.43
	His	212	A	A	.	B	.	.	.	0.21	0.07	*	*	.	-0.30	0.35
	Glu	213	A	A	.	.	.	.	.	0.21	0.76	.	.	.	-0.60	0.39
	Phe	214	A	A	.	.	.	.	.	0.21	0.51	.	*	.	-0.60	0.84
	His	215	A	A	.	.	.	.	.	0.82	-0.13	*	.	.	0.45	1.04
20	Leu	216	A	A	.	.	.	.	.	1.79	0.13	*	.	.	0.04	0.94
	Asn	217	A	.	.	.	.	T	.	1.52	0.13	*	.	.	0.93	2.12
	Asp	218	A	.	.	.	.	T	.	0.67	-0.27	*	.	F	2.02	2.09
	Tyr	219	.	.	.	.	T	T	.	1.41	-0.13	*	.	F	2.76	1.88
	Arg	220	.	.	.	.	T	T	.	1.44	-0.81	*	.	F	3.40	2.34
25	Ser	221	A	.	.	.	.	.	.	1.40	-1.21	*	.	F	2.46	2.34
	Val	222	.	A	B	.	.	.	.	0.54	-0.57	*	.	F	1.92	1.11
	Lys	223	.	A	B	.	.	.	.	0.54	-0.69	*	.	F	1.43	0.42
	Asp	224	.	A	B	.	.	.	.	0.20	-0.69	*	.	F	1.09	0.54
	Val	225	A	A	.	.	.	.	.	-0.50	-0.57	*	.	.	0.60	0.74
30	Val	226	A	A	.	.	.	.	.	-0.50	-0.71	*	.	.	0.60	0.37
	Glu	227	A	A	.	.	.	.	.	0.32	-0.33	*	.	.	0.30	0.30
	Ala	228	A	A	.	.	.	.	.	-0.61	0.17	*	.	.	-0.30	0.55
	Ala	229	A	A	.	.	.	.	.	-0.61	0.21	*	.	.	-0.30	0.52
	Ser	230	A	A	.	.	.	.	.	0.24	-0.43	*	*	.	0.30	0.52
35	His	231	A	A	.	.	.	.	.	1.21	-0.03	*	*	.	0.64	0.89
	Ile	232	A	A	.	.	.	.	.	0.87	-0.53	*	*	.	1.43	1.72
	Glu	233	A	A	.	.	.	.	.	1.11	-0.60	*	*	F	1.92	1.27
	Gln	234	.	.	.	.	T	T	.	1.39	-0.56	*	*	F	2.91	0.92
	Arg	235	.	.	.	.	T	T	.	1.69	-0.57	.	*	F	3.40	1.90
40	Gly	236	.	.	.	.	T	T	.	1.41	-1.26	*	*	F	3.06	1.90
	Gly	237	.	.	.	.	.	T	C	2.41	-0.77	*	*	F	2.68	1.59
	Thr	238	.	.	.	.	.	.	C	2.10	-1.17	*	*	F	2.30	1.59
	Glu	239	.	.	.	.	.	.	C	1.51	-0.69	*	*	F	2.12	2.31
	Thr	240	.	.	B	.	.	.	.	0.70	-0.61	*	*	F	1.74	2.36
	Arg	241	.	.	B	.	.	.	.	0.70	-0.26	.	*	F	1.60	1.42

	Thr	242	.	.	B	.	.	.	0.16	-0.31	.	*	F	1.29	0.81	
	Ala	243	A	A	.	.	.	.	0.47	0.37	.	*	.	0.18	0.39	
	Phe	244	A	A	.	.	.	.	-0.23	-0.11	.	*	.	0.62	0.35	
	Gly	245	A	A	.	.	.	.	-0.51	0.67	.	*	.	-0.44	0.21	
5	Ile	246	A	A	.	.	.	.	-0.51	0.69	.	*	.	-0.60	0.21	
	Glu	247	A	A	.	.	.	.	-0.50	0.19	.	.	.	-0.30	0.47	
	Phe	248	A	A	.	.	.	.	0.09	-0.21	.	.	.	0.30	0.64	
	Ala	249	A	A	.	.	.	.	0.20	-0.64	.	.	.	0.75	1.58	
	Arg	250	A	A	.	.	.	.	-0.16	-0.83	.	.	F	0.75	0.92	
10	Ser	251	A	A	.	.	.	.	0.73	-0.04	.	.	F	0.45	0.92	
	Glu	252	A	A	.	.	.	.	0.78	-0.43	.	.	F	0.60	1.58	
	Ala	253	A	A	.	.	.	.	1.13	-0.93	.	.	F	0.90	1.61	
	Phe	254	A	A	.	.	.	.	1.38	-0.50	*	*	F	0.60	1.19	
	Gln	255	A	.	.	.	.	T	1.38	-0.46	*	.	F	0.85	0.68	
15	Lys	256	A	.	.	.	.	T	1.72	-0.46	*	.	F	1.00	1.32	
	Gly	257	A	.	.	.	.	T	1.38	-0.96	*	.	F	1.30	3.05	
	Gly	258	A	.	.	.	.	T	1.38	-1.31	*	.	F	1.30	1.74	
	Arg	259	A	A	.	.	.	.	2.12	-1.21	*	.	F	0.75	0.88	
	Lys	260	A	A	.	.	.	.	2.17	-1.21	*	.	F	0.90	1.78	
20	Gly	261	A	A	.	.	.	.	1.27	-1.64	*	.	F	0.90	3.59	
	Ala	262	A	A	.	.	.	.	1.01	-1.43	*	.	F	0.90	1.36	
	Lys	263	A	.	.	B	.	.	0.47	-0.81	*	.	F	0.75	0.67	
	Lys	264	.	.	B	B	.	.	-0.50	-0.13	*	.	.	0.30	0.48	
	Val	265	.	.	B	B	.	.	-1.43	0.09	*	.	.	-0.30	0.35	
25	Met	266	.	.	B	B	.	.	-1.40	0.27	*	.	.	-0.30	0.12	
	Ile	267	.	.	B	B	.	.	-0.81	0.76	*	.	.	-0.60	0.09	
	Val	268	.	.	B	B	.	.	-1.20	0.76	*	.	.	-0.60	0.20	
	Ile	269	.	.	B	.	.	T	-1.24	0.54	.	.	.	-0.20	0.20	
	Thr	270	.	.	B	.	.	T	-0.69	-0.07	.	.	F	0.85	0.49	
30	Asp	271	.	.	B	.	.	T	-0.12	-0.37	.	.	F	0.85	0.89	
	Gly	272	.	.	.	.	.	T	C	0.77	-0.51	.	.	F	1.50	1.73
	Glu	273	.	.	.	.	.	.	C	1.32	-1.20	.	.	F	1.60	2.00
	Ser	274	.	.	.	.	.	.	C	2.00	-1.30	.	.	F	1.90	1.60
	His	275	.	.	.	.	.	.	C	2.31	-0.87	.	.	F	2.20	2.51
35	Asp	276	.	.	.	.	.	.	C	1.50	-1.30	.	*	F	2.50	2.42
	Ser	277	.	.	.	.	.	T	C	1.84	-0.61	.	.	F	3.00	1.49
	Pro	278	A	.	.	.	.	T	.	1.89	-1.00	.	.	F	2.50	1.89
	Asp	279	A	.	.	.	.	T	.	1.33	-1.50	*	.	F	2.20	2.27
	Leu	280	A	.	.	.	.	T	.	0.48	-0.86	*	.	F	1.90	1.25
40	Glu	281	A	A	.	.	.	.	0.48	-0.56	*	.	F	1.05	0.57	
	Lys	282	A	A	.	.	.	.	0.78	-0.59	*	.	F	0.75	0.59	

280

5	Val	283	A	A	.	.	.	.	0.69	-0.19	*	.	.	0.45	1.24	
	Ile	284	A	A	.	.	.	.	0.69	-0.49	*	.	F	0.45	0.96	
	Gln	285	.	A	B	.	.	.	1.61	-0.49	*	.	F	0.79	0.83	
	Gln	286	A	A	.	.	.	.	1.61	-0.49	*	.	F	1.28	2.19	
	Ser	287	A	A	.	.	.	.	1.57	-1.13	*	*	F	1.92	5.22	
	Glu	288	.	.	.	.	T	C	1.57	-1.41	*	.	F	2.86	4.85	
	Arg	289	.	.	.	.	T	T	.	2.14	-1.17	*	.	F	3.40	2.08
	Asp	290	.	.	.	.	T	T	.	2.26	-1.09	.	.	F	3.06	2.24
10	Asn	291	.	.	.	.	T	T	.	2.01	-1.47	*	.	F	2.72	2.53
	Val	292	.	.	B	B	.	.	1.72	-0.71	.	.	F	1.58	2.02	
	Thr	293	.	.	B	B	.	.	0.87	-0.21	.	.	F	0.94	1.22	
	Arg	294	.	.	B	B	.	.	0.17	0.43	*	.	.	-0.60	0.57	
15	Tyr	295	.	.	B	B	.	.	-0.69	0.53	*	.	.	-0.60	0.77	
	Ala	296	.	.	B	B	.	.	-1.50	0.53	*	.	.	-0.60	0.40	
	Val	297	.	.	B	B	.	.	-0.99	0.73	*	.	.	-0.60	0.17	
	Ala	298	.	.	B	B	.	.	-0.92	1.16	*	.	.	-0.60	0.11	
20	Val	299	.	.	B	B	.	.	-1.28	1.16	*	.	.	-0.60	0.16	
	Leu	300	.	.	B	B	.	.	-1.03	1.41	*	.	.	-0.60	0.34	
	Gly	301	.	.	B	B	.	.	-0.33	1.17	*	.	.	-0.60	0.55	
	Tyr	302	.	.	B	B	.	.	0.63	0.67	*	.	.	-0.45	1.45	
25	Tyr	303	.	.	B	.	.	.	0.88	0.03	*	.	.	0.39	3.44	
	Asn	304	.	.	B	.	.	T	0.84	-0.23	*	.	.	1.53	3.44	
	Arg	305	.	.	.	.	T	T	.	1.66	0.03	*	.	F	1.82	1.54
	Arg	306	.	.	.	.	T	T	.	1.79	-0.33	*	.	F	2.76	1.58
	Gly	307	.	.	.	.	T	T	.	2.03	-0.66	*	.	F	3.40	1.52
	Ile	308	.	.	.	.	.	C	1.97	-1.06	.	.	F	2.66	1.34	
	Asn	309	.	.	.	.	.	T	C	1.27	-0.57	*	.	F	2.37	0.99
	Pro	310	.	.	.	.	.	T	C	0.34	0.21	*	.	F	1.13	0.86
30	Glu	311	.	.	B	.	.	T	.	0.23	0.47	.	.	F	0.44	1.02
	Thr	312	.	.	B	.	.	T	.	0.58	0.19	*	.	F	0.40	1.02
	Phe	313	A	A	.	.	.	.	0.58	-0.21	.	*	.	0.45	1.14	
	Leu	314	A	A	.	.	.	.	0.62	0.04	*	*	.	-0.30	0.46	
35	Asn	315	A	A	.	.	.	.	0.59	0.04	*	.	.	-0.30	0.64	
	Glu	316	A	A	.	.	.	.	-0.30	0.31	*	.	F	0.00	1.16	
	Ile	317	A	A	.	.	.	.	-0.58	0.21	*	.	.	-0.30	0.98	
	Lys	318	A	A	.	.	.	.	-0.18	0.03	*	.	.	-0.30	0.62	
40	Tyr	319	.	A	B	.	.	.	0.63	0.01	*	.	.	-0.30	0.48	
	Ile	320	.	A	B	.	.	.	0.42	0.01	*	.	.	-0.15	1.14	
	Ala	321	.	A	B	.	.	.	0.42	-0.24	*	.	.	0.64	0.88	
	Ser	322	.	A	B	.	.	.	1.31	-0.24	*	.	.	0.98	0.94	
	Asp	323	.	.	.	.	T	C	1.31	-1.00	.	.	F	2.52	2.23	

	Pro	324	A	.	.	.	.	T	.	1.52	-1.69	.	.	F	2.66	4.42
	Asp	325	.	.	.	.	.	T	T	1.71	-1.69	.	.	F	3.40	4.49
	Asp	326	A	.	.	.	.	T	.	1.60	-1.29	.	.	F	2.66	2.33
	Lys	327	A	A	.	.	.	.	.	1.90	-0.50	.	.	F	1.62	1.30
5	His	328	A	A	.	.	.	.	.	1.04	-0.53	.	*	.	1.43	1.26
	Phe	329	.	A	B	.	.	.	.	0.94	0.11	*	.	.	0.04	0.56
	Phe	330	.	A	B	.	.	.	.	0.94	0.60	*	.	.	-0.60	0.40
	Asn	331	A	A	.	.	.	.	.	0.94	0.60	*	.	.	-0.60	0.49
	Val	332	A	A	.	.	.	.	.	0.31	0.10	*	.	.	-0.30	0.99
10	Thr	333	A	A	.	.	.	.	.	-0.24	-0.19	*	.	F	0.60	1.15
	Asp	334	A	A	.	.	.	.	.	-0.36	-0.47	*	*	F	0.45	0.72
	Glu	335	A	A	.	.	.	.	.	0.39	-0.19	.	*	.	0.30	0.81
	Ala	336	A	A	.	.	.	.	.	0.39	-0.83	.	.	.	0.75	1.12
	Ala	337	A	A	.	.	.	.	.	0.36	-1.31	.	.	.	0.75	1.12
15	Leu	338	A	A	.	.	.	.	.	-0.19	-0.63	*	.	.	0.60	0.45
	Lys	339	A	A	.	.	.	.	.	-0.19	0.01	*	.	.	-0.30	0.33
	Asp	340	A	A	.	.	.	.	.	-0.78	-0.49	*	.	.	0.30	0.55
	Ile	341	A	A	.	.	.	.	.	-1.00	-0.49	*	.	.	0.30	0.67
	Val	342	A	A	.	.	.	.	.	-0.76	-0.49	*	.	.	0.30	0.28
20	Asp	343	A	A	.	.	.	.	.	0.06	-0.06	*	.	.	0.30	0.16
	Ala	344	A	A	.	.	.	.	.	0.12	-0.06	*	.	.	0.30	0.39
	Leu	345	A	.	.	.	.	T	.	-0.77	-0.74	*	.	.	1.15	1.03
	Gly	346	A	.	.	.	.	T	.	-0.58	-0.70	*	.	.	1.00	0.43
	Asp	347	A	.	.	.	.	T	.	-0.02	0.09	*	.	.	0.10	0.37
25	Arg	348	.	.	B	.	.	T	.	-0.83	-0.03	*	.	.	0.70	0.60
	Ile	349	.	.	B	.	.	.	.	-0.24	-0.03	*	.	.	0.50	0.50
	Phe	350	.	.	B	.	.	.	.	0.22	-0.46	*	.	.	0.50	0.52
	Ser	351	.	.	B	.	.	.	.	0.26	-0.03	*	.	.	0.50	0.26
	Leu	352	.	.	B	.	.	.	.	0.26	0.46	.	.	.	-0.10	0.54
30	Glu	353	.	.	.	.	.	.	C	0.19	0.17	.	.	F	1.00	1.01
	Gly	354	.	.	.	.	.	.	C	1.08	-0.61	.	.	F	2.20	1.50
	Thr	355	.	.	.	.	.	.	C	1.78	-0.60	.	*	F	2.50	2.93
	Asn	356	.	.	.	.	.	T	C	1.77	-1.29	.	.	F	3.00	2.93
	Lys	357	.	.	.	.	.	T	C	2.28	-0.80	.	*	F	2.70	4.28
35	Asn	358	.	.	.	.	.	T	C	1.58	-0.84	.	.	F	2.40	3.97
	Glu	359	A	.	.	.	.	T	.	1.58	-0.54	.	.	F	1.90	2.14
	Thr	360	A	.	.	.	.	T	.	1.08	-0.51	.	*	F	1.60	1.06
	Ser	361	A	.	.	.	.	T	.	1.08	0.17	.	*	F	0.25	0.54
	Phe	362	A	.	.	.	.	T	.	0.43	-0.23	.	*	.	0.70	0.54
40	Gly	363	A	.	.	.	.	T	.	0.13	0.39	.	.	.	0.10	0.37
	Leu	364	A	.	.	.	.	.	.	0.13	0.29	.	*	.	-0.10	0.37

	Glu	365	A	.	.	.	.	.	.	0.13	0.30	.	.	.	-0.10	0.74
	Met	366	A	.	.	.	.	.	.	0.09	0.00	.	.	.	0.05	1.09
	Ser	367	A	.	.	.	.	T	.	0.09	0.00	.	.	F	0.40	1.30
	Gln	368	A	.	.	.	.	T	.	0.13	0.10	.	.	F	0.25	0.65
5	Thr	369	.	.	.	.	.	T	C	0.64	0.49	.	.	F	0.15	0.88
	Gly	370	.	.	.	.	.	T	C	0.61	0.26	.	.	F	0.45	0.88
	Phe	371	.	.	.	.	.	.	C	0.36	0.37	.	.	F	0.25	0.69
	Ser	372	.	.	.	B	.	.	C	-0.20	0.61	.	.	F	-0.25	0.36
	Ser	373	.	.	.	B	.	.	C	-0.20	0.77	.	.	.	-0.40	0.27
10	His	374	.	.	B	B	.	.	.	0.11	0.34	.	.	.	-0.30	0.53
	Val	375	.	.	B	B	.	.	.	0.11	-0.44	.	.	.	0.30	0.67
	Val	376	.	.	B	.	.	T	.	-0.04	-0.40	.	.	.	0.70	0.49
	Glu	377	.	.	B	.	.	T	.	-0.56	-0.14	.	.	.	0.70	0.27
	Asp	378	A	.	.	.	.	T	.	-1.07	0.04	.	.	.	0.10	0.30
15	Gly	379	A	.	.	.	.	T	.	-1.38	0.09	.	.	.	0.10	0.33
	Val	380	A	A	.	.	.	.	.	-1.11	-0.13	.	.	.	0.30	0.19
	Leu	381	A	A	.	.	.	.	.	-1.11	0.37	.	.	.	-0.30	0.11
	Leu	382	.	A	B	.	.	.	.	-1.46	1.01	.	.	.	-0.60	0.09
	Gly	383	.	A	B	.	.	.	.	-2.04	1.01	.	.	.	-0.60	0.11
20	Ala	384	.	A	B	.	.	.	.	-1.94	0.87	.	.	.	-0.60	0.14
	Val	385	.	A	B	.	.	.	.	-1.09	0.94	.	.	.	-0.60	0.27
	Gly	386	.	.	B	.	.	.	.	-0.57	0.26	.	.	.	-0.10	0.45
	Ala	387	.	.	B	.	.	.	.	0.24	0.74	.	.	.	-0.40	0.47
	Tyr	388	.	.	B	.	.	.	.	0.24	0.64	.	.	.	-0.25	1.01
25	Asp	389	.	.	.	.	T	.	.	0.24	0.43	.	.	.	0.15	1.01
	Trp	390	A	.	.	.	.	.	.	0.24	0.50	.	.	.	-0.25	1.01
	Asn	391	A	.	.	.	.	.	.	-0.22	0.64	*	.	.	-0.40	0.48
	Gly	392	A	A	.	.	.	.	.	0.41	0.57	*	.	.	-0.60	0.24
	Ala	393	A	A	.	.	.	.	.	0.66	0.57	.	.	.	-0.60	0.45
30	Val	394	A	A	.	.	.	.	.	0.34	-0.34	.	.	.	0.30	0.49
	Leu	395	A	A	.	.	.	.	.	0.33	-0.26	.	.	F	0.45	0.71
	Lys	396	A	A	.	.	.	.	.	-0.26	-0.30	.	.	F	0.45	0.94
	Glu	397	A	A	.	.	.	.	.	-0.26	-0.30	.	.	F	0.60	1.28
	Thr	398	A	A	.	.	.	.	.	0.38	-0.51	.	.	F	0.90	1.54
35	Ser	399	A	.	.	.	.	T	.	0.38	-1.20	.	.	F	1.30	1.54
	Ala	400	A	.	.	.	.	T	.	0.30	-0.56	.	.	F	1.15	0.66
	Gly	401	A	.	.	.	.	T	.	0.04	0.13	.	.	F	0.25	0.32
	Lys	402	.	.	B	.	.	T	.	-0.77	0.07	.	.	F	0.25	0.37
	Val	403	.	.	B	.	.	.	.	-0.34	0.37	.	.	.	-0.10	0.30
40	Ile	404	.	.	B	.	.	.	.	-0.04	-0.13	.	.	.	0.50	0.60
	Pro	405	.	.	B	.	.	.	.	0.24	-0.56	.	.	.	0.80	0.52



	Leu	406	.	.	B	.	.	.	.	0.34	-0.17	.	.	.	0.50	0.93
	Arg	407	A	.	.	.	.	.	.	-0.51	-0.06	.	.	F	0.80	2.08
	Glu	408	A	.	.	.	.	.	.	0.39	-0.06	.	.	F	0.80	1.11
	Ser	409	A	.	.	.	.	.	.	1.28	-0.49	.	*	F	0.80	2.69
5	Tyr	410	A	A	.	.	.	.	.	0.79	-1.17	.	.	F	0.90	2.38
	Leu	411	A	A	.	.	.	.	.	1.39	-0.39	.	.	F	0.60	1.19
	Lys	412	A	A	.	.	.	.	.	1.28	0.04	.	.	F	0.00	1.37
	Glu	413	A	A	.	.	.	.	.	1.28	-0.34	*	.	F	0.60	1.52
	Phe	414	A	A	.	.	.	.	.	0.77	-1.10	*	.	F	0.90	3.19
10	Pro	415	A	A	.	.	.	.	.	1.06	-1.10	*	.	F	0.90	1.31
	Glu	416	A	A	.	.	.	.	.	1.87	-1.10	*	.	F	0.90	1.52
	Glu	417	A	A	.	.	.	.	.	1.79	-0.70	*	*	F	0.90	2.82
	Leu	418	A	A	.	.	.	.	.	1.44	-0.99	*	*	F	0.90	2.48
	Lys	419	A	A	.	.	.	.	.	1.56	-0.99	*	*	F	0.90	1.42
15	Asn	420	A	.	.	.	.	T	.	1.52	-0.49	*	.	.	0.70	0.83
	His	421	A	.	.	.	.	T	.	0.71	0.27	*	.	.	0.25	1.57
	Gly	422	A	.	.	.	.	T	.	0.37	0.27	.	.	.	0.10	0.65
	Ala	423	.	.	B	.	.	T	.	0.93	0.70	.	.	.	-0.20	0.40
	Tyr	424	.	.	B	B	.	.	.	0.58	1.06	.	.	.	-0.60	0.46
20	Leu	425	.	.	B	B	.	.	.	-0.28	1.04	.	.	.	-0.60	0.67
	Gly	426	.	.	B	B	.	.	.	-0.56	1.26	.	.	.	-0.60	0.49
	Tyr	427	.	.	B	B	.	.	.	-0.51	1.24	.	.	.	-0.60	0.45
	Thr	428	.	.	B	B	.	.	.	-0.78	0.87	.	.	.	-0.60	0.74
	Val	429	.	.	B	B	.	.	.	-1.39	0.83	*	.	.	-0.60	0.55
25	Thr	430	.	.	B	B	.	.	.	-0.88	1.04	*	.	.	-0.60	0.26
	Ser	431	.	.	B	B	.	.	.	-0.83	0.67	.	.	.	-0.60	0.24
	Val	432	.	.	B	B	.	.	.	-0.48	0.57	.	.	.	-0.60	0.44
	Val	433	.	.	B	B	.	.	.	-0.17	-0.07	.	.	F	0.79	0.60
	Ser	434	.	.	B	.	.	T	.	0.34	-0.16	.	.	F	1.53	0.77
30	Ser	435	.	.	B	.	.	T	.	0.77	-0.11	.	.	F	2.02	1.03
	Arg	436	.	.	B	.	.	T	.	0.21	-0.76	.	.	F	2.66	2.71
	Gln	437	.	.	.	.	T	T	.	0.82	-0.76	.	*	F	3.40	1.50
	Gly	438	.	.	B	B	.	.	.	0.82	-0.39	*	*	F	1.96	1.75
	Arg	439	.	.	B	B	.	.	.	0.53	-0.13	*	*	F	1.47	0.66
35	Val	440	.	.	B	B	.	.	.	0.49	0.37	*	*	.	0.38	0.39
	Tyr	441	.	.	B	B	.	.	.	-0.21	0.40	*	*	.	-0.26	0.39
	Val	442	.	.	B	B	.	.	.	-0.42	0.47	*	*	.	-0.60	0.20
	Ala	443	.	.	B	B	.	.	.	0.03	0.90	*	*	.	-0.60	0.42
	Gly	444	.	.	B	B	.	.	.	-0.78	0.26	*	*	.	-0.30	0.52
40	Ala	445	.	.	B	.	.	.	.	0.08	0.29	.	*	.	-0.10	0.61
	Pro	446	.	.	.	.	.	C	.	0.29	0.04	*	*	F	0.25	0.97

5	Arg	447	.	.	B	.	.	.	0.83	0.04	*	*	F	0.20	1.33	
	Phe	448	.	.	B	.	.	.	1.08	0.10	*	*	.	0.18	1.90	
	Asn	449	.	.	.	.	T	.	1.47	0.03	*	*	.	0.71	1.22	
	His	450	.	.	.	.	T	T	1.20	-0.40	*	*	F	1.79	1.24	
	Thr	451	.	.	.	.	.	T	C	0.52	0.24	*	*	F	1.12	1.06
	Gly	452	.	.	.	.	T	T	-0.40	0.14	*	*	F	1.30	0.46	
	Lys	453	.	.	B	.	.	T	-0.40	0.43	*	*	F	0.47	0.28	
10	Val	454	.	.	B	B	.	.	-0.71	0.71	.	.	.	-0.21	0.17	
	Ile	455	.	.	B	B	.	.	-1.28	0.71	.	.	.	-0.34	0.25	
	Leu	456	.	.	B	B	.	.	-1.00	0.90	.	.	.	-0.47	0.12	
	Phe	457	.	.	B	B	.	.	-0.66	1.40	.	.	.	-0.60	0.22	
	Thr	458	.	.	B	B	.	.	-0.70	1.16	.	.	.	-0.60	0.51	
15	Met	459	.	.	B	B	.	.	0.27	0.87	.	.	.	-0.32	1.00	
	His	460	.	.	.	.	.	T	C	0.86	0.19	.	.	.	1.01	2.26
	Asn	461	.	.	.	.	.	T	C	0.86	-0.21	.	.	F	2.04	2.10
	Asn	462	.	.	.	.	.	T	C	1.24	-0.01	.	.	F	2.32	1.75
	Arg	463	.	.	.	.	T	T	0.67	-0.14	.	.	F	2.80	1.85	
20	Ser	464	.	.	.	.	.	.	C	1.23	0.04	.	.	F	1.37	0.81
	Leu	465	A	A	.	.	.	.	1.27	0.14	.	.	.	0.54	0.68	
	Thr	466	.	A	B	.	.	.	0.68	0.14	.	.	.	0.26	0.60	
	Ile	467	.	A	B	.	.	.	0.08	0.64	.	*	.	-0.32	0.46	
	His	468	.	A	B	.	.	.	0.08	0.87	.	*	.	-0.60	0.55	
25	Gln	469	.	A	B	.	.	.	0.03	0.19	*	*	.	-0.30	0.74	
	Ala	470	.	A	B	.	.	.	0.84	0.13	*	*	.	0.02	1.05	
	Met	471	.	.	B	.	.	T	1.16	-0.16	*	.	.	1.19	1.33	
	Arg	472	.	.	B	.	.	T	1.16	-0.26	*	*	F	1.51	1.33	
	Gly	473	.	.	B	.	.	T	0.84	0.03	*	.	F	0.93	0.92	
30	Gln	474	.	.	B	.	.	T	0.54	-0.04	.	.	F	1.70	0.92	
	Gln	475	.	.	B	.	.	.	0.89	-0.27	*	.	F	1.33	0.63	
	Ile	476	.	.	B	.	.	.	0.79	0.49	*	.	F	0.41	1.00	
	Gly	477	.	.	B	.	.	T	0.33	0.84	*	.	F	0.29	0.50	
	Ser	478	.	.	B	.	.	T	0.38	0.87	*	.	F	0.12	0.29	
35	Tyr	479	.	.	.	.	.	T	C	0.38	0.86	*	.	.	0.00	0.55
	Phe	480	.	.	B	.	.	T	-0.51	0.17	*	.	F	0.25	0.96	
	Gly	481	.	.	.	B	.	.	C	0.07	0.43	*	.	F	-0.25	0.50
	Ser	482	.	.	.	B	.	.	C	0.11	0.53	*	.	F	-0.25	0.46
	Glu	483	.	.	B	B	.	.	-0.44	0.16	*	.	F	-0.15	0.71	
40	Ile	484	.	.	B	B	.	.	-0.20	0.01	.	.	F	-0.15	0.54	
	Thr	485	.	.	B	B	.	.	-0.39	-0.41	.	*	F	0.45	0.67	
	Ser	486	.	.	B	B	.	.	-0.04	-0.11	.	*	F	0.45	0.27	
	Val	487	.	.	B	B	.	.	-0.09	-0.11	.	*	F	0.76	0.64	

5	Asp	488	.	.	B	B	.	.	-0.09	-0.37	.	*	F	1.07	0.44
	Ile	489	.	.	B	.	.	.	0.46	-0.86	.	*	F	1.88	0.55
	Asp	490	.	.	.	.	T	T	-0.09	-0.81	.	*	F	2.79	0.73
	Gly	491	.	.	.	.	T	T	-0.10	-0.81	.	*	F	3.10	0.33
	Asp	492	.	.	.	.	T	T	0.76	-0.33	*	*	F	2.49	0.67
10	Gly	493	.	.	B	.	.	T	-0.10	-1.01	*	*	F	2.08	0.67
	Val	494	.	.	B	B	.	.	-0.02	-0.37	.	*	F	1.07	0.50
	Thr	495	.	.	B	B	.	.	-0.83	-0.11	.	.	F	0.76	0.25
	Asp	496	.	.	B	B	.	.	-1.34	0.57	*	.	F	-0.45	0.21
	Val	497	.	.	B	B	.	.	-1.69	0.79	*	.	.	-0.60	0.21
15	Leu	498	.	.	B	B	.	.	-1.93	0.57	.	.	.	-0.60	0.14
	Leu	499	.	.	B	B	.	.	-1.29	0.59	.	.	.	-0.60	0.09
	Val	500	.	.	B	B	.	.	-1.58	1.01	.	.	.	-0.60	0.18
	Gly	501	.	.	B	B	.	.	-1.82	0.99	.	.	.	-0.60	0.21
	Ala	502	.	.	B	.	.	.	-1.67	1.06	.	.	.	-0.40	0.41
20	Pro	503	.	.	B	.	.	.	-0.86	1.16	.	.	.	-0.40	0.48
	Met	504	.	.	B	.	.	.	-0.04	0.91	.	.	.	-0.40	0.77
	Tyr	505	.	.	B	.	.	.	0.47	0.49	.	.	.	-0.25	1.33
	Phe	506	.	.	B	.	.	.	0.92	0.41	*	.	.	-0.40	0.85
	Asn	507	A	.	.	.	.	T	1.51	-0.01	.	*	.	0.85	1.68
25	Glu	508	A	.	.	.	.	T	1.83	-0.63	.	*	F	1.30	1.86
	Gly	509	A	.	.	.	.	T	2.09	-1.39	.	*	F	1.30	4.20
	Arg	510	A	.	.	.	.	T	2.38	-1.74	.	*	F	1.30	2.58
	Glu	511	A	.	.	.	.	.	2.22	-2.14	.	*	F	1.10	2.98
	Arg	512	.	.	.	B	T	.	1.98	-1.50	.	*	F	1.30	2.24
30	Gly	513	.	.	.	B	T	.	1.12	-1.17	.	*	F	1.30	1.79
	Lys	514	.	.	B	B	.	.	1.22	-0.53	.	*	F	0.75	0.77
	Val	515	.	.	B	B	.	.	1.11	0.23	.	*	.	-0.30	0.61
	Tyr	516	.	.	B	B	.	.	0.30	0.23	.	*	.	-0.15	1.07
	Val	517	.	.	B	B	.	.	0.30	0.49	.	*	.	-0.60	0.44
35	Tyr	518	.	.	B	.	.	.	0.64	0.49	*	*	.	0.01	1.17
	Glu	519	.	.	B	.	.	.	0.60	0.24	*	.	.	0.57	1.29
	Leu	520	.	.	B	.	.	.	1.57	-0.11	.	.	.	1.43	2.80
	Arg	521	A	.	.	.	.	T	1.11	-0.76	.	.	F	2.34	3.50
	Gln	522	.	.	B	.	.	T	1.11	-0.73	.	.	F	2.60	1.75
40	Asn	523	.	.	B	.	.	T	1.11	-0.09	*	.	F	2.04	1.57
	Arg	524	.	.	B	.	.	T	1.11	-0.01	*	*	F	1.78	1.26
	Phe	525	.	.	B	.	.	.	1.58	0.39	*	.	.	0.57	1.17
	Val	526	.	.	B	.	.	T	1.16	0.41	*	*	.	0.06	0.72
	Tyr	527	.	.	B	.	.	T	0.34	0.50	.	*	.	-0.20	0.53
	Asn	528	.	.	B	.	.	T	0.39	1.19	.	*	F	0.29	0.50

	Gly	529	.	.	.	.	T	T	.	0.28	0.40	*	*	F	1.18	1.36
	Thr	530	.	.	.	.	.	.	C	0.68	-0.24	.	.	F	2.02	1.45
	Leu	531	.	.	.	.	.	T	C	1.50	-0.61	.	.	F	2.86	1.21
	Lys	532	.	.	.	.	T	T	.	1.44	-0.51	.	*	F	3.40	1.66
5	Asp	533	.	.	B	.	.	T	.	1.20	-0.56	.	*	F	2.66	1.54
	Ser	534	.	.	B	.	.	T	.	1.54	-0.29	.	.	F	2.02	2.93
	His	535	.	.	B	.	.	T	.	1.86	-0.57	.	.	.	1.83	2.54
	Ser	536	.	.	B	.	.	T	.	2.08	-0.17	.	*	.	1.19	2.44
	Tyr	537	.	.	B	.	.	T	.	2.14	0.33	.	*	.	0.25	1.84
10	Gln	538	.	.	B	.	.	T	.	1.44	-0.06	.	*	.	0.85	2.65
	Asn	539	.	.	B	.	.	.	.	1.40	0.23	.	*	.	0.05	1.71
	Ala	540	.	.	B	.	.	.	.	1.13	0.27	.	*	.	0.05	1.08
	Arg	541	.	.	B	.	.	.	.	1.13	-0.10	*	*	.	0.50	0.84
	Phe	542	.	.	B	.	.	.	.	0.49	-0.11	*	*	F	0.65	0.70
15	Gly	543	.	.	.	.	T	T	.	-0.10	0.17	*	*	F	0.65	0.48
	Ser	544	.	.	.	.	.	T	C	-0.40	0.17	*	*	F	0.45	0.25
	Ser	545	.	.	B	.	.	T	.	-0.67	0.56	.	*	F	-0.05	0.39
	Ile	546	.	.	B	.	.	T	.	-0.67	0.41	*	*	.	-0.20	0.29
	Ala	547	.	.	B	B	.	.	.	0.03	-0.01	*	.	.	0.30	0.42
20	Ser	548	.	.	B	B	.	.	.	-0.43	-0.40	.	.	.	0.30	0.53
	Val	549	.	.	B	B	.	.	.	-0.13	-0.10	*	.	.	0.64	0.62
	Arg	550	.	.	B	B	.	.	.	0.17	-0.39	*	.	F	1.13	0.99
	Asp	551	.	.	B	.	.	.	.	1.06	-0.49	*	.	F	1.82	1.28
	Leu	552	.	.	B	.	.	.	.	1.34	-0.87	*	.	F	2.46	2.88
25	Asn	553	.	.	.	.	T	T	.	1.40	-1.13	*	.	F	3.40	1.97
	Gln	554	.	.	.	.	T	T	.	2.26	-0.37	*	.	F	2.76	1.85
	Asp	555	.	.	.	.	T	T	.	2.14	0.03	*	.	F	1.82	3.60
	Ser	556	.	.	.	.	T	T	.	1.29	-0.66	*	.	F	2.38	3.74
	Tyr	557	.	.	.	B	T	.	.	1.24	-0.41	.	.	F	1.34	1.60
30	Asn	558	.	.	B	B	.	.	.	0.39	-0.17	.	.	F	0.45	0.71
	Asp	559	.	.	B	B	.	.	.	0.04	0.47	.	.	.	-0.60	0.39
	Val	560	.	.	B	B	.	.	.	-0.54	0.51	*	.	.	-0.60	0.25
	Val	561	.	.	B	B	.	.	.	-0.46	0.26	.	.	.	-0.30	0.16
	Val	562	.	.	B	B	.	.	.	-1.02	0.29	.	.	.	-0.30	0.14
35	Gly	563	.	.	B	B	.	.	.	-1.02	0.97	.	.	.	-0.60	0.16
	Ala	564	.	A	B	.	.	.	.	-1.02	0.33	.	.	.	-0.30	0.38
	Pro	565	A	A	.	.	.	.	.	-0.17	-0.31	.	.	.	0.30	0.85
	Leu	566	A	A	.	.	.	.	.	0.66	-0.56	.	.	.	0.75	1.37
	Glu	567	A	A	.	.	.	.	.	0.92	-0.49	.	.	F	0.60	1.85
40	Asp	568	A	A	.	.	.	.	.	0.92	-0.49	.	.	.	0.45	1.21
	Asn	569	A	A	.	.	.	.	.	0.92	-0.49	.	.	.	0.45	1.45

	His	570	A	A	.	.	.	.	0.24	-0.67	.	.	.	0.60	0.85	
	Ala	571	A	.	.	B	.	.	0.81	0.01	.	.	.	-0.30	0.36	
	Gly	572	A	.	.	B	.	.	-0.08	0.77	.	.	.	-0.60	0.35	
	Ala	573	A	.	.	B	.	.	-0.78	1.06	.	.	.	-0.60	0.18	
5	Ile	574	.	.	B	B	.	.	-0.81	1.34	.	.	.	-0.60	0.15	
	Tyr	575	.	.	B	B	.	.	-1.12	1.34	.	.	.	-0.60	0.21	
	Ile	576	.	.	B	B	.	.	-1.23	1.34	*	*	.	-0.60	0.21	
	Phe	577	.	.	B	B	.	.	-0.78	1.63	*	*	.	-0.60	0.25	
	His	578	.	.	B	B	.	.	-0.53	0.94	*	*	.	-0.60	0.32	
10	Gly	579	.	.	.	B	T	.	0.06	0.61	*	*	.	-0.20	0.45	
	Phe	580	.	.	.	.	T	T	-0.59	0.31	*	*	.	0.50	0.69	
	Arg	581	.	.	.	.	T	T	-0.51	0.21	*	*	F	0.65	0.36	
	Gly	582	.	.	.	.	T	T	0.23	0.40	.	.	F	0.35	0.30	
	Ser	583	.	.	.	.	T	T	-0.04	-0.03	.	.	F	1.25	0.69	
15	Ile	584	.	.	.	.	.	.	C	0.09	-0.33	*	*	F	1.15	0.51
	Leu	585	.	.	.	.	.	.	C	0.83	0.10	*	*	F	0.85	0.79
	Lys	586	.	.	.	.	.	.	C	0.72	-0.33	.	*	F	1.90	1.18
	Thr	587	.	.	.	.	.	T	C	1.18	-0.31	*	*	F	2.40	2.92
	Pro	588	.	.	.	.	.	T	C	0.59	-1.00	*	*	F	3.00	6.94
20	Lys	589	.	.	B	.	.	T	.	1.17	-1.00	*	*	F	2.50	2.43
	Gln	590	.	.	B	.	.	T	.	1.39	-0.51	*	*	F	2.20	2.43
	Arg	591	.	.	B	B	.	.	1.04	-0.50	.	*	F	1.20	1.59	
	Ile	592	.	.	B	B	.	.	1.36	-0.54	.	*	F	1.20	1.06	
	Thr	593	.	A	B	B	.	.	0.76	-0.54	.	*	F	0.90	1.06	
25	Ala	594	.	A	B	B	.	.	0.12	-0.26	.	*	F	0.45	0.45	
	Ser	595	.	A	B	.	.	.	-0.19	0.24	.	.	F	-0.15	0.65	
	Glu	596	.	A	B	.	.	.	-0.64	0.04	.	*	F	-0.15	0.65	
	Leu	597	A	A	.	B	.	.	-0.57	-0.01	.	.	F	0.45	0.63	
	Ala	598	A	A	.	B	.	.	-0.26	0.17	*	.	.	-0.30	0.39	
30	Thr	599	A	A	.	B	.	.	0.09	0.19	*	.	.	-0.30	0.39	
	Gly	600	A	A	.	B	.	.	-0.31	0.94	*	.	.	-0.60	0.74	
	Leu	601	.	.	B	B	.	.	-0.66	1.04	*	.	.	-0.60	0.63	
	Gln	602	.	.	B	B	.	.	-0.51	0.97	*	.	.	-0.60	0.44	
	Tyr	603	.	.	.	.	T	T	-0.22	1.06	*	.	.	0.20	0.24	
35	Phe	604	.	.	B	.	.	T	-0.80	1.01	*	.	.	-0.20	0.38	
	Gly	605	.	.	B	.	.	T	-0.49	1.01	*	.	.	-0.20	0.15	
	Cys	606	.	.	B	.	.	T	-0.02	1.11	.	*	.	-0.20	0.13	
	Ser	607	.	.	B	B	.	.	-0.02	0.79	.	*	.	-0.60	0.15	
	Ile	608	.	.	B	B	.	.	-0.59	0.40	.	*	.	-0.60	0.27	
40	His	609	.	.	B	B	.	.	0.11	0.66	.	*	.	-0.60	0.41	
	Gly	610	.	.	B	B	.	.	-0.36	0.09	.	*	.	-0.30	0.52	

	Gln	611	.	.	B	.	.	.	0.31	0.39	.	*	.	-0.10	0.61
	Leu	612	.	.	B	.	.	.	0.61	0.10	.	*	.	-0.10	0.72
	Asp	613	.	.	B	.	.	.	1.50	-0.40	.	*	.	0.65	1.26
	Leu	614	.	.	B	.	.	.	1.19	-0.83	.	*	.	0.95	1.21
5	Asn	615	A	.	.	.	.	T	0.72	-0.80	.	*	F	1.30	1.45
	Glu	616	A	.	.	.	.	T	-0.17	-0.80	.	*	F	1.15	0.72
	Asp	617	A	.	.	.	.	T	0.64	-0.11	.	*	F	0.85	0.61
	Gly	618	A	.	.	.	.	T	-0.17	-0.80	.	*	F	1.15	0.63
	Leu	619	A	.	.	B	.	.	0.06	-0.51	.	*	.	0.60	0.30
10	Ile	620	A	.	.	B	.	.	-0.80	-0.01	.	*	.	0.30	0.18
	Asp	621	.	.	B	B	.	.	-1.14	0.63	.	*	.	-0.60	0.14
	Leu	622	.	.	B	B	.	.	-1.73	0.63	*	*	.	-0.60	0.16
	Ala	623	.	.	B	B	.	.	-2.20	0.44	.	.	.	-0.60	0.24
	Val	624	A	.	.	B	.	.	-1.73	0.44	*	.	.	-0.60	0.12
15	Gly	625	A	A	.	.	.	.	-0.84	0.87	*	*	.	-0.60	0.14
	Ala	626	A	A	.	.	.	.	-1.43	0.59	.	.	.	-0.60	0.22
	Leu	627	A	A	.	.	.	.	-1.48	0.59	.	.	.	-0.60	0.30
	Gly	628	A	A	.	.	.	.	-1.78	0.59	.	.	.	-0.60	0.23
	Asn	629	.	A	B	B	.	.	-1.73	0.84	.	.	.	-0.60	0.16
20	Ala	630	.	A	B	B	.	.	-1.68	1.03	.	.	.	-0.60	0.16
	Val	631	.	A	B	B	.	.	-1.39	1.26	*	.	.	-0.60	0.17
	Ile	632	.	A	B	B	.	.	-0.47	1.21	*	.	.	-0.60	0.14
	Leu	633	.	A	B	B	.	.	-0.33	0.81	*	.	.	-0.60	0.27
	Trp	634	.	A	B	B	.	.	-1.19	0.74	*	.	.	-0.60	0.57
25	Ser	635	.	A	B	B	.	.	-1.46	0.74	*	.	.	-0.60	0.60
	Arg	636	.	.	B	B	.	.	-0.60	0.70	*	*	F	-0.45	0.54
	Pro	637	.	.	B	B	.	.	-0.60	0.41	*	*	.	-0.60	0.89
	Val	638	.	.	B	B	.	.	0.21	0.19	*	*	.	-0.30	0.46
	Val	639	.	.	B	B	.	.	-0.09	0.20	*	*	.	-0.30	0.38
30	Gln	640	.	.	B	B	.	.	-0.09	0.70	*	*	.	-0.60	0.25
	Ile	641	.	.	B	B	.	.	-1.01	0.66	*	*	.	-0.60	0.45
	Asn	642	.	.	B	.	.	T	-0.83	0.70	.	*	.	-0.20	0.50
	Ala	643	.	.	B	.	.	T	-0.68	0.56	.	*	.	-0.20	0.39
	Ser	644	.	.	B	.	.	T	0.18	0.94	.	*	.	-0.20	0.48
35	Leu	645	A	.	.	.	.	T	-0.03	0.26	.	*	.	0.10	0.52
	His	646	A	.	.	.	.	.	0.56	0.29	.	*	.	0.18	0.80
	Phe	647	A	.	.	.	.	.	0.60	0.17	.	*	.	0.46	0.80
	Glu	648	A	.	.	.	.	T	0.30	-0.21	.	*	F	1.84	1.94
	Pro	649	A	.	.	.	.	T	0.60	-0.21	.	*	F	1.97	1.00
40	Ser	650	.	.	.	.	T	T	0.52	-0.31	.	*	F	2.80	1.85
	Lys	651	A	.	.	.	.	T	-0.14	-0.41	.	.	F	1.97	0.75

	Ile	652	A	.	.	B	.	.	.	0.52	0.37	*	*	F	0.69	0.42
	Asn	653	A	.	.	B	.	.	.	0.63	0.44	*	*	.	-0.04	0.43
	Ile	654	A	.	.	B	.	.	.	0.84	0.06	*	*	.	-0.02	0.42
	Phe	655	.	.	B	B	.	.	.	0.48	0.06	*	*	.	0.04	1.00
5	His	656	.	.	B	.	.	T	.	0.48	-0.06	*	*	.	1.38	0.33
	Arg	657	.	.	B	.	.	T	.	1.48	-0.46	*	*	.	1.72	0.95
	Asp	658	.	.	.	.	T	T	.	1.18	-1.14	*	.	F	3.06	2.14
	Cys	659	.	.	.	.	T	T	.	1.72	-1.54	*	.	F	3.40	2.11
	Lys	660	.	.	.	.	T	.	.	2.53	-1.61	*	.	F	2.86	1.07
10	Arg	661	.	.	.	.	T	T	.	2.57	-1.61	*	.	F	3.03	1.25
	Ser	662	.	.	.	.	T	T	.	1.87	-1.61	*	.	F	3.00	3.90
	Gly	663	.	.	.	.	T	T	.	1.56	-1.69	*	.	F	2.97	1.97
	Arg	664	.	.	.	.	T	T	.	1.56	-1.20	*	.	F	2.94	1.45
	Asp	665	.	.	.	.	T	T	.	0.70	-0.63	*	.	F	3.10	0.58
15	Ala	666	.	.	B	.	.	T	.	0.00	-0.33	*	.	F	2.09	0.48
	Thr	667	.	.	B	.	.	T	.	-0.29	-0.26	.	.	.	1.63	0.25
	Cys	668	.	.	B	.	.	T	.	-0.64	0.24	*	.	.	0.72	0.15
	Leu	669	A	A	.	.	.	.	.	-1.57	1.03	*	.	.	-0.29	0.13
	Ala	670	A	A	.	.	.	.	.	-2.23	1.21	.	.	.	-0.60	0.07
20	Ala	671	A	A	.	.	.	.	.	-2.34	1.30	.	.	.	-0.60	0.07
	Phe	672	A	A	.	.	.	.	.	-2.34	1.51	.	.	.	-0.60	0.08
	Leu	673	A	A	.	.	.	.	.	-1.89	1.31	.	.	.	-0.60	0.11
	Cys	674	.	A	B	.	.	.	.	-1.97	1.24	.	.	.	-0.60	0.17
	Phe	675	.	.	B	B	.	.	.	-2.08	1.43	.	.	.	-0.60	0.14
25	Thr	676	.	.	B	B	.	.	.	-2.30	1.43	.	.	.	-0.60	0.14
	Pro	677	.	.	B	B	.	.	.	-2.19	1.43	.	.	.	-0.60	0.22
	Ile	678	.	A	.	B	T	.	.	-1.59	1.36	.	.	.	-0.20	0.26
	Phe	679	.	A	B	B	.	.	.	-0.96	1.00	.	.	.	-0.60	0.28
	Leu	680	.	A	B	B	.	.	.	-0.96	1.01	.	.	.	-0.60	0.24
30	Ala	681	.	A	.	B	.	.	C	-0.64	1.37	.	.	.	-0.40	0.30
	Pro	682	.	A	.	B	.	.	C	-0.74	1.09	.	.	.	-0.40	0.60
	His	683	.	A	.	B	T	.	.	-0.17	0.79	.	.	.	-0.05	1.05
	Phe	684	.	A	.	B	T	.	.	0.22	0.59	.	.	.	-0.05	1.51
	Gln	685	.	A	B	B	.	.	.	0.18	0.57	.	.	F	-0.30	1.41
35	Thr	686	.	A	B	B	.	.	.	0.42	0.79	.	.	F	-0.45	0.77
	Thr	687	.	.	B	B	.	.	.	-0.26	0.71	*	*	F	-0.45	0.88
	Thr	688	.	.	B	B	.	.	.	-0.11	0.61	*	*	F	-0.45	0.35
	Val	689	.	.	B	B	.	.	.	0.34	0.21	.	*	.	-0.30	0.48
	Gly	690	.	.	B	B	.	.	.	0.34	0.49	.	*	.	-0.60	0.52
40	Ile	691	.	.	B	B	.	.	.	0.07	0.40	.	*	.	-0.60	0.58
	Arg	692	.	.	B	B	.	.	.	0.07	0.41	.	*	.	-0.60	0.79

5	Tyr	693	.	.	B	B	.	.	.	-0.22	0.26	.	*	.	-0.15	1.16
	Asn	694	.	A	B	B	.	.	.	0.63	0.44	.	*	.	-0.45	1.63
	Ala	695	.	A	B	B	.	.	.	0.98	-0.24	*	*	.	0.45	1.39
	Thr	696	.	A	B	B	.	.	.	1.98	-0.24	.	*	.	0.45	1.54
	Met	697	.	A	B	B	.	.	.	1.98	-1.00	.	*	F	0.90	1.87
	Asp	698	.	A	B	.	.	.	.	1.98	-1.40	.	.	F	0.90	3.63
	Glu	699	.	A	B	.	.	.	.	1.67	-1.14	.	.	F	1.20	3.94
	Arg	700	.	A	B	.	.	.	.	2.04	-1.14	*	*	F	1.50	5.75
10	Arg	701	.	A	.	.	T	.	.	2.47	-1.33	*	*	F	2.20	5.33
	Tyr	702	.	A	.	.	T	.	.	2.48	-1.33	*	*	F	2.50	6.02
	Thr	703	.	.	.	.	.	T	C	2.44	-0.83	.	*	F	3.00	3.11
	Pro	704	.	.	.	.	.	T	C	1.63	-0.33	.	*	F	2.40	2.16
15	Arg	705	.	.	B	.	.	T	.	1.52	0.36	.	*	.	1.15	1.14
	Ala	706	.	.	B	.	.	T	.	1.41	-0.40	*	*	.	1.45	1.31
	His	707	.	.	B	.	.	.	.	1.31	-0.89	.	*	.	1.59	1.47
	Leu	708	.	.	B	.	.	.	.	1.28	-0.89	*	*	F	1.63	0.74
20	Asp	709	.	.	B	.	.	T	.	1.49	-0.46	.	*	F	1.87	0.73
	Glu	710	.	.	.	.	T	T	.	1.49	-0.96	*	*	F	2.91	0.89
	Gly	711	.	.	.	.	T	T	.	1.38	-1.46	*	*	F	3.40	2.12
	Gly	712	.	.	.	.	T	T	.	1.10	-1.36	*	.	F	3.06	1.10
	Asp	713	.	.	.	.	T	.	.	1.91	-0.87	*	*	F	2.37	0.92
	Arg	714	A	.	.	.	.	.	.	2.02	-0.47	*	*	F	1.48	1.49
	Phe	715	A	.	.	.	.	.	.	1.43	-0.90	*	*	F	1.44	2.95
	Thr	716	.	.	B	.	.	.	.	0.92	-0.83	*	*	F	1.10	1.79
25	Asn	717	.	A	B	.	.	.	.	0.46	-0.19	*	*	F	0.45	0.68
	Arg	718	.	A	B	.	.	.	.	-0.36	0.50	*	*	F	-0.45	0.64
	Ala	719	.	A	B	.	.	.	.	-0.77	0.40	*	*	.	-0.60	0.37
	Val	720	.	A	B	.	.	.	.	-0.37	0.30	.	.	.	-0.06	0.31
30	Leu	721	.	A	B	.	.	.	.	-0.40	0.29	.	.	.	0.18	0.21
	Leu	722	.	A	B	.	.	.	.	-0.40	0.71	.	.	F	0.27	0.21
	Ser	723	.	.	.	.	.	T	C	-0.51	0.61	.	.	F	1.11	0.48
	Ser	724	.	.	.	.	.	T	C	-0.73	-0.03	.	.	F	2.40	1.01
35	Gly	725	.	.	.	.	.	T	C	-0.54	-0.03	*	.	F	2.16	1.01
	Gln	726	A	.	.	.	.	T	.	0.27	-0.14	*	.	F	1.57	0.40
	Glu	727	A	A	.	.	.	.	.	1.19	-0.53	*	*	F	1.23	0.52
	Leu	728	A	A	.	.	.	.	.	0.60	-0.91	*	*	F	1.14	1.03
40	Cys	729	A	A	.	.	.	.	.	0.90	-0.66	*	*	.	0.60	0.42
	Glu	730	A	A	.	.	.	.	.	0.54	-0.66	*	*	.	0.60	0.39
	Arg	731	A	A	.	.	.	.	.	0.51	0.13	*	*	.	-0.30	0.41
	Ile	732	A	A	.	.	.	.	.	-0.34	-0.06	*	*	.	0.45	1.03
	Asn	733	A	A	.	.	.	.	.	-0.34	0.01	*	*	.	-0.30	0.44



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5	Phe	734	A	A	.	.	.	.	0.32	0.70	*	*	.	-0.60	0.19	
	His	735	.	A	B	.	.	.	0.01	0.70	*	*	.	-0.60	0.44	
	Val	736	.	A	B	.	.	.	-0.69	0.50	*	*	.	-0.60	0.40	
	Leu	737	.	A	B	.	.	.	0.20	0.60	.	*	.	-0.60	0.46	
	Asp	738	A	A	.	.	.	.	-0.04	-0.19	.	.	F	0.62	0.57	
	Thr	739	A	.	.	.	.	T	-0.20	0.07	.	.	F	0.74	1.20	
	Ala	740	A	.	.	.	.	T	-0.12	0.07	*	.	F	0.91	1.08	
	Asp	741	A	.	.	.	.	T	0.52	-0.61	*	.	.	1.83	1.30	
10	Tyr	742	.	.	B	.	.	T	0.48	-0.19	*	.	.	1.70	1.39	
	Val	743	.	.	B	B	.	.	0.17	-0.03	.	.	.	1.13	1.02	
	Lys	744	.	.	B	B	.	.	-0.22	-0.04	.	.	F	0.96	0.88	
	Pro	745	.	.	B	B	.	.	0.07	0.74	*	.	F	-0.11	0.49	
15	Val	746	.	.	B	B	.	.	-0.79	0.37	*	.	.	-0.13	0.88	
	Thr	747	.	.	B	B	.	.	-0.54	0.37	*	*	.	-0.30	0.33	
	Phe	748	.	.	B	B	.	.	0.07	0.37	.	*	.	-0.30	0.37	
	Ser	749	.	.	B	B	.	.	-0.28	0.70	.	*	.	-0.60	0.77	
	Val	750	.	.	B	B	.	.	-0.88	0.44	.	*	.	-0.60	0.72	
20	Glu	751	.	.	B	B	.	.	-0.02	0.64	.	*	.	-0.60	0.68	
	Tyr	752	.	.	B	.	.	.	0.29	-0.14	.	*	.	0.50	0.88	
	Ser	753	.	.	.	.	.	.	C	0.78	-0.53	.	*	.	1.49	1.99
	Leu	754	.	.	.	.	T	.	1.08	-0.74	*	.	.	2.03	1.78	
	Glu	755	A	.	.	.	.	.	1.90	-0.74	*	.	F	2.12	1.89	
25	Asp	756	A	.	.	.	.	T	1.56	-1.00	.	.	F	2.66	1.92	
	Pro	757	.	.	.	.	T	T	1.59	-0.96	.	.	F	3.40	2.31	
	Asp	758	.	.	.	.	T	T	1.29	-1.21	.	.	F	3.06	2.06	
	His	759	.	.	.	.	.	T	C	1.29	-0.60	.	.	F	2.52	1.22
	Gly	760	.	.	.	.	.	.	C	1.29	0.09	.	.	F	0.93	0.65
30	Pro	761	.	.	B	.	.	.	1.29	-0.34	.	.	F	0.99	0.65	
	Met	762	.	.	B	.	.	.	1.16	-0.34	*	.	.	0.50	0.80	
	Leu	763	.	.	B	.	.	.	0.87	-0.41	*	.	F	0.89	0.80	
	Asp	764	.	.	.	.	T	T	0.69	0.07	.	.	F	1.13	0.54	
	Asp	765	.	.	.	.	T	T	0.72	0.07	.	.	F	1.37	0.85	
35	Gly	766	.	.	.	.	T	T	0.62	-0.06	.	.	F	2.36	1.48	
	Trp	767	.	.	.	.	.	T	C	0.41	-0.26	*	*	F	2.40	1.28
	Pro	768	.	.	.	B	.	.	C	1.33	0.43	*	*	F	0.71	0.63
	Thr	769	.	.	B	B	.	.	0.48	0.43	*	*	F	0.42	1.25	
	Thr	770	.	.	B	B	.	.	0.18	0.64	*	*	F	0.03	0.89	
40	Leu	771	.	.	B	B	.	.	-0.33	0.11	.	*	.	-0.06	0.77	
	Arg	772	.	.	B	B	.	.	-0.26	0.33	*	*	.	-0.30	0.39	
	Val	773	.	.	B	B	.	.	-0.74	0.27	*	*	.	-0.30	0.42	
	Ser	774	.	.	B	B	.	.	-0.72	0.57	*	*	.	-0.60	0.44	

5	Val	775	.	.	B	B	.	.	-0.41	0.80	*	*	.	-0.60	0.24	
	Pro	776	.	.	B	B	.	.	0.06	1.20	*	*	.	-0.60	0.52	
	Phe	777	.	.	.	B	T	.	-0.72	0.99	*	*	.	-0.20	0.38	
	Trp	778	.	.	.	.	T	T	0.13	1.17	.	.	.	0.20	0.28	
	Asn	779	.	.	.	.	.	T	C	0.43	0.93	.	.	.	0.00	0.29
	Gly	780	.	.	.	.	T	T	1.29	0.50	.	.	.	0.20	0.57	
	Cys	781	.	.	.	.	T	T	1.50	-0.29	.	.	F	1.25	0.91	
	Asn	782	.	A	.	.	T	.	2.17	-1.20	.	.	F	1.15	0.98	
10	Glu	783	.	A	.	.	T	.	1.79	-1.10	.	.	F	1.30	1.35	
	Asp	784	.	A	.	.	T	.	0.93	-0.96	.	.	F	1.30	1.35	
	Glu	785	.	A	.	.	T	.	1.07	-0.89	.	.	F	1.15	0.62	
	His	786	.	A	.	.	T	.	1.73	-0.86	*	.	.	1.00	0.56	
15	Cys	787	A	A	.	.	.	.	0.92	-0.86	*	.	.	0.60	0.56	
	Val	788	A	.	.	.	.	.	0.07	-0.17	.	.	.	0.50	0.26	
	Pro	789	A	.	.	.	.	.	-0.74	0.47	.	.	F	-0.25	0.14	
	Asp	790	A	A	.	.	.	.	-0.74	0.66	*	.	F	-0.45	0.22	
	Leu	791	A	A	.	.	.	.	-1.30	0.09	*	*	.	-0.30	0.50	
20	Val	792	A	A	.	.	.	.	-0.52	-0.06	*	*	.	0.30	0.33	
	Leu	793	A	A	.	.	.	.	0.03	-0.49	*	*	.	0.30	0.38	
	Asp	794	.	A	B	.	.	.	0.24	-0.10	.	*	.	0.30	0.62	
	Ala	795	A	A	.	.	.	.	-0.57	-0.79	.	*	F	0.90	1.40	
	Arg	796	A	.	.	.	.	T	0.03	-0.74	.	*	F	1.30	1.40	
25	Ser	797	A	.	.	.	.	T	0.58	-1.00	.	*	F	1.30	1.29	
	Asp	798	A	.	.	.	.	T	C	0.80	-0.51	.	*	F	1.50	1.85
	Leu	799	.	.	.	.	.	T	C	0.20	-0.51	*	*	F	1.35	0.95
	Pro	800	.	A	.	.	.	.	C	0.79	0.10	*	*	F	0.05	0.70
	Thr	801	A	A	.	.	.	.	0.43	-0.29	.	*	.	0.30	0.73	
30	Ala	802	A	A	.	.	.	.	0.07	0.47	.	.	.	-0.45	1.39	
	Met	803	A	A	.	.	.	.	0.07	0.36	*	.	.	-0.30	0.48	
	Glu	804	A	A	.	.	.	.	0.99	0.33	*	*	.	-0.30	0.58	
	Tyr	805	A	.	.	B	.	.	0.34	-0.16	*	.	.	0.45	1.12	
	Cys	806	A	.	.	B	.	.	-0.16	-0.01	*	.	.	0.30	0.84	
35	Gln	807	A	.	.	B	.	.	0.54	0.06	*	.	.	-0.30	0.40	
	Arg	808	A	.	.	B	.	.	1.19	0.06	*	.	.	-0.30	0.50	
	Val	809	A	.	.	B	.	.	0.98	-0.70	*	.	.	0.75	1.86	
	Leu	810	.	.	B	B	.	.	0.63	-0.84	*	.	F	1.20	1.66	
	Arg	811	.	.	B	B	.	.	1.30	-0.74	*	.	F	1.35	0.86	
40	Lys	812	.	.	B	B	.	.	1.30	-0.34	*	.	F	1.50	2.00	
	Pro	813	.	.	.	.	T	.	0.52	-0.99	*	.	F	2.70	4.06	
	Ala	814	.	.	.	.	T	.	1.08	-1.10	*	.	F	3.00	1.11	
	Gln	815	.	.	B	.	.	T	1.30	-0.71	*	.	F	2.35	0.74	

5	Asp	816	.	.	B	.	.	T	.	0.94	-0.21	*	.	F	1.75	0.49
	Cys	817	.	.	B	.	.	T	.	0.59	0.11	.	.	.	0.70	0.75
	Ser	818	.	.	B	.	.	T	.	-0.01	0.10	.	.	.	0.40	0.63
	Ala	819	.	.	B	B	.	.	.	0.28	0.39	.	.	.	-0.30	0.31
	Tyr	820	.	.	B	B	.	.	.	-0.42	0.77	.	.	.	-0.60	0.78
10	Thr	821	.	.	B	B	.	.	.	-0.42	0.99	.	.	.	-0.60	0.50
	Leu	822	.	.	B	B	.	.	.	-0.07	0.60	.	.	.	-0.60	0.83
	Ser	823	.	.	B	B	.	.	.	-0.08	0.59	.	*	.	-0.60	0.76
	Phe	824	.	.	B	B	.	.	.	-0.34	0.31	.	*	.	-0.30	0.76
	Asp	825	.	.	B	B	.	.	.	-0.80	0.47	.	*	F	-0.45	0.69
15	Thr	826	.	.	B	B	.	.	.	-1.38	0.57	.	*	F	-0.45	0.44
	Thr	827	.	.	B	B	.	.	.	-1.46	0.87	.	*	F	-0.45	0.36
	Val	828	.	.	B	B	.	.	.	-1.16	0.77	.	.	.	-0.60	0.15
	Phe	829	.	.	B	B	.	.	.	-0.76	0.77	.	.	.	-0.60	0.18
	Ile	830	.	.	B	B	.	.	.	-1.07	0.67	.	.	.	-0.60	0.17
20	Ile	831	.	.	B	B	.	.	.	-0.64	0.67	.	.	.	-0.60	0.33
	Glu	832	A	.	.	B	.	.	.	-0.33	0.03	.	*	F	-0.15	0.74
	Ser	833	A	.	.	.	.	T	.	0.63	-0.36	.	*	F	1.00	1.83
	Thr	834	A	.	.	.	.	T	.	0.48	-1.04	.	*	F	1.30	5.10
	Arg	835	A	.	.	.	.	T	.	0.78	-1.09	.	*	F	1.30	2.19
25	Gln	836	A	.	.	.	.	T	.	0.81	-0.59	.	*	F	1.30	1.65
	Arg	837	A	A	.	.	.	.	.	0.81	-0.33	.	*	F	0.45	0.85
	Val	838	.	A	B	.	.	.	.	0.52	-0.81	.	*	.	0.60	0.75
	Ala	839	.	A	B	.	.	.	.	0.52	-0.31	.	*	.	0.30	0.44
	Val	840	.	A	B	.	.	.	.	-0.40	-0.23	.	*	.	0.30	0.32
30	Glu	841	A	A	.	.	.	.	.	-0.40	0.46	.	*	.	-0.60	0.36
	Ala	842	A	A	.	.	.	.	.	-0.51	-0.19	.	*	.	0.30	0.61
	Thr	843	A	A	.	.	.	.	.	0.46	-0.29	.	*	.	0.45	1.33
	Leu	844	A	A	.	.	.	.	.	0.70	-0.93	.	*	F	0.90	1.50
	Glu	845	A	A	.	.	.	.	.	1.56	-0.50	.	*	F	0.60	1.47
35	Asn	846	A	.	.	.	.	T	.	1.56	-1.00	.	*	F	1.60	1.77
	Arg	847	A	.	.	.	.	T	.	1.56	-1.09	*	*	F	1.90	3.45
	Gly	848	A	.	.	.	.	T	.	1.62	-1.27	*	*	F	2.20	2.01
	Glu	849	A	.	.	.	.	T	.	2.13	-0.51	*	*	F	2.50	1.96
	Asn	850	.	.	.	.	.	T	C	1.82	-0.53	*	.	F	3.00	1.34
40	Ala	851	A	.	.	.	.	T	.	0.97	-0.04	*	.	F	2.20	1.95
	Tyr	852	.	.	B	.	.	T	.	0.04	0.17	*	.	.	1.00	0.84
	Ser	853	.	.	B	.	.	T	.	0.39	0.86	*	.	.	0.40	0.43
	Thr	854	.	.	B	B	.	.	.	-0.50	0.86	*	.	.	-0.30	0.68
	Val	855	.	.	B	B	.	.	.	-0.80	1.04	*	.	.	-0.60	0.31
	Leu	856	.	.	B	B	.	.	.	-0.21	0.67	*	.	.	-0.60	0.31

5	Asn	857	.	.	B	B	.	.	.	-0.27	0.69	*	.	.	-0.60	0.37
	Ile	858	.	.	B	B	.	.	.	-0.56	0.59	*	.	F	-0.45	0.66
	Ser	859	.	.	B	.	.	.	.	-0.24	0.44	.	*	F	-0.25	0.81
	Gln	860	.	.	B	.	.	.	C	-0.20	0.16	.	*	F	0.25	0.81
	Ser	861	.	.	.	.	.	T	C	0.61	0.44	.	*	F	0.15	0.96
10	Ala	862	.	.	B	.	.	T	.	-0.09	0.16	.	*	F	0.40	1.23
	Asn	863	.	.	B	.	.	T	.	0.21	0.56	.	*	.	-0.20	0.62
	Leu	864	A	.	.	.	.	T	.	0.21	0.66	.	.	.	-0.20	0.47
	Gln	865	A	A	.	.	.	.	.	-0.60	0.66	.	*	.	-0.60	0.62
	Phe	866	A	A	.	.	.	.	.	-1.19	0.84	.	*	.	-0.60	0.32
15	Ala	867	A	A	.	.	.	.	.	-0.60	1.13	*	*	.	-0.60	0.27
	Ser	868	A	A	.	.	.	.	.	-0.56	0.84	*	*	.	-0.60	0.27
	Leu	869	A	A	.	.	.	.	.	0.26	0.44	*	.	.	-0.60	0.62
	Ile	870	A	A	.	.	.	.	.	0.26	-0.34	*	.	.	0.45	1.07
	Gln	871	A	A	.	.	.	.	.	0.66	-0.84	*	.	F	1.24	1.33
20	Lys	872	A	A	.	.	.	.	.	1.24	-0.84	*	.	F	1.58	2.16
	Glu	873	A	A	.	.	.	.	.	1.20	-1.53	*	.	F	1.92	5.14
	Asp	874	.	.	.	.	T	T	.	1.71	-1.79	.	*	F	3.06	2.94
	Ser	875	.	.	.	.	T	T	.	1.71	-1.80	.	*	F	3.40	1.97
	Asp	876	.	.	.	.	T	T	.	1.71	-1.11	.	*	F	2.91	0.80
25	Gly	877	.	.	.	.	T	T	.	1.00	-1.11	.	*	F	2.57	0.83
	Ser	878	A	A	.	.	.	.	.	0.14	-0.54	.	.	F	1.43	0.33
	Ile	879	A	A	.	.	.	.	.	0.14	-0.29	.	*	.	0.64	0.15
	Glu	880	A	A	.	.	.	.	.	0.44	0.11	.	.	.	-0.30	0.24
	Cys	881	.	A	B	.	.	.	.	0.44	-0.31	.	*	.	0.30	0.31
30	Val	882	A	A	.	.	.	.	.	0.90	-0.70	*	.	.	0.60	0.76
	Asn	883	A	A	.	.	.	.	.	1.31	-1.39	*	.	F	0.75	0.86
	Glu	884	A	A	.	.	.	.	.	1.39	-1.39	*	*	F	0.90	3.15
	Glu	885	A	A	.	.	.	.	.	1.39	-1.27	*	.	F	0.90	3.50
	Arg	886	A	A	.	.	.	.	.	2.10	-1.51	*	.	F	0.90	3.77
35	Arg	887	A	A	.	.	.	.	.	2.96	-1.91	*	*	F	0.90	4.35
	Leu	888	A	A	.	.	.	.	.	2.10	-1.51	*	.	F	0.90	4.35
	Gln	889	A	A	.	.	.	.	.	1.43	-0.87	*	.	F	0.90	1.65
	Lys	890	A	A	.	.	.	.	.	1.43	-0.30	*	.	F	0.45	0.45
	Gln	891	.	A	B	.	.	.	.	0.47	0.10	*	.	.	-0.30	0.88
40	Val	892	.	A	B	.	.	.	.	0.06	0.06	*	*	.	-0.30	0.38
	Cys	893	.	A	B	.	.	.	.	0.62	0.04	*	.	.	-0.30	0.25
	Asn	894	.	.	B	.	.	T	.	0.41	0.80	*	.	.	-0.20	0.23
	Val	895	.	.	B	.	.	T	.	-0.33	0.83	*	.	.	-0.20	0.48
	Ser	896	.	.	B	.	.	T	.	-1.03	0.97	*	.	.	-0.20	0.77
	Tyr	897	.	.	B	.	.	T	.	-0.07	1.19	*	.	.	-0.20	0.41

	Pro	898	.	.	B	B	.	.	.	0.01	0.79	*	*	.	-0.45	1.09
	Phe	899	A	A	.	B	.	.	.	0.06	0.64	*	*	.	-0.60	0.82
	Phe	900	A	A	.	B	.	.	.	0.32	0.26	*	*	.	-0.15	1.05
	Arg	901	A	A	.	B	.	.	.	0.67	0.00	*	*	.	-0.30	0.69
5	Ala	902	A	A	.	.	.	.	.	0.06	-0.43	*	*	.	0.45	1.59
	Lys	903	A	A	.	.	.	.	.	-0.32	-0.57	*	*	F	0.90	1.36
	Ala	904	A	A	.	.	.	.	.	-0.32	-0.86	*	*	F	0.75	0.70
	Lys	905	A	A	.	B	.	.	.	0.49	-0.07	*	*	.	0.30	0.60
	Val	906	A	A	.	B	.	.	.	-0.43	-0.57	*	*	.	0.60	0.59
10	Ala	907	A	A	.	B	.	.	.	0.16	0.11	.	*	.	-0.30	0.48
	Phe	908	A	A	.	B	.	.	.	-0.59	-0.39	.	*	.	0.30	0.40
	Arg	909	A	A	.	B	.	.	.	0.00	0.40	*	*	.	-0.60	0.47
	Leu	910	A	A	.	.	.	.	.	-0.74	-0.24	*	*	.	0.30	0.80
	Asp	911	A	A	.	.	.	.	.	-0.19	0.04	*	*	.	-0.30	0.80
15	Phe	912	A	A	.	.	.	.	.	0.44	-0.36	*	*	.	0.30	0.55
	Glu	913	A	A	.	.	.	.	.	0.84	-0.36	*	*	.	0.45	1.33
	Phe	914	A	A	.	.	.	.	.	-0.16	-0.66	*	*	.	0.75	1.07
	Ser	915	A	.	.	.	.	T	.	-0.04	0.03	.	*	F	0.25	0.87
	Lys	916	A	.	.	.	.	T	.	-0.86	0.03	.	*	F	0.25	0.43
20	Ser	917	A	.	.	.	.	T	.	-0.19	0.71	.	.	.	-0.20	0.41
	Ile	918	A	.	.	.	.	T	.	-0.22	0.43	.	.	.	-0.20	0.42
	Phe	919	A	A	.	.	.	.	.	-0.33	0.54	.	.	.	-0.60	0.28
	Leu	920	A	A	.	.	.	.	.	-0.03	1.23	.	.	.	-0.60	0.18
	His	921	A	A	.	.	.	.	.	-0.97	0.84	.	*	.	-0.60	0.43
25	His	922	A	A	.	.	.	.	.	-0.67	0.84	.	*	.	-0.60	0.35
	Leu	923	A	A	.	.	.	.	.	-0.59	0.06	.	*	.	-0.30	0.74
	Glu	924	A	A	.	.	.	.	.	-0.48	0.06	.	*	.	-0.30	0.45
	Ile	925	A	A	.	.	.	.	.	-0.26	0.06	.	*	.	-0.30	0.33
	Glu	926	A	A	.	.	.	.	.	-0.57	0.06	.	*	.	-0.30	0.41
30	Leu	927	A	A	.	.	.	.	.	-0.83	-0.20	.	*	.	0.30	0.23
	Ala	928	A	A	.	.	.	.	.	-0.02	0.19	.	*	.	-0.30	0.44
	Ala	929	A	A	.	.	.	.	.	-0.32	-0.50	.	*	.	0.30	0.43
	Gly	930	A	.	.	.	.	T	.	0.57	-0.11	.	*	F	0.85	0.69
	Ser	931	.	.	.	.	.	T	C	0.57	-0.40	*	*	F	1.20	1.11
35	Asp	932	.	.	.	.	.	T	C	1.49	-0.90	.	.	F	1.50	1.89
	Ser	933	.	.	.	.	.	T	C	2.08	-1.40	.	.	F	1.84	3.75
	Asn	934	.	.	.	.	.	.	C	2.37	-1.83	.	.	F	1.98	4.67
	Glu	935	A	.	.	.	.	.	.	2.40	-1.83	*	*	F	2.12	3.75
	Arg	936	A	.	.	.	.	.	.	2.74	-1.34	.	.	F	2.46	4.04
40	Asp	937	.	.	.	.	T	T	.	2.74	-1.73	.	*	F	3.40	5.02
	Ser	938	.	.	.	.	.	T	C	3.04	-2.13	.	.	F	2.86	5.02

	Thr	939	A	.	.	.	.	T	.	3.04	-2.13	.	.	F	2.32	4.28
	Lys	940	A	.	.	.	.	T	.	2.19	-1.73	*	.	F	1.98	4.12
	Glu	941	A	A	.	.	.	.	.	1.49	-1.09	*	.	F	1.24	2.28
	Asp	942	A	A	.	.	.	.	.	1.28	-0.97	.	.	F	0.90	1.60
5	Asn	943	A	A	.	.	.	.	.	0.77	-1.03	.	*	F	0.90	1.24
	Val	944	A	A	.	.	.	.	.	1.19	-0.34	.	*	.	0.30	0.59
	Ala	945	A	A	.	.	.	.	.	0.44	-0.34	.	*	.	0.30	0.69
	Pro	946	A	A	.	.	.	.	.	0.41	0.44	.	*	.	-0.60	0.37
	Leu	947	A	A	.	.	.	.	.	-0.40	0.54	.	*	.	-0.60	0.68
10	Arg	948	A	A	.	.	.	.	.	-0.36	0.59	.	*	.	-0.60	0.56
	Phe	949	A	A	.	.	.	.	.	0.26	0.09	.	*	.	-0.30	0.72
	His	950	A	A	.	.	.	.	.	0.84	0.41	.	*	.	-0.45	1.37
	Leu	951	A	A	.	.	.	.	.	0.47	-0.27	*	*	.	0.45	1.21
	Lys	952	A	A	.	.	.	.	.	1.28	0.23	*	*	.	-0.15	1.41
15	Tyr	953	A	A	.	.	.	.	.	0.31	-0.56	*	*	.	0.75	1.73
	Glu	954	A	A	.	.	.	.	.	0.20	-0.41	.	*	.	0.45	1.56
	Ala	955	A	.	.	B	.	.	.	-0.47	-0.41	.	*	.	0.30	0.64
	Asp	956	A	.	.	B	.	.	.	0.03	0.37	.	*	.	-0.30	0.35
	Val	957	A	.	.	B	.	.	.	0.10	0.10	.	*	.	-0.30	0.30
20	Leu	958	A	.	.	B	.	.	.	0.04	0.10	.	.	.	-0.30	0.57
	Phe	959	A	.	.	B	.	.	.	-0.26	-0.01	.	.	.	0.30	0.46
	Thr	960	A	.	.	B	.	.	.	0.03	0.37	.	.	F	0.06	0.83
	Arg	961	A	.	.	B	.	.	.	-0.78	0.11	.	.	F	0.42	1.35
	Ser	962	.	.	.	.	T	T	.	-0.22	0.11	.	.	F	1.43	1.29
25	Ser	963	.	.	.	.	.	T	C	0.56	-0.29	.	.	F	2.04	1.19
	Ser	964	.	.	.	.	.	T	C	1.01	-0.27	.	.	F	2.10	0.83
	Leu	965	.	.	.	.	.	T	C	1.32	0.49	.	.	F	0.99	0.97
	Ser	966	.	.	.	.	.	.	C	0.36	0.10	.	*	.	0.88	1.25
	His	967	.	.	B	.	.	.	.	0.70	0.36	.	*	.	0.32	0.69
30	Tyr	968	.	.	B	.	.	.	.	0.19	-0.03	.	*	.	0.86	1.68
	Glu	969	.	.	B	.	.	.	.	0.49	-0.03	.	*	.	0.65	1.04
	Val	970	A	.	.	.	.	.	.	1.00	-0.01	.	*	.	0.65	1.22
	Lys	971	A	.	.	.	.	.	.	1.00	-0.13	.	*	F	0.80	1.05
	Leu	972	A	.	.	.	.	.	.	0.22	-0.50	.	*	F	0.65	0.81
35	Asn	973	.	.	.	.	.	T	C	0.47	0.19	*	*	F	0.45	0.90
	Ser	974	A	.	.	.	.	T	.	0.58	-0.46	*	*	F	0.85	0.78
	Ser	975	A	.	.	.	.	T	.	1.19	-0.46	*	*	F	1.00	1.85
	Leu	976	.	.	B	.	.	T	.	1.14	-0.39	*	*	F	1.31	1.80
	Glu	977	.	.	B	.	.	.	.	1.61	-0.79	*	.	F	1.72	2.25
40	Arg	978	.	.	B	.	.	T	.	0.72	-0.74	*	.	F	2.23	1.66
	Tyr	979	.	.	B	.	.	T	.	0.68	-0.44	.	.	F	2.24	1.41

5	Asp	980	.	.	.	.	T	T	.	0.77	-0.70	.	.	F	3.10	0.81
	Gly	981	.	.	.	.	T	T	.	1.37	-0.27	*	.	F	2.49	0.64
	Ile	982	.	.	.	.	T	.	.	0.67	0.16	*	.	F	1.38	0.63
	Gly	983	.	.	.	.	.	.	C	0.26	0.19	.	*	F	0.87	0.33
	Pro	984	.	.	.	.	.	T	C	-0.17	0.57	*	.	F	0.46	0.44
10	Pro	985	.	.	.	.	T	T	.	-1.06	0.71	*	.	F	0.35	0.34
	Phe	986	.	.	.	.	T	T	.	-1.41	0.71	*	*	.	0.20	0.24
	Ser	987	.	.	B	.	.	T	.	-0.41	1.07	*	*	.	-0.20	0.13
	Cys	988	.	.	B	B	.	.	.	-0.96	0.64	*	*	.	-0.60	0.17
	Ile	989	.	.	B	B	.	.	.	-0.74	0.90	*	*	.	-0.60	0.14
15	Phe	990	.	.	B	B	.	.	.	-0.53	0.51	*	*	.	-0.60	0.18
	Arg	991	.	.	B	B	.	.	.	-0.64	0.53	*	*	.	-0.60	0.53
	Ile	992	.	.	B	B	.	.	.	-0.69	0.64	*	*	.	-0.60	0.63
	Gln	993	.	.	B	B	.	.	.	-0.83	0.39	*	*	.	-0.30	0.72
	Asn	994	.	.	.	B	T	.	.	-0.64	0.29	*	*	.	0.10	0.30
20	Leu	995	.	.	.	B	T	.	.	-0.16	1.07	.	*	.	-0.20	0.37
	Gly	996	.	.	.	B	T	.	.	-1.16	0.81	*	*	.	-0.20	0.33
	Leu	997	.	.	.	.	.	.	C	-0.30	1.10	.	.	.	-0.20	0.14
	Phe	998	.	.	B	.	.	.	.	-0.64	1.20	.	.	.	-0.40	0.24
	Pro	999	.	.	B	.	.	.	.	-1.53	0.94	.	.	.	-0.40	0.24
25	Ile	1000	A	.	.	B	.	.	.	-1.32	1.20	.	.	.	-0.60	0.20
	His	1001	A	.	.	B	.	.	.	-1.58	1.13	.	.	.	-0.60	0.23
	Gly	1002	A	.	.	B	.	.	.	-0.72	0.96	*	.	.	-0.60	0.15
	Ile	1003	A	.	.	B	.	.	.	-0.91	0.53	.	*	.	-0.60	0.42
	Met	1004	A	.	.	B	.	.	.	-1.01	0.53	.	*	.	-0.60	0.22
30	Met	1005	.	.	B	B	.	.	.	-1.01	0.51	.	*	.	-0.60	0.32
	Lys	1006	.	.	B	B	.	.	.	-1.19	0.77	.	*	.	-0.60	0.32
	Ile	1007	.	.	B	B	.	.	.	-1.73	0.51	.	*	.	-0.60	0.50
	Thr	1008	.	.	B	B	.	.	.	-1.43	0.59	.	*	.	-0.60	0.35
	Ile	1009	.	.	B	B	.	.	.	-1.14	0.47	*	*	.	-0.60	0.18
35	Pro	1010	.	.	B	B	.	.	.	-0.43	0.96	*	*	.	-0.60	0.37
	Ile	1011	.	.	B	B	.	.	.	-0.78	0.27	*	*	.	0.04	0.50
	Ala	1012	.	.	B	B	.	.	.	-0.23	0.17	*	*	.	0.38	0.95
	Thr	1013	.	.	B	.	.	T	.	0.08	-0.09	*	*	F	1.87	0.61
	Arg	1014	.	.	.	.	T	T	.	1.08	-0.11	*	*	F	2.76	1.40
40	Ser	1015	.	.	.	.	T	T	.	0.48	-0.80	*	*	F	3.40	2.71
	Gly	1016	.	.	.	.	T	T	.	0.56	-0.61	*	*	F	3.06	1.55
	Asn	1017	.	A	.	.	T	.	.	1.19	-0.41	*	.	F	1.87	0.65
	Arg	1018	.	A	B	.	.	.	.	0.69	-0.41	*	*	F	1.13	0.97
	Leu	1019	.	A	B	.	.	.	.	0.69	-0.11	*	*	F	0.79	0.81
	Leu	1020	.	A	B	.	.	.	.	0.99	-0.54	.	.	F	0.75	0.99

	Lys	1021	.	A	B	.	.	.	.	0.63	-0.94	*	.	F	0.75	0.84
	Leu	1022	.	A	B	.	.	.	.	-0.18	-0.16	*	.	F	0.45	0.88
	Arg	1023	.	A	B	.	.	.	.	-0.60	-0.16	*	.	F	0.45	0.88
	Asp	1024	.	A	B	.	.	.	.	0.21	-0.36	*	*	F	0.45	0.64
5	Phe	1025	.	A	B	.	.	.	.	1.02	-0.36	*	*	.	0.45	1.29
	Leu	1026	A	A	.	.	.	.	.	0.12	-1.04	*	*	F	0.90	1.14
	Thr	1027	A	A	.	.	.	.	.	0.34	-0.40	*	.	F	0.45	0.51
	Asp	1028	A	A	.	.	.	.	.	0.23	0.10	.	.	F	-0.15	0.59
	Glu	1029	A	A	.	.	.	.	.	-0.08	-0.29	*	.	.	0.45	1.15
10	Val	1030	A	A	.	.	.	.	.	0.32	-0.49	.	.	.	0.45	1.15
	Ala	1031	A	A	.	.	.	.	.	0.47	-0.59	*	.	.	0.60	0.93
	Asn	1032	.	.	.	.	T	T	.	0.78	-0.01	*	.	F	1.25	0.29
	Thr	1033	.	.	.	.	T	T	.	-0.11	0.39	*	.	F	0.65	0.62
	Ser	1034	.	.	B	.	.	T	.	-0.40	0.43	*	.	F	-0.05	0.43
15	Cys	1035	.	.	B	.	.	T	.	0.11	0.84	*	*	.	-0.20	0.28
	Asn	1036	.	.	.	.	T	.	.	0.70	0.87	.	*	.	0.16	0.19
	Ile	1037	.	.	.	.	T	.	.	0.40	0.79	.	*	.	0.32	0.23
	Trp	1038	.	.	.	.	T	T	.	0.40	0.79	.	.	.	0.68	0.58
	Gly	1039	.	.	.	.	.	T	C	0.70	0.70	.	.	F	0.79	0.52
20	Asn	1040	.	.	.	.	T	T	.	1.12	0.30	.	*	F	1.60	1.28
	Ser	1041	.	.	.	.	.	T	C	1.23	0.37	.	*	F	1.24	1.91
	Thr	1042	.	.	.	.	.	.	C	1.91	-0.54	.	*	F	1.78	3.79
	Glu	1043	.	.	.	.	T	.	.	1.89	-0.54	.	*	F	1.82	3.64
	Tyr	1044	.	.	.	.	T	.	.	2.02	-0.46	.	.	F	1.66	3.92
25	Arg	1045	.	.	.	.	.	T	C	1.17	-0.41	.	.	F	1.80	4.20
	Pro	1046	.	.	.	.	.	T	C	1.47	-0.26	.	.	F	2.10	1.80
	Thr	1047	.	.	.	.	.	T	C	1.78	-0.26	.	.	F	2.40	1.99
	Pro	1048	.	.	.	.	.	T	C	1.78	-1.01	.	*	F	3.00	1.76
	Val	1049	A	A	.	.	.	.	.	1.21	-1.01	.	*	F	2.10	1.90
30	Glu	1050	A	A	.	.	.	.	.	1.21	-0.76	*	.	F	1.80	1.09
	Glu	1051	A	A	.	.	.	.	.	1.53	-1.24	*	.	F	1.50	1.38
	Asp	1052	A	A	.	.	.	.	.	1.26	-1.67	*	.	F	1.20	3.63
	Leu	1053	A	A	.	.	.	.	.	1.26	-1.81	*	.	F	0.90	2.12
	Arg	1054	A	A	.	.	.	.	.	2.11	-1.39	*	*	F	0.90	1.89
35	Arg	1055	A	A	.	.	.	.	.	1.30	-0.99	*	*	F	0.90	1.96
	Ala	1056	A	A	.	.	.	.	.	1.30	-0.30	*	.	F	0.60	1.96
	Pro	1057	A	A	.	.	.	.	.	1.27	-0.59	*	*	F	0.90	1.61
	Gln	1058	A	A	.	.	.	.	.	1.78	-0.09	*	.	F	0.60	1.12
	Leu	1059	.	A	B	.	.	.	.	1.67	0.30	*	.	.	0.13	1.48
40	Asn	1060	.	A	.	.	.	.	C	1.26	0.20	.	.	.	0.61	1.54
	His	1061	.	.	.	.	.	T	C	1.84	0.16	.	.	F	1.44	1.19



5	Ser	1062	.	.	.	.	.	T	C	1.20	-0.24	.	.	F	2.32	2.42
	Asn	1063	.	.	.	.	T	T	.	0.34	-0.29	*	.	F	2.80	1.12
	Ser	1064	.	.	.	.	T	T	.	0.86	-0.04	*	.	F	2.37	0.61
	Asp	1065	.	.	B	B	.	.	.	-0.03	-0.16	.	.	F	1.29	0.61
	Val	1066	.	.	B	B	.	.	.	0.00	0.14	.	.	F	0.41	0.27
	Val	1067	.	.	B	B	.	.	.	-0.37	0.14	.	.	.	-0.02	0.32
10	Ser	1068	.	.	B	.	.	T	.	-0.37	0.33	.	*	.	0.10	0.10
	Ile	1069	.	.	B	.	.	T	.	-0.96	0.73	*	*	.	-0.20	0.22
	Asn	1070	.	.	B	.	.	T	.	-0.84	0.77	.	*	.	-0.20	0.21
	Cys	1071	.	.	B	.	.	T	.	-0.80	0.13	*	*	.	0.10	0.31
	Asn	1072	.	.	B	B	.	.	.	-0.80	0.43	*	*	.	-0.60	0.36
	Ile	1073	.	.	B	B	.	.	.	-0.71	0.39	*	*	.	-0.30	0.17
15	Arg	1074	.	.	B	B	.	.	.	0.18	0.41	*	*	.	-0.60	0.48
	Leu	1075	.	.	B	B	.	.	.	0.18	0.24	*	*	.	-0.30	0.48
	Val	1076	.	.	B	.	.	T	.	0.84	0.24	.	*	F	0.40	1.18
	Pro	1077	.	.	.	.	.	T	C	-0.04	-0.44	*	*	F	1.20	1.05
	Asn	1078	.	.	.	.	T	T	.	0.84	0.24	*	*	F	0.65	0.89
	Gln	1079	A	.	.	.	.	T	.	0.03	-0.04	*	*	F	1.00	1.93
20	Glu	1080	.	A	B	.	.	.	.	0.81	0.10	.	*	F	0.00	1.08
	Ile	1081	.	A	B	.	.	.	.	0.86	0.17	.	*	F	-0.15	0.91
	Asn	1082	.	A	B	.	.	.	.	0.26	0.46	.	*	.	-0.60	0.43
	Phe	1083	.	A	B	.	.	.	.	-0.09	0.74	.	*	.	-0.60	0.21
	His	1084	.	A	B	.	.	.	.	-0.09	1.17	.	*	.	-0.60	0.29
	Leu	1085	.	A	B	.	.	.	.	-0.90	0.89	.	*	.	-0.60	0.29
25	Leu	1086	.	A	.	.	.	.	C	-0.30	1.17	.	*	.	-0.40	0.28
	Gly	1087	.	A	.	.	T	.	.	-1.11	1.30	*	*	.	-0.20	0.22
	Asn	1088	A	A	.	.	.	.	.	-0.30	1.49	*	*	.	-0.60	0.22
	Leu	1089	A	A	.	.	.	.	.	-0.57	0.80	*	*	.	-0.60	0.51
	Trp	1090	A	A	.	.	.	.	.	-0.57	0.50	*	*	.	-0.60	0.69
	Leu	1091	A	A	.	.	.	.	.	0.29	0.76	*	.	.	-0.60	0.35
30	Arg	1092	A	A	.	.	.	.	.	0.04	0.36	*	*	.	-0.30	0.86
	Ser	1093	A	A	.	.	.	.	.	-0.77	0.17	*	.	.	-0.30	0.83
	Leu	1094	A	A	.	.	.	.	.	0.09	-0.06	*	.	F	0.45	0.83
	Lys	1095	A	A	.	.	.	.	.	0.13	-0.74	*	.	F	0.75	0.84
	Ala	1096	A	A	.	.	.	.	.	0.99	0.01	*	*	.	-0.30	0.99
	Leu	1097	A	A	.	.	.	.	.	0.58	-0.37	*	.	.	0.45	2.39
35	Lys	1098	A	A	.	.	.	.	.	0.28	-0.67	.	.	F	0.90	1.60
	Tyr	1099	A	A	.	.	.	.	.	1.13	-0.06	*	.	F	0.60	1.57
	Lys	1100	A	A	.	.	.	.	.	0.20	-0.56	*	.	F	0.90	3.81
	Ser	1101	A	A	.	.	.	.	.	0.19	-0.56	.	*	F	0.90	1.34
	Met	1102	A	A	.	.	.	.	.	0.14	0.06	.	*	.	-0.30	0.84

300

	Lys	1103	A	A	.	.	.	.	0.10	-0.06	.	*	.	0.30 0.31
	Ile	1104	.	A	B	.	.	.	-0.24	0.34	*	*	.	-0.30 0.38
	Met	1105	A	A	.	.	.	.	-0.88	0.46	*	*	.	-0.60 0.38
	Val	1106	A	A	.	.	.	.	-1.39	0.34	*	*	.	-0.30 0.19
5	Asn	1107	A	A	.	.	.	.	-0.79	1.03	.	*	.	-0.60 0.23
	Ala	1108	A	A	.	.	.	.	-0.72	0.74	.	*	.	-0.60 0.40
	Ala	1109	A	A	.	.	.	.	0.17	0.13	.	*	.	-0.15 1.05
	Leu	1110	A	A	.	.	.	.	0.07	-0.11	*	.	.	0.45 1.13
	Gln	1111	A	A	.	.	.	.	0.89	0.27	*	.	.	-0.30 0.97
10	Arg	1112	A	A	.	.	.	.	0.59	0.27	*	.	.	-0.15 1.31
	Gln	1113	.	A	B	.	.	.	0.97	0.16	*	.	.	-0.15 2.13
	Phe	1114	.	A	.	.	T	.	0.86	-0.10	*	.	.	0.85 1.90
	His	1115	.	A	.	.	.	C	0.78	0.29	*	.	.	-0.10 0.84
	Ser	1116	.	A	.	.	.	C	0.08	0.97	.	*	.	-0.40 0.34
15	Pro	1117	.	.	.	B	.	C	0.08	1.36	.	*	.	-0.40 0.34
	Phe	1118	.	A	.	B	.	C	0.08	0.57	.	*	.	-0.40 0.49
	Ile	1119	.	A	B	B	.	.	0.78	0.07	.	*	.	-0.30 0.63
	Phe	1120	.	A	B	B	.	.	0.81	-0.31	.	.	.	0.30 0.71
	Arg	1121	A	A	.	B	.	.	0.90	-0.74	.	.	F	1.24 1.37
20	Glu	1122	.	A	.	.	T	.	0.81	-1.10	*	*	F	1.98 3.01
	Glu	1123	.	A	.	.	.	C	1.62	-1.40	*	*	F	2.12 4.66
	Asp	1124	.	.	.	.	T	C	2.51	-2.19	*	.	F	2.86 4.66
	Pro	1125	.	.	.	.	T	T	2.32	-1.79	*	*	F	3.40 4.66
	Ser	1126	.	.	.	.	T	T	1.36	-1.10	*	.	F	3.06 1.89
25	Arg	1127	A	.	.	.	T	.	0.66	-0.46	.	.	F	1.87 0.84
	Gln	1128	A	.	.	B	.	.	0.66	0.33	*	.	F	0.53 0.47
	Ile	1129	A	.	.	B	.	.	-0.23	-0.10	*	.	.	0.64 0.61
	Val	1130	A	.	.	B	.	.	-0.32	0.20	*	.	.	-0.30 0.22
	Phe	1131	.	.	B	B	.	.	0.02	0.59	*	.	.	-0.60 0.17
30	Glu	1132	.	.	B	B	.	.	-0.09	0.19	*	.	.	-0.30 0.48
	Ile	1133	.	.	B	B	.	.	-0.09	-0.10	*	*	F	0.60 1.12
	Ser	1134	.	A	.	.	.	C	0.80	-0.74	.	*	F	1.10 2.24
	Lys	1135	.	A	.	.	T	.	1.37	-1.53	.	.	F	1.30 2.16
	Gln	1136	.	A	.	.	T	.	2.07	-0.61	.	*	F	1.30 3.24
35	Glu	1137	A	A	.	.	.	.	1.21	-0.90	.	*	F	0.90 4.18
	Asp	1138	.	A	.	B	T	.	1.89	-0.64	.	*	F	1.30 1.55
	Trp	1139	.	A	.	B	T	.	1.30	-0.21	.	*	.	0.85 1.39
	Gln	1140	.	A	B	B	.	.	0.97	0.07	.	*	.	-0.30 0.56
	Val	1141	.	A	B	B	.	.	0.08	0.99	.	*	.	-0.60 0.35
40	Pro	1142	.	A	B	B	.	.	-0.81	1.67	.	*	.	-0.60 0.24
	Ile	1143	.	.	B	B	.	.	-1.67	1.44	.	*	.	-0.60 0.10

	Trp	1144	.	.	B	B	.	.	.	-1.72	1.69	.	*	.	-0.60	0.10
	Ile	1145	.	.	B	B	.	.	.	-2.02	1.47	.	.	.	-0.60	0.06
	Ile	1146	.	.	B	B	.	.	.	-1.48	1.43	.	.	.	-0.60	0.12
	Val	1147	.	.	B	B	.	.	.	-2.08	1.23	.	.	.	-0.60	0.16
5	Gly	1148	.	.	B	B	.	.	.	-1.53	1.00	.	.	F	-0.45	0.19
	Ser	1149	.	.	.	B	.	.	C	-1.59	0.74	.	.	F	-0.25	0.27
	Thr	1150	.	.	.	B	.	.	C	-1.51	0.49	.	.	F	-0.25	0.35
	Leu	1151	.	.	.	B	.	.	C	-1.43	0.53	.	.	F	-0.25	0.30
	Gly	1152	.	.	.	B	T	.	.	-1.39	0.79	.	.	F	-0.05	0.18
10	Gly	1153	.	A	B	B	.	.	.	-1.86	1.09	.	.	.	-0.60	0.10
	Leu	1154	.	A	B	B	.	.	.	-2.14	1.29	.	.	.	-0.60	0.10
	Leu	1155	.	A	B	B	.	.	.	-2.64	1.10	.	.	.	-0.60	0.11
	Leu	1156	A	A	.	B	.	.	.	-2.64	1.36	.	.	.	-0.60	0.09
	Leu	1157	A	A	.	B	.	.	.	-3.16	1.61	.	.	.	-0.60	0.09
15	Ala	1158	A	A	.	B	.	.	.	-3.62	1.57	.	.	.	-0.60	0.08
	Leu	1159	A	A	.	B	.	.	.	-3.40	1.57	.	.	.	-0.60	0.08
	Leu	1160	A	A	.	B	.	.	.	-3.40	1.39	.	.	.	-0.60	0.10
	Val	1161	A	A	.	B	.	.	.	-2.88	1.39	.	.	.	-0.60	0.08
	Leu	1162	A	A	.	B	.	.	.	-2.02	1.80	*	.	.	-0.60	0.10
20	Ala	1163	A	A	.	B	.	.	.	-2.24	1.11	.	.	.	-0.60	0.25
	Leu	1164	A	A	.	B	.	.	.	-1.78	1.11	.	*	.	-0.60	0.27
	Trp	1165	A	A	.	B	.	.	.	-1.67	0.90	.	.	.	-0.60	0.33
	Lys	1166	A	A	.	B	.	.	.	-1.51	1.00	.	.	.	-0.60	0.28
	Leu	1167	A	A	.	B	.	.	.	-0.59	1.29	.	.	.	-0.60	0.29
25	Gly	1168	A	.	.	B	.	.	.	-0.30	0.60	.	.	.	-0.60	0.55
	Phe	1169	.	.	B	B	.	.	.	-0.08	0.07	*	.	.	-0.30	0.37
	Phe	1170	.	.	B	B	.	.	.	0.32	0.57	*	.	.	-0.60	0.45
	Arg	1171	.	.	B	B	.	.	.	0.39	-0.11	*	.	.	0.30	0.89
	Ser	1172	.	.	.	B	.	.	C	1.31	-0.54	*	.	F	1.10	2.02
30	Ala	1173	.	.	.	.	.	.	C	1.77	-1.33	*	.	F	1.30	4.57
	Arg	1174	.	.	.	.	.	.	C	2.47	-2.11	*	.	F	1.30	4.57
	Arg	1175	.	.	.	.	T	.	.	2.96	-2.11	*	.	F	1.84	5.90
	Arg	1176	.	.	.	.	T	.	.	2.50	-2.07	*	.	F	2.18	9.03
	Arg	1177	.	.	.	.	T	.	.	1.99	-2.14	.	.	F	2.52	4.56
35	Glu	1178	.	.	.	.	.	T	C	2.58	-1.46	.	.	F	2.86	1.92
	Pro	1179	.	.	.	.	T	T	.	2.26	-1.46	.	.	F	3.40	1.64
	Gly	1180	.	.	.	.	T	T	.	1.83	-1.03	.	.	F	3.06	1.29
	Leu	1181	.	.	.	.	.	T	C	1.51	-0.54	.	*	F	2.69	1.08
	Asp	1182	.	.	.	.	.	T	C	1.44	-0.11	.	*	F	2.22	1.08
40	Pro	1183	.	.	.	.	.	T	C	0.59	-0.54	*	*	F	2.35	2.18
	Thr	1184	.	.	.	.	.	T	C	-0.01	-0.33	*	.	F	1.88	1.96

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5	Pro	1185	.	.	B	.	.	T	.	0.33	-0.33	*	.	F	1.70	0.97
	Lys	1186	.	A	B	.	.	.	.	0.76	-0.33	*	*	F	1.28	1.08
	Val	1187	.	A	B	.	.	.	.	0.37	-0.33	*	.	F	0.96	0.96
	Leu	1188	A	A	.	.	.	.	.	0.19	-0.39	*	.	.	0.64	0.79
	Glu	1189	A	A	.	.	.	.	.	0.11	-0.39	*	.	.	0.47	0.51
	Ter	1190	A	A	.	.	.	.	.	-0.07	0.04	*	.	.	-0.30	0.87

Table VIII

	Res	Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
5	Met	1	A	A	.	.	.	.	.	-1.47	0.70	.	.	.	-0.60	0.31
	Ala	2	A	A	.	.	.	.	.	-1.38	0.96	.	.	.	-0.60	0.20
	Leu	3	A	A	.	.	.	.	.	-1.80	0.91	.	.	.	-0.60	0.21
	Met	4	A	A	.	.	.	.	.	-2.27	1.17	.	.	.	-0.60	0.17
	Leu	5	A	A	.	.	.	.	.	-2.69	1.20	.	.	.	-0.60	0.13
10	Ser	6	A	A	.	.	.	.	.	-2.39	1.39	.	*	.	-0.60	0.13
	Leu	7	A	A	.	.	.	.	.	-2.61	1.09	.	.	.	-0.60	0.17
	Val	8	A	A	.	.	.	.	.	-2.61	1.16	*	.	.	-0.60	0.17
	Leu	9	A	A	.	.	.	.	.	-1.97	1.16	*	.	.	-0.60	0.11
	Ser	10	A	A	.	.	.	.	.	-1.97	0.77	*	.	.	-0.60	0.26
15	Leu	11	.	A	B	.	.	.	.	-2.01	0.77	*	.	.	-0.60	0.28
	Leu	12	.	A	B	.	.	.	.	-1.50	0.56	*	.	.	-0.60	0.34
	Lys	13	.	A	B	.	.	.	.	-0.99	0.26	*	.	F	-0.15	0.34
	Leu	14	.	A	.	.	.	.	C	-0.18	0.30	.	.	F	0.05	0.41
	Gly	15	.	.	.	.	T	T	.	-0.17	0.01	*	.	F	0.65	0.86
20	Ser	16	.	.	.	.	.	T	C	0.64	0.24	*	*	F	0.45	0.45
	Gly	17	.	.	.	.	.	T	C	0.60	0.64	*	.	F	0.15	0.95
	Gln	18	.	.	B	.	.	T	.	-0.14	0.60	*	.	F	-0.05	0.71
	Trp	19	.	.	B	B	.	.	.	0.32	0.96	.	.	.	-0.60	0.46
	Gln	20	.	.	B	B	.	.	.	0.46	1.00	.	*	.	-0.60	0.46
25	Val	21	.	.	B	B	.	.	.	0.76	1.00	.	*	.	-0.60	0.41
	Phe	22	.	.	B	B	.	.	.	1.14	0.60	.	*	.	-0.30	0.65
	Gly	23	.	.	.	.	.	T	C	0.93	-0.31	.	.	.	1.50	0.75
	Pro	24	.	.	.	.	T	T	.	0.37	-0.29	.	.	F	2.30	1.57
	Asp	25	.	.	.	.	.	T	C	0.37	-0.29	.	.	F	2.40	1.34
30	Lys	26	.	.	.	.	.	T	C	0.63	-0.67	*	.	F	3.00	2.35
	Pro	27	.	.	.	B	.	.	C	0.52	-0.60	*	.	F	2.30	1.54
	Val	28	.	.	B	B	.	.	.	0.01	-0.34	*	.	.	1.20	0.76
	Gln	29	.	.	B	B	.	.	.	-0.12	0.30	*	.	.	0.30	0.28
	Ala	30	.	.	B	B	.	.	.	-0.12	0.73	.	.	.	-0.30	0.18
35	Leu	31	.	.	B	B	.	.	.	-0.17	0.30	.	.	.	-0.30	0.42
	Val	32	.	.	B	B	.	.	.	-0.54	-0.34	.	.	.	0.30	0.41
	Gly	33	A	.	.	B	.	.	.	-0.28	-0.24	.	.	F	0.45	0.41
	Glu	34	A	A	.	.	.	.	.	-0.98	-0.24	.	.	F	0.45	0.50
	Asp	35	A	A	.	.	.	.	.	-0.69	-0.14	.	.	F	0.45	0.58
40	Ala	36	A	A	.	.	.	.	.	-0.54	-0.40	.	.	.	0.30	0.79

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	Ala	37	A	A	.	B	.	.	.	-0.39	-0.26	.	.	.	0.30	0.24
	Phe	38	A	A	.	B	.	.	.	-0.86	0.53	.	.	.	-0.60	0.13
	Ser	39	A	A	.	B	.	.	.	-1.16	1.21	.	.	.	-0.60	0.10
	Cys	40	A	A	.	B	.	.	.	-1.37	1.10	.	.	.	-0.60	0.14
5	Phe	41	A	A	.	B	.	.	.	-0.73	1.03	.	.	.	-0.60	0.24
	Leu	42	.	A	.	B	.	.	C	-0.46	0.24	.	.	.	-0.10	0.36
	Ser	43	.	.	.	.	.	T	C	0.24	0.34	.	*	F	0.45	0.98
	Pro	44	.	.	.	.	.	T	C	-0.04	0.17	.	*	F	0.60	1.82
	Lys	45	.	.	.	.	.	T	C	0.62	-0.11	.	*	F	1.20	2.23
10	Thr	46	A	.	.	.	.	T	.	0.73	-0.80	.	*	F	1.30	2.88
	Asn	47	A	A	.	.	.	.	.	0.94	-0.69	.	*	F	0.90	1.88
	Ala	48	A	A	.	.	.	.	.	1.24	-0.50	.	*	.	0.30	0.93
	Glu	49	A	A	.	.	.	.	.	0.60	-0.50	.	*	.	0.45	1.12
	Ala	50	A	A	.	.	.	.	.	0.67	-0.34	.	*	.	0.30	0.52
15	Met	51	A	A	.	.	.	.	.	0.28	-0.74	*	*	.	0.60	1.00
	Glu	52	A	A	.	.	.	.	.	-0.42	-0.46	*	.	.	0.30	0.50
	Val	53	A	A	.	.	.	.	.	0.28	0.33	*	.	.	-0.30	0.43
	Arg	54	A	A	.	.	.	.	.	-0.07	-0.17	*	.	.	0.30	0.85
	Phe	55	A	A	.	.	.	.	.	0.52	-0.36	*	*	.	0.30	0.48
20	Phe	56	A	.	.	.	.	T	.	0.42	0.04	*	*	.	0.25	1.13
	Arg	57	A	.	.	.	.	T	.	0.12	0.19	*	*	.	0.10	0.50
	Gly	58	.	.	.	.	T	T	.	0.68	0.57	*	.	F	0.35	0.77
	Gln	59	.	.	.	.	T	T	.	-0.29	0.17	*	*	F	0.80	1.20
	Phe	60	.	.	.	B	.	.	C	-0.44	0.03	*	*	F	0.05	0.45
25	Ser	61	.	.	.	B	.	.	C	0.22	0.67	*	*	F	-0.25	0.34
	Ser	62	.	.	B	B	.	.	.	-0.70	0.74	*	*	.	-0.60	0.27
	Val	63	.	.	B	B	.	.	.	-0.60	1.03	*	.	.	-0.60	0.25
	Val	64	.	.	B	B	.	.	.	-0.49	1.00	*	.	.	-0.60	0.30
	His	65	.	.	B	B	.	.	.	0.21	0.61	*	.	.	-0.26	0.43
30	Leu	66	.	.	B	B	.	.	.	0.17	0.23	*	.	.	0.38	0.98
	Tyr	67	.	.	B	.	.	T	.	0.51	0.01	*	.	.	1.27	1.30
	Arg	68	.	.	.	.	T	T	.	1.37	-0.63	*	.	F	3.06	1.92
	Asp	69	.	.	.	.	T	T	.	2.22	-1.13	*	.	F	3.40	3.88
	Gly	70	.	.	.	.	T	T	.	2.04	-1.41	*	.	F	3.06	4.29
35	Lys	71	.	.	.	.	T	.	.	2.16	-1.74	*	.	F	2.52	3.39
	Asp	72	.	.	.	.	.	.	C	1.80	-0.96	.	.	F	1.98	1.76
	Gln	73	.	.	.	.	.	.	C	1.69	-0.34	.	.	F	1.34	1.76
	Pro	74	.	.	B	.	.	.	.	1.09	-0.37	.	.	F	0.80	1.52
	Phe	75	.	.	B	.	.	.	.	1.22	0.24	.	.	.	-0.10	0.90
40	Met	76	.	.	B	.	.	.	.	1.18	0.67	.	.	.	-0.40	0.80
	Gln	77	.	.	B	.	.	.	.	0.93	0.67	.	.	.	-0.40	0.90

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	Met	78	.	.	B	.	.	.	0.93	1.00	*	.	.	-0.25	1.63
	Pro	79	.	.	B	.	.	.	0.80	0.61	*	*	.	0.09	2.85
	Gln	80	.	.	.	.	T	.	1.61	0.43	*	*	F	0.98	1.63
	Tyr	81	.	.	.	.	T	T	1.90	0.03	.	*	F	1.82	3.23
5	Gln	82	A	.	.	.	.	T	1.94	-0.10	.	*	F	2.36	3.01
	Gly	83	.	.	.	.	T	T	1.73	-0.53	.	*	F	3.40	3.48
	Arg	84	.	.	B	.	.	T	1.09	-0.24	.	*	F	2.36	1.83
	Thr	85	.	.	B	.	.	.	1.13	-0.36	.	*	F	1.90	0.78
	Lys	86	.	.	B	.	.	.	1.38	-0.76	.	*	F	2.24	1.59
10	Leu	87	.	.	B	.	.	.	1.08	-1.19	*	*	F	2.13	1.35
	Val	88	.	.	B	.	.	T	0.53	-0.80	.	*	F	2.22	1.26
	Lys	89	.	.	B	.	.	T	-0.17	-0.60	.	.	F	2.30	0.44
	Asp	90	.	.	B	.	.	T	0.14	-0.10	*	.	F	1.77	0.54
	Ser	91	.	.	B	.	.	T	-0.24	-0.79	*	.	.	1.84	1.26
15	Ile	92	A	A	.	.	.	.	0.68	-1.00	*	*	.	1.06	0.62
	Ala	93	A	A	.	.	.	.	0.64	-1.00	.	*	F	0.98	0.73
	Glu	94	A	A	.	.	.	.	0.30	-0.31	.	*	F	0.45	0.38
	Gly	95	A	A	.	.	.	.	-0.51	-0.31	*	*	F	0.45	0.73
	Arg	96	A	A	.	.	.	.	-0.10	-0.31	*	*	F	0.45	0.60
20	Ile	97	A	A	.	.	.	.	-0.02	-0.81	.	*	F	0.75	0.67
	Ser	98	A	A	.	.	.	.	0.57	-0.13	*	*	.	0.30	0.56
	Leu	99	A	A	.	.	.	.	0.57	-0.56	*	*	.	0.60	0.50
	Arg	100	A	A	.	.	.	.	0.02	-0.16	*	*	.	0.45	1.14
	Leu	101	A	A	.	.	.	.	-0.40	-0.16	*	*	.	0.30	0.60
25	Glu	102	.	A	B	.	.	.	-0.37	-0.06	.	*	.	0.45	1.04
	Asn	103	.	A	B	.	.	.	-0.88	-0.10	.	*	.	0.30	0.40
	Ile	104	.	A	B	.	.	.	-0.07	0.59	.	*	.	-0.60	0.40
	Thr	105	.	A	B	.	.	.	-0.77	-0.10	.	.	.	0.30	0.38
	Val	106	.	A	B	.	.	.	-0.30	0.40	.	.	.	-0.60	0.24
30	Leu	107	.	A	B	.	.	.	-1.11	0.43	.	.	.	-0.60	0.34
	Asp	108	.	A	B	.	.	.	-1.36	0.43	.	.	.	-0.60	0.19
	Ala	109	.	A	B	.	.	.	-0.81	0.70	.	.	.	-0.60	0.41
	Gly	110	.	.	.	.	T	.	-1.17	0.49	*	.	.	0.00	0.49
	Leu	111	.	.	B	.	.	T	-0.20	0.37	*	.	.	0.10	0.16
35	Tyr	112	.	.	B	.	.	T	-0.28	0.37	*	*	.	0.10	0.30
	Gly	113	.	.	B	.	.	T	-0.58	0.56	*	*	.	-0.20	0.22
	Cys	114	.	.	B	.	.	T	-0.29	0.51	*	*	.	-0.20	0.35
	Arg	115	.	.	B	B	.	.	0.06	0.21	*	*	.	-0.30	0.30
	Ile	116	.	.	B	B	.	.	0.57	-0.14	*	*	F	0.45	0.52
40	Ser	117	.	.	B	B	.	.	0.57	-0.19	*	*	F	0.76	1.31
	Ser	118	.	.	B	.	.	T	0.67	0.00	*	*	F	1.32	1.05

	Gln	119	.	.	B	.	.	T	.	1.33	0.76	.	*	F	0.58 2.35
	Ser	120	.	.	.	.	.	T	T	1.27	0.47	.	*	F	1.14 3.03
	Tyr	121	.	.	.	.	.	T	T	1.57	0.09	.	.	F	1.60 4.52
	Tyr	122	.	A	.	.	.	T	.	0.98	0.20	.	.	.	0.89 2.64
5	Gln	123	.	A	B	.	.	.	.	0.99	0.49	.	.	.	0.03 1.38
	Lys	124	.	A	B	.	.	.	.	0.99	1.01	*	.	.	-0.28 0.93
	Ala	125	.	A	B	.	.	.	.	0.48	0.26	*	.	.	0.01 1.02
	Ile	126	.	A	B	.	.	.	.	0.72	0.19	.	*	.	-0.30 0.49
	Trp	127	.	A	B	.	.	.	.	0.11	0.19	.	*	.	-0.30 0.42
10	Glu	128	A	A	.	.	.	.	.	-0.19	0.83	*	*	.	-0.60 0.31
	Leu	129	A	A	.	.	.	.	.	-0.82	0.71	*	*	.	-0.60 0.59
	Gln	130	.	A	B	.	.	.	.	-1.04	0.53	.	*	.	-0.60 0.57
	Val	131	.	A	B	.	.	.	.	-0.50	0.30	.	*	.	-0.30 0.27
	Ser	132	.	A	.	.	.	.	C	-0.51	0.73	.	*	.	-0.40 0.33
15	Ala	133	.	A	.	.	.	.	C	-1.37	0.43	.	*	.	-0.40 0.25
	Leu	134	.	A	B	.	.	.	.	-0.77	0.67	.	*	.	-0.60 0.25
	Gly	135	.	A	.	.	.	T	.	-1.58	0.46	.	.	.	-0.20 0.29
	Ser	136	.	.	B	B	.	.	.	-1.61	0.76	.	.	.	-0.60 0.24
	Val	137	.	.	B	B	.	.	.	-1.61	0.94	.	.	.	-0.60 0.20
20	Pro	138	.	.	B	B	.	.	.	-1.91	0.64	.	.	.	-0.60 0.27
	Leu	139	.	.	B	B	.	.	.	-1.69	0.90	.	.	.	-0.60 0.14
	Ile	140	.	.	B	B	.	.	.	-1.69	1.01	.	.	.	-0.60 0.19
	Ser	141	.	.	B	B	.	.	.	-1.63	0.80	.	.	.	-0.60 0.12
	Ile	142	.	.	B	B	.	.	.	-1.63	1.13	.	.	.	-0.60 0.24
25	Ala	143	.	.	B	B	.	.	.	-1.42	1.09	*	.	.	-0.60 0.25
	Gly	144	.	.	B	B	.	.	.	-0.50	0.40	*	.	.	-0.34 0.31
	Tyr	145	.	.	B	B	.	.	.	0.39	0.01	*	*	.	0.22 0.87
	Val	146	.	.	B	B	.	.	.	-0.20	-0.67	*	.	.	1.53 1.44
	Asp	147	.	.	B	.	.	T	.	0.69	-0.49	*	*	F	2.04 1.02
30	Arg	148	.	.	B	.	.	T	.	0.47	-0.51	*	.	F	2.60 1.13
	Asp	149	.	.	B	.	.	T	.	0.00	-0.59	*	.	F	2.34 1.25
	Ile	150	.	.	B	.	.	T	.	-0.42	-0.54	*	.	.	1.78 0.62
	Gln	151	.	A	B	.	.	.	.	0.43	0.03	*	.	.	0.22 0.17
	Leu	152	.	A	B	.	.	.	.	0.13	0.43	*	.	.	-0.34 0.18
35	Leu	153	.	A	B	.	.	.	.	-0.28	0.81	*	.	.	-0.60 0.34
	Cys	154	.	A	B	.	.	.	.	-0.62	0.51	.	*	.	-0.60 0.26
	Gln	155	.	A	.	.	.	T	.	-0.02	0.54	*	*	F	-0.05 0.31
	Ser	156	.	.	.	.	.	T	T	-0.72	0.77	*	.	F	0.35 0.40
	Ser	157	.	.	.	.	.	T	T	-0.12	0.87	*	.	F	0.35 0.64
40	Gly	158	.	.	.	.	.	T	T	0.80	0.73	*	.	F	0.35 0.57
	Trp	159	.	.	.	.	.	T	T	1.26	0.33	*	.	F	0.65 0.84



307

	Phe	160	.	.	.	.	.	T	C	0.94	0.37	*	.	F	0.45	0.97
	Pro	161	.	.	.	.	.	T	C	0.66	0.47	*	*	F	0.30	1.41
	Arg	162	.	.	.	.	.	T	C	1.00	0.54	*	*	F	0.30	1.36
	Pro	163	.	.	.	.	T	T	.	1.06	-0.37	*	*	F	1.40	3.13
5	Thr	164	.	.	.	.	T	.	.	1.39	-0.24	*	*	F	1.20	2.13
	Ala	165	.	.	.	.	T	.	.	1.74	-0.67	*	*	F	1.50	2.17
	Lys	166	.	.	.	.	T	.	.	1.74	-0.24	.	*	F	1.20	1.39
	Trp	167	.	.	.	.	T	.	.	1.63	-0.24	.	*	F	1.54	1.49
	Lys	168	.	.	.	.	.	.	C	1.50	-0.33	.	*	F	1.68	2.55
10	Gly	169	.	.	.	.	.	.	C	1.81	-0.40	.	*	F	2.02	1.26
	Pro	170	.	.	.	.	.	T	C	2.40	0.00	.	*	F	1.96	2.08
	Gln	171	.	.	.	.	T	T	.	1.54	-0.91	.	*	F	3.40	1.74
	Gly	172	.	.	.	.	.	T	C	1.53	-0.23	.	.	F	2.56	1.45
	Gln	173	.	.	B	.	.	T	.	1.18	-0.27	.	.	F	2.02	1.26
15	Asp	174	.	.	B	.	.	.	.	1.52	-0.21	.	.	F	1.82	1.05
	Leu	175	.	.	B	.	.	.	.	1.43	-0.61	*	*	F	2.12	1.77
	Ser	176	.	.	B	.	.	T	.	1.54	-0.66	*	*	F	2.32	1.37
	Thr	177	.	.	B	.	.	T	.	1.58	-1.06	*	*	F	2.66	1.60
	Asp	178	.	.	.	.	T	T	.	1.58	-0.57	*	*	F	3.40	2.80
20	Ser	179	.	.	.	.	.	T	C	1.69	-0.86	*	*	F	2.86	3.37
	Arg	180	.	.	.	.	T	T	.	2.50	-1.24	*	*	F	3.06	4.57
	Thr	181	.	.	.	.	T	T	.	2.20	-1.73	*	.	F	3.06	4.57
	Asn	182	.	.	.	.	T	T	.	2.48	-1.11	*	.	F	3.06	3.37
	Arg	183	.	.	B	.	.	T	.	2.13	-1.00	*	.	F	2.66	2.34
25	Asp	184	.	.	.	.	T	T	.	1.62	-0.57	*	.	F	3.40	1.61
	Met	185	.	.	B	.	.	T	.	0.81	-0.37	*	.	.	2.06	0.82
	His	186	.	.	B	.	.	T	.	1.12	0.01	*	.	.	1.12	0.36
	Gly	187	.	.	B	.	.	T	.	0.27	0.01	*	*	.	0.78	0.36
	Leu	188	.	.	B	B	.	.	.	0.16	0.66	*	*	.	-0.26	0.27
30	Phe	189	A	.	.	B	.	.	.	-0.73	0.04	.	*	.	-0.30	0.35
	Asp	190	A	.	.	B	.	.	.	-0.43	0.23	.	*	.	-0.30	0.25
	Val	191	A	.	.	B	.	.	.	-1.21	0.19	.	*	.	-0.30	0.40
	Glu	192	A	.	.	B	.	.	.	-1.18	0.19	.	*	.	-0.30	0.38
	Ile	193	A	.	.	B	.	.	.	-1.22	-0.11	.	*	.	0.30	0.33
35	Ser	194	A	.	.	B	.	.	.	-0.52	0.53	.	*	.	-0.60	0.33
	Leu	195	A	A	.	B	.	.	.	-0.52	0.29	.	*	.	-0.30	0.33
	Thr	196	A	A	.	B	.	.	.	0.33	0.29	.	*	.	-0.30	0.81
	Val	197	A	A	.	B	.	.	.	-0.26	0.00	.	*	.	0.55	0.98
	Gln	198	A	A	.	B	.	.	.	0.29	0.11	.	*	F	0.50	1.20
40	Glu	199	A	A	.	B	.	.	.	0.29	-0.14	.	.	F	1.20	0.82
	Asn	200	.	.	.	.	T	T	.	0.21	-0.24	.	.	F	2.40	1.48

	Ala	201	.	.	.	.	T	T	.	0.22	-0.20	.	.	F	2.50	0.60
	Gly	202	.	.	.	.	T	T	.	0.41	-0.21	.	.	F	2.25	0.46
	Ser	203	.	.	.	.	T	T	.	0.11	0.36	.	.	F	1.40	0.15
	Ile	204	A	.	.	.	.	.	.	-0.49	0.34	*	*	.	0.40	0.21
5	Ser	205	A	.	.	.	.	.	.	-0.38	0.46	*	*	.	-0.15	0.21
	Cys	206	.	.	B	.	.	.	.	0.18	0.03	*	*	.	-0.10	0.30
	Ser	207	.	A	B	.	.	.	.	-0.07	0.14	*	*	.	-0.30	0.58
	Met	208	A	A	.	.	.	.	.	0.20	-0.04	*	*	.	0.30	0.44
	Arg	209	A	A	.	.	.	.	.	0.28	0.07	*	*	.	-0.15	1.11
10	His	210	A	A	.	.	.	.	.	0.28	0.19	.	.	.	-0.30	0.69
	Ala	211	A	A	.	.	.	.	.	1.06	0.19	.	.	.	-0.30	0.93
	His	212	A	A	.	.	.	.	.	1.36	-0.43	*	.	.	0.30	0.93
	Leu	213	A	A	.	.	.	.	.	1.10	-0.43	*	.	.	0.45	1.18
	Ser	214	A	A	.	.	.	.	.	0.99	-0.29	*	.	.	0.30	0.87
15	Arg	215	A	A	.	.	.	.	.	0.72	-0.79	*	*	F	0.90	1.10
	Glu	216	A	A	.	.	.	.	.	1.42	-0.90	*	*	F	0.90	1.79
	Val	217	A	.	.	B	.	.	.	0.60	-1.59	*	*	F	0.90	2.62
	Glu	218	A	.	.	B	.	.	.	1.41	-1.33	*	*	F	0.75	0.99
	Ser	219	A	.	.	B	.	.	.	0.82	-0.93	*	*	F	0.75	0.99
20	Arg	220	.	.	B	B	.	.	.	0.37	-0.24	*	*	F	0.45	0.94
	Val	221	.	.	B	B	.	.	.	0.37	-0.46	.	*	F	0.45	0.54
	Gln	222	A	.	.	B	.	.	.	0.93	-0.46	.	*	.	0.64	0.67
	Ile	223	A	.	.	.	.	T	.	1.04	0.07	*	*	.	0.78	0.36
	Gly	224	A	.	.	.	.	T	.	1.46	0.07	*	*	F	1.27	0.95
25	Asp	225	.	.	.	.	T	T	.	1.39	-0.57	.	*	F	3.06	1.07
	Trp	226	.	.	.	.	T	T	.	2.21	-0.97	.	.	F	3.40	3.06
	Arg	227	.	.	B	.	.	.	.	1.87	-1.16	*	.	F	2.46	4.20
	Arg	228	.	.	.	.	T	T	.	2.76	-1.16	*	.	F	2.72	2.49
	Lys	229	.	.	.	.	T	T	.	2.51	-0.76	*	.	F	2.38	4.10
30	His	230	.	.	.	.	T	T	.	2.17	-1.17	*	.	F	2.38	2.12
	Gly	231	.	.	.	.	.	T	C	2.50	-0.74	*	.	F	2.18	1.07
	Gln	232	.	.	.	.	T	.	.	2.50	-0.74	*	.	F	2.52	1.07
	Ala	233	.	.	.	.	.	.	C	2.43	-0.74	*	.	F	2.66	1.54
	Gly	234	.	.	.	.	T	T	.	2.14	-1.24	*	.	F	3.40	3.11
35	Lys	235	.	.	B	.	.	T	.	1.88	-0.91	*	.	F	2.66	2.81
	Arg	236	.	.	.	.	T	T	.	1.92	-0.93	*	.	F	2.77	3.73
	Lys	237	.	.	.	.	T	T	.	1.62	-1.04	*	.	F	2.48	5.05
	Tyr	238	.	.	B	.	.	T	.	2.18	-1.09	.	.	F	1.79	3.39
	Ser	239	.	.	B	.	.	T	.	1.63	-0.59	.	.	F	1.50	2.35
40	Ser	240	.	.	B	.	.	T	.	1.34	0.10	.	.	F	0.50	0.82
	Ser	241	.	.	B	.	.	T	.	1.23	0.86	.	.	F	0.15	0.82

	His	242	.	.	B	.	.	.	0.89	0.10	*	.	0.20	1.03
	Ile	243	.	.	B	.	.	.	0.43	0.10	*	.	0.15	1.03
	Tyr	244	.	.	B	.	.	.	0.52	0.50	*	.	-0.35	0.66
	Asp	245	.	.	B	.	.	.	0.52	0.54	*	.	-0.40	0.75
5	Ser	246	.	.	B	.	.	.	0.01	0.43	*	.	F	-0.10 1.44
	Phe	247	.	.	B	.	.	T	-0.26	0.43	*	.	F	-0.05 0.76
	Pro	248	.	.	.	.	.	T	-0.07	0.06	*	.	F	0.45 0.61
	Ser	249	.	.	.	.	.	T	-0.42	0.84	.	.	F	0.15 0.39
	Leu	250	.	.	.	.	.	T	-0.42	1.07	.	.	.	0.00 0.45
10	Ser	251	.	.	B	.	.	.	-0.82	0.29	.	.	.	-0.10 0.49
	Phe	252	.	.	B	B	.	.	-0.37	0.64	.	.	.	-0.60 0.31
	Met	253	.	.	B	B	.	.	-1.04	1.01	.	.	.	-0.60 0.60
	Asp	254	.	.	B	B	.	.	-1.56	1.01	.	.	.	-0.60 0.31
	Phe	255	.	.	B	B	.	.	-0.63	1.31	.	.	.	-0.60 0.30
15	Tyr	256	.	.	B	B	.	.	-0.54	0.53	.	.	.	-0.60 0.59
	Ile	257	.	.	B	B	.	.	-0.70	0.34	.	.	.	-0.30 0.54
	Leu	258	.	.	B	B	.	.	-0.44	0.99	*	.	.	-0.60 0.47
	Arg	259	.	.	B	B	.	.	-0.66	0.63	*	.	.	-0.35 0.29
	Pro	260	.	.	.	B	T	.	-0.62	0.30	.	*	F	0.75 0.65
20	Val	261	.	.	.	B	T	.	-0.27	0.19	*	*	F	1.00 0.42
	Gly	262	.	.	.	.	.	T	0.03	-0.50	*	*	F	2.35 0.42
	Pro	263	.	.	.	.	T	T	0.89	0.00	*	*	F	2.50 0.28
	Cys	264	.	.	B	.	.	T	-0.03	-0.43	*	*	F	1.85 0.74
	Arg	265	.	.	B	.	.	T	-0.68	-0.39	.	*	.	1.45 0.62
25	Ala	266	.	A	B	.	.	.	-0.42	-0.17	.	*	.	0.80 0.30
	Lys	267	.	A	B	.	.	.	-0.42	0.01	.	*	.	-0.05 0.55
	Leu	268	.	A	B	.	.	.	-0.52	-0.13	.	*	.	0.30 0.28
	Val	269	.	A	B	.	.	.	-0.67	0.36	.	*	.	-0.30 0.40
	Met	270	A	A	.	.	.	.	-0.73	0.54	.	*	.	-0.60 0.16
30	Gly	271	A	A	.	.	.	.	-0.96	0.54	*	*	.	-0.60 0.40
	Thr	272	A	A	.	.	.	.	-1.00	0.54	.	*	.	-0.60 0.44
	Leu	273	A	A	.	.	.	.	-1.08	0.30	.	*	.	-0.30 0.77
	Lys	274	A	A	.	.	.	.	-1.03	0.37	.	*	.	-0.30 0.55
	Leu	275	A	A	.	.	.	.	-0.78	0.63	.	*	.	-0.60 0.31
35	Gln	276	A	A	.	.	.	.	-0.43	0.57	.	*	.	-0.60 0.37
	Ile	277	.	A	B	.	.	.	-0.98	-0.11	.	*	.	0.30 0.32
	Leu	278	A	A	.	.	.	.	-0.20	0.53	.	*	.	-0.60 0.29
	Gly	279	A	A	.	.	.	.	-0.94	0.34	.	*	.	-0.30 0.23
	Glu	280	A	A	.	.	.	.	-0.99	0.73	.	*	.	-0.60 0.28
40	Val	281	A	A	.	.	.	.	-0.99	0.69	*	*	.	-0.60 0.26
	His	282	A	A	.	.	.	.	-0.06	0.00	*	*	.	0.30 0.45

	Phe	283	A	A	.	.	.	.	.	0.54	-0.43	.	.	.	0.30	0.52
	Val	284	A	A	.	.	.	.	.	0.86	0.00	.	*	.	0.45	1.07
	Glu	285	A	A	.	.	.	.	.	0.56	-0.14	.	.	F	0.60	1.07
	Lys	286	A	.	.	.	.	T	.	0.60	-0.26	*	.	F	1.00	1.66
5	Pro	287	A	.	.	.	.	T	.	-0.18	-0.36	*	.	F	1.00	1.85
	His	288	A	.	.	.	.	T	.	0.52	-0.31	*	.	F	0.85	0.88
	Ser	289	A	.	.	.	.	T	.	0.49	0.09	*	.	.	0.10	0.76
	Leu	290	A	.	.	B	.	.	.	0.19	0.77	.	*	.	-0.60	0.35
	Leu	291	.	.	B	B	.	.	.	-0.20	0.73	.	*	.	-0.60	0.34
10	Gln	292	.	.	B	B	.	.	.	-0.33	0.66	.	.	.	-0.60	0.25
	Ile	293	.	.	B	B	.	.	.	-0.60	0.70	.	.	F	-0.45	0.30
	Ser	294	.	.	B	.	.	T	.	-0.61	0.40	.	.	F	0.25	0.49
	Gly	295	.	.	.	.	T	T	.	-0.11	0.20	.	.	F	0.65	0.41
	Gly	296	.	.	.	.	T	T	.	-0.11	0.29	.	*	F	0.65	0.84
15	Ser	297	.	.	.	.	.	T	C	-0.07	0.29	*	.	F	0.45	0.52
	Thr	298	.	.	B	B	.	.	.	0.87	-0.10	*	.	F	0.90	1.04
	Thr	299	.	.	B	B	.	.	.	0.82	-0.53	*	.	F	1.50	2.11
	Leu	300	.	.	B	B	.	.	.	0.96	-0.53	*	.	F	1.80	1.56
	Lys	301	.	.	.	B	T	.	.	1.30	-0.49	*	.	F	2.20	1.67
20	Lys	302	.	.	.	.	T	.	.	1.39	-0.57	*	.	F	3.00	1.86
	Gly	303	.	.	.	.	.	T	C	1.41	-0.63	*	.	F	2.70	3.49
	Pro	304	.	.	.	.	.	T	C	1.42	-0.40	*	.	F	2.10	1.83
	Asn	305	.	.	.	.	.	T	C	1.53	-0.01	*	.	F	1.80	1.23
	Pro	306	.	.	.	.	T	T	.	1.28	0.77	*	.	F	0.80	1.08
25	Trp	307	.	.	.	.	T	.	.	0.93	0.77	.	.	.	0.15	1.08
	Ser	308	.	.	.	.	.	.	C	1.07	0.73	.	.	.	-0.20	0.90
	Phe	309	.	.	B	.	.	.	.	0.61	0.76	.	.	F	-0.25	0.90
	Pro	310	.	.	B	.	.	.	.	0.02	0.90	.	.	F	-0.25	0.46
	Ser	311	.	.	.	.	.	T	C	-0.58	0.49	.	.	F	0.15	0.34
30	Pro	312	.	.	.	.	T	T	.	-0.99	0.79	.	.	F	0.35	0.33
	Cys	313	.	.	.	.	T	T	.	-0.90	0.79	.	.	.	0.20	0.18
	Ala	314	.	.	B	.	T	T	.	-0.51	0.79	.	.	.	0.20	0.21
	Leu	315	.	.	B	.	.	.	.	-0.69	0.89	.	.	.	-0.40	0.20
	Phe	316	.	.	B	.	.	.	.	-0.78	0.89	.	.	.	-0.40	0.47
35	Pro	317	.	.	B	.	.	.	.	-0.96	0.74	.	.	.	-0.40	0.60
	Thr	318	.	.	B	.	.	.	.	-0.68	0.67	.	.	.	-0.40	0.93
	Ter	319	.	.	B	.	.	.	.	-0.48	0.41	.	.	.	-0.25	1.37

Table IX

	Res Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
5	Met 1	.	.	B	.	.	.	.	-0.69	0.51	.	.	.	-0.40	0.26
	Ala 2	.	.	B	.	.	.	.	-0.64	0.51	.	.	.	-0.40	0.31
	Gly 3	.	.	B	.	.	.	.	-1.07	0.51	.	.	.	-0.40	0.24
	Ile 4	.	.	B	.	.	.	.	-1.49	0.77	.	.	.	-0.40	0.20
	Pro 5	.	.	B	.	.	.	.	-1.80	0.84	.	.	F	-0.25	0.17
10	Gly 6	.	.	B	B	.	.	.	-2.01	1.13	.	.	.	-0.60	0.14
	Leu 7	.	.	B	B	.	.	.	-2.23	1.39	.	.	.	-0.60	0.17
	Leu 8	.	.	B	B	.	.	.	-2.59	1.39	.	.	.	-0.60	0.09
	Phe 9	.	.	B	B	.	.	.	-2.40	1.74	.	.	.	-0.60	0.08
	Leu 10	.	.	B	B	.	.	.	-3.00	2.10	.	.	.	-0.60	0.08
15	Leu 11	.	.	B	B	.	.	.	-3.47	2.10	.	.	.	-0.60	0.08
	Phe 12	.	.	B	B	.	.	.	-3.32	2.10	.	.	.	-0.60	0.08
	Phe 13	.	.	B	B	.	.	.	-3.10	1.89	.	.	.	-0.60	0.05
	Leu 14	.	.	B	B	.	.	.	-3.26	1.70	.	.	.	-0.60	0.06
	Leu 15	.	.	B	B	.	.	.	-2.79	1.66	.	.	.	-0.60	0.05
20	Cys 16	.	.	B	B	.	.	.	-1.98	1.30	*	.	.	-0.60	0.06
	Ala 17	.	.	B	B	T	.	.	-2.13	0.91	.	.	.	-0.20	0.13
	Val 18	.	.	B	B	.	.	.	-1.73	0.87	.	.	.	-0.60	0.12
	Gly 19	.	.	B	B	.	.	.	-1.13	0.57	*	.	.	-0.60	0.29
	Gln 20	.	.	B	B	.	.	.	-0.57	0.43	.	.	F	-0.45	0.45
25	Val 21	.	.	B	B	.	.	.	-0.20	0.69	.	.	F	-0.45	0.95
	Ser 22	.	.	B	.	.	T	.	-0.20	0.43	.	.	F	0.10	1.28
	Pro 23	.	.	B	.	.	T	.	0.44	0.50	.	.	F	-0.05	0.75
	Tyr 24	.	.	.	.	T	T	.	0.50	0.53	.	*	.	0.35	1.56
	Ser 25	.	.	.	.	.	T	C	0.54	0.80	.	*	.	0.15	1.22
30	Ala 26	.	.	.	.	.	.	C	1.19	0.41	.	.	.	-0.05	1.58
	Pro 27	.	.	.	.	T	.	.	1.18	0.41	.	*	.	0.15	1.56
	Trp 28	.	.	.	.	T	.	.	1.10	0.14	.	*	.	0.45	1.68
	Lys 29	.	.	.	.	.	T	C	1.13	0.67	.	*	F	0.30	1.75
	Pro 30	.	.	.	.	T	T	.	0.84	0.60	.	*	F	0.50	1.75
35	Thr 31	.	.	.	.	T	T	.	1.19	0.67	*	*	F	0.50	1.68
	Trp 32	.	.	B	.	.	T	.	1.51	0.51	*	*	.	-0.05	1.32
	Pro 33	.	.	B	.	.	T	.	0.99	0.51	*	*	.	-0.05	1.67
	Ala 34	.	.	.	.	T	T	.	0.73	0.77	*	*	.	0.20	0.95
	Tyr 35	.	.	.	.	T	T	.	0.09	0.71	.	.	.	0.35	1.40
40	Arg 36	.	.	B	.	.	T	.	-0.46	0.44	.	*	.	-0.20	0.67

	Leu	37	.	.	B	B	.	.	.	-0.98	0.66	.	*	.	-0.60	0.49
	Pro	38	.	.	B	B	.	.	.	-0.98	0.84	*	*	.	-0.60	0.26
	Val	39	.	.	B	B	.	.	.	-0.39	0.51	*	*	.	-0.60	0.21
	Val	40	.	.	B	B	.	.	.	-0.44	0.91	*	*	.	-0.60	0.43
5	Leu	41	.	.	B	B	.	.	.	-0.87	0.61	*	*	F	-0.45	0.37
	Pro	42	.	.	B	.	.	T	.	-0.87	0.67	.	.	F	-0.05	0.73
	Gln	43	.	.	B	.	.	T	.	-0.66	0.71	.	*	F	-0.05	0.81
	Ser	44	.	.	B	.	.	T	.	-0.61	0.47	.	.	F	0.10	1.57
	Thr	45	.	.	B	.	.	T	.	-0.34	0.47	*	.	F	-0.05	0.84
10	Leu	46	.	.	B	.	.	.	.	0.51	0.54	*	.	F	-0.25	0.49
	Asn	47	.	.	B	.	.	.	.	0.51	0.14	.	.	.	0.14	0.73
	Leu	48	.	.	B	.	.	.	.	0.51	0.19	*	*	.	0.38	0.78
	Ala	49	.	.	B	.	.	.	.	0.11	-0.30	.	.	.	1.37	1.59
	Lys	50	.	.	.	.	.	T	C	0.08	-0.20	.	.	F	2.01	0.85
15	Pro	51	.	.	.	.	.	T	C	0.30	-0.17	.	*	F	2.40	1.02
	Asp	52	.	.	.	.	.	T	C	0.30	-0.36	.	*	F	2.16	1.02
	Phe	53	.	.	B	.	.	T	.	0.52	-0.86	.	*	.	1.72	0.89
	Gly	54	A	A	.	.	.	.	.	1.16	-0.36	.	*	.	0.78	0.58
	Ala	55	A	A	.	.	.	.	.	0.30	-0.79	.	*	.	0.84	0.69
20	Glu	56	A	A	.	.	.	.	.	0.51	-0.10	.	*	.	0.30	0.66
	Ala	57	A	A	.	.	.	.	.	-0.34	-0.89	.	*	F	0.90	1.16
	Lys	58	A	A	.	.	.	.	.	0.06	-0.67	.	*	F	0.75	0.85
	Leu	59	.	A	B	.	.	.	.	0.10	-0.79	.	*	.	0.60	0.66
	Glu	60	.	A	B	.	.	.	.	0.39	-0.40	.	*	.	0.30	0.87
25	Val	61	.	A	B	.	.	.	.	-0.28	-0.51	.	*	F	1.00	0.58
	Ser	62	.	A	.	.	.	T	.	-0.03	0.06	.	*	F	0.75	0.38
	Ser	63	.	.	.	.	.	T	T	-0.29	-0.20	.	*	F	2.00	0.22
	Ser	64	.	.	.	.	.	T	T	0.52	0.23	.	*	F	1.65	0.45
	Cys	65	.	.	.	.	.	T	T	-0.14	-0.01	.	.	F	2.50	0.58
30	Gly	66	.	.	.	.	.	T	C	0.68	0.17	.	.	F	1.45	0.23
	Pro	67	.	.	.	.	.	T	.	1.02	0.29	.	.	F	1.45	0.24
	Gln	68	.	.	.	.	.	T	.	0.98	-0.10	.	.	.	1.90	0.89
	Cys	69	.	.	B	.	.	.	.	0.97	-0.24	.	.	.	1.50	0.89
	His	70	.	.	.	.	.	T	T	1.42	-0.19	.	.	F	2.25	0.83
35	Lys	71	.	.	.	.	.	T	T	0.96	-0.19	.	.	F	2.50	0.74
	Gly	72	.	.	.	.	.	T	T	0.96	0.10	.	.	F	1.80	1.14
	Thr	73	.	.	.	.	.	T	C	0.64	-0.04	.	.	F	1.95	1.29
	Pro	74	.	.	.	.	.	.	C	1.07	-0.06	.	.	F	1.35	0.93
	Leu	75	.	.	.	.	.	.	C	1.10	0.70	.	.	F	0.61	1.48
40	Pro	76	.	.	.	.	.	T	C	1.06	0.27	.	.	F	1.12	1.77
	Thr	77	.	.	B	.	.	T	.	0.81	-0.21	.	.	F	1.78	1.98

	Tyr	78	.	.	B	.	.	T	.	1.17	-0.14	.	.	F	2.04	2.43
	Glu	79	.	.	B	.	.	T	.	1.38	-0.83	.	.	F	2.60	3.14
	Glu	80	.	A	B	.	.	.	.	1.94	-0.86	*	.	F	1.94	3.77
	Ala	81	A	A	.	.	.	.	.	1.34	-0.59	*	.	F	1.68	3.77
5	Lys	82	.	A	B	.	.	.	.	1.36	-0.66	*	.	F	1.42	1.79
	Gln	83	.	A	B	.	.	.	.	1.36	-0.27	*	.	F	0.86	1.39
	Tyr	84	.	A	B	.	.	.	.	1.36	0.49	.	.	.	-0.45	2.15
	Leu	85	.	.	B	B	.	.	.	1.04	-0.01	.	*	.	0.45	1.87
	Ser	86	.	.	B	B	.	.	.	0.82	0.47	.	.	.	-0.45	1.55
10	Tyr	87	.	A	B	B	.	.	.	0.53	0.76	.	.	.	-0.60	0.82
	Glu	88	.	A	B	B	.	.	.	-0.06	0.76	.	.	.	-0.45	1.55
	Thr	89	.	A	B	B	.	.	.	0.19	0.57	.	.	.	-0.45	1.17
	Leu	90	.	A	B	B	.	.	.	0.66	0.59	.	.	.	-0.45	1.20
	Tyr	91	.	.	B	.	.	T	.	0.66	0.26	*	.	.	0.36	0.69
15	Ala	92	.	.	.	.	.	T	C	1.01	0.64	*	.	.	0.52	0.64
	Asn	93	.	.	.	.	.	T	C	0.70	0.16	*	.	F	1.38	1.52
	Gly	94	.	.	.	.	.	T	C	1.01	-0.04	*	.	F	2.24	1.40
	Ser	95	.	.	.	.	.	.	C	1.51	-0.80	*	.	F	2.60	2.39
	Arg	96	.	.	.	B	.	.	C	1.76	-0.81	*	*	F	2.14	2.15
20	Thr	97	.	.	B	B	.	.	.	1.49	-0.81	*	*	F	1.68	3.76
	Glu	98	.	.	B	B	.	.	.	1.14	-0.60	*	*	F	1.42	2.08
	Thr	99	.	.	B	B	.	.	.	0.60	-0.56	.	*	F	1.16	1.05
	Gln	100	.	.	B	B	.	.	.	0.66	0.13	*	*	F	-0.15	0.51
	Val	101	.	.	B	B	.	.	.	-0.34	0.40	*	*	.	-0.60	0.46
25	Gly	102	.	.	B	B	.	.	.	-0.84	1.09	.	*	.	-0.60	0.22
	Ile	103	.	.	B	B	.	.	.	-1.14	1.29	.	*	.	-0.60	0.11
	Tyr	104	.	.	B	B	.	.	.	-1.13	1.27	.	.	.	-0.60	0.19
	Ile	105	.	.	B	B	.	.	.	-1.43	1.01	.	.	.	-0.60	0.26
	Leu	106	.	.	B	B	.	.	.	-0.92	0.97	.	.	.	-0.35	0.50
30	Ser	107	.	.	B	.	.	T	.	-0.58	0.71	.	.	F	0.45	0.32
	Ser	108	.	.	.	.	.	T	C	-0.03	-0.04	*	.	F	1.80	0.75
	Ser	109	.	.	.	.	.	T	C	-0.38	-0.30	*	.	F	2.05	0.90
	Gly	110	.	.	.	.	T	T	.	0.51	-0.49	*	.	F	2.50	0.68
	Asp	111	.	A	.	.	T	.	.	1.29	-0.47	.	*	F	1.85	0.88
35	Gly	112	.	A	.	.	.	.	C	1.70	-0.36	.	.	F	1.40	0.89
	Ala	113	.	A	B	.	.	.	.	2.00	-0.74	.	.	F	1.40	1.77
	Gln	114	.	A	B	.	.	.	.	2.00	-1.17	.	.	.	1.34	1.77
	His	115	.	A	B	.	.	.	.	2.00	-0.79	.	.	F	1.58	2.39
	Arg	116	.	A	B	.	.	.	.	1.70	-0.79	.	.	F	1.92	2.34
40	Asp	117	.	.	.	.	T	T	.	1.74	-0.90	.	.	F	3.06	1.81
	Ser	118	.	.	.	.	T	T	.	1.99	-0.91	.	*	F	3.40	1.79

	Gly	119	.	.	.	.	T	T	.	2.03	-0.99	*	.	F	2.91	0.90
	Ser	120	.	.	.	.	T	T	.	1.77	-0.99	.	*	F	3.02	1.08
	Ser	121	.	.	.	.	.	.	C	1.77	-0.60	.	.	F	2.58	1.08
	Gly	122	.	.	.	.	.	T	C	1.88	-0.99	.	*	F	2.74	2.14
5	Lys	123	.	.	.	.	T	T	.	2.22	-1.41	.	.	F	2.90	3.13
	Ser	124	.	.	.	.	.	T	C	2.68	-1.80	.	.	F	3.00	4.66
	Arg	125	.	.	B	.	.	T	.	2.98	-2.19	.	.	F	2.50	9.23
	Arg	126	.	.	B	.	.	.	.	2.39	-2.21	.	.	F	2.00	7.99
	Lys	127	.	.	B	B	.	.	.	2.49	-1.53	.	.	F	1.50	4.18
10	Arg	128	.	.	B	B	.	.	.	2.10	-1.16	.	.	F	1.20	3.35
	Gln	129	.	.	B	B	.	.	.	2.16	-0.73	.	.	.	0.75	1.69
	Ile	130	.	.	B	B	.	.	.	2.04	0.03	.	.	.	-0.15	1.32
	Tyr	131	.	.	B	B	.	.	.	1.63	0.03	.	.	.	-0.15	1.13
	Gly	132	.	.	B	.	.	.	.	1.70	0.41	*	*	.	-0.40	0.87
15	Tyr	133	.	.	B	.	.	.	.	0.89	0.01	*	*	.	0.05	2.44
	Asp	134	.	.	B	.	.	T	.	0.59	0.11	.	*	F	0.40	1.35
	Ser	135	.	.	B	.	.	T	.	0.59	-0.26	.	*	F	1.00	1.83
	Arg	136	.	.	B	.	.	T	.	0.13	0.00	.	*	F	0.25	0.82
	Phe	137	.	.	B	.	.	T	.	0.13	0.03	.	*	.	0.10	0.42
20	Ser	138	.	.	B	B	.	.	.	0.42	0.46	.	*	.	-0.47	0.31
	Ile	139	.	.	B	B	.	.	.	0.42	0.07	*	*	.	-0.04	0.32
	Phe	140	.	.	B	B	.	.	.	0.02	0.07	*	*	.	0.09	0.62
	Gly	141	.	.	.	.	T	T	.	-0.90	0.07	*	*	.	1.02	0.40
	Lys	142	.	.	.	.	T	T	.	-1.01	0.37	.	.	F	1.30	0.47
25	Asp	143	.	.	.	.	T	T	.	-0.71	0.37	.	.	F	1.17	0.45
	Phe	144	.	.	B	.	.	T	.	-0.07	-0.01	.	.	.	1.09	0.73
	Leu	145	.	.	B	.	.	.	.	0.42	0.31	.	.	.	0.16	0.57
	Leu	146	.	.	B	.	.	.	.	0.07	0.74	.	.	.	-0.27	0.53
	Asn	147	.	.	B	.	.	.	.	-0.28	1.53	.	.	.	-0.40	0.53
30	Tyr	148	.	.	.	.	.	T	C	-0.59	1.13	.	*	.	0.00	0.85
	Pro	149	.	.	.	.	T	T	.	-0.19	0.93	.	*	.	0.35	1.50
	Phe	150	.	.	.	.	T	T	.	-0.23	0.63	*	*	.	0.35	1.25
	Ser	151	.	.	B	.	.	T	.	0.62	0.87	*	*	F	-0.05	0.59
	Thr	152	.	.	B	B	.	.	.	-0.19	0.11	.	*	F	-0.15	0.76
35	Ser	153	.	.	B	B	.	.	.	-0.24	0.37	.	*	F	-0.15	0.73
	Val	154	.	.	B	B	.	.	.	-0.34	-0.03	.	*	F	0.45	0.73
	Lys	155	.	.	B	B	.	.	.	0.01	0.07	.	*	F	-0.15	0.73
	Leu	156	.	.	B	B	.	.	.	-0.36	0.01	.	*	F	-0.15	0.54
	Ser	157	.	.	B	.	.	T	.	-0.36	0.20	.	*	F	0.25	0.39
40	Thr	158	.	.	B	.	.	T	.	-0.40	0.04	.	*	F	0.25	0.28
	Gly	159	.	.	.	.	T	T	.	0.14	0.47	.	*	F	0.35	0.34



	Cys	160	.	.	.	.	T	T	.	-0.71	0.27	.	.	F	0.65	0.36
	Thr	161	.	.	B	.	.	.	.	-0.76	0.57	.	.	F	-0.25	0.21
	Gly	162	.	.	B	.	.	.	.	-1.04	0.73	.	.	F	-0.25	0.16
	Thr	163	.	A	B	.	.	.	.	-0.73	0.80	.	.	F	-0.45	0.29
5	Leu	164	.	A	B	.	.	.	.	-0.34	0.23	.	.	.	-0.30	0.35
	Val	165	.	A	B	.	.	.	.	0.29	-0.26	.	.	.	0.30	0.71
	Ala	166	.	A	B	.	.	.	.	-0.26	-0.19	.	.	.	0.30	0.67
	Glu	167	A	A	.	.	.	.	.	-0.72	-0.03	.	.	.	0.30	0.60
	Lys	168	A	A	.	.	.	.	.	-0.72	-0.03	.	.	.	0.30	0.67
10	His	169	A	A	.	.	.	.	.	-0.50	-0.19	.	.	.	0.30	0.95
	Val	170	A	A	.	.	.	.	.	-0.23	-0.19	*	.	.	0.30	0.56
	Leu	171	A	A	.	.	.	.	.	0.32	0.31	*	.	.	-0.30	0.28
	Thr	172	A	A	.	.	.	.	.	-0.34	0.81	*	.	.	-0.60	0.28
	Ala	173	A	A	.	.	.	.	.	-1.28	0.89	*	.	.	-0.60	0.20
15	Ala	174	A	A	.	.	.	.	.	-1.28	0.93	*	.	.	-0.60	0.17
	His	175	.	A	B	.	.	.	.	-0.42	0.74	*	.	.	-0.32	0.16
	Cys	176	.	A	B	.	.	.	.	0.04	0.26	.	.	.	0.26	0.27
	Ile	177	.	A	B	.	.	.	.	0.40	0.19	*	.	.	0.54	0.26
	His	178	.	.	.	.	T	T	.	0.68	-0.31	*	.	.	2.22	0.39
20	Asp	179	.	.	.	.	T	T	.	1.02	-0.33	*	.	F	2.80	1.04
	Gly	180	.	.	.	.	T	T	.	0.20	-0.14	*	*	F	2.52	2.33
	Lys	181	.	.	.	.	T	T	.	0.91	-0.19	*	*	F	2.24	1.27
	Thr	182	.	.	B	B	.	.	.	1.46	-0.69	*	*	F	1.46	1.52
	Tyr	183	.	.	B	B	.	.	.	1.18	-0.26	*	*	F	0.88	1.52
25	Val	184	.	.	B	B	.	.	.	1.18	-0.20	*	*	F	0.60	1.10
	Lys	185	.	.	B	B	.	.	.	1.57	0.20	*	*	F	0.12	1.32
	Gly	186	.	.	B	.	.	.	.	0.71	-0.29	*	*	F	1.04	1.68
	Thr	187	.	.	B	.	.	.	.	1.13	-0.36	.	*	F	1.16	1.87
	Gln	188	.	.	B	.	.	.	.	0.52	-1.00	*	*	F	1.58	1.83
30	Lys	189	.	.	B	B	.	.	.	1.03	-0.36	*	*	F	1.20	1.37
	Leu	190	.	.	B	B	.	.	.	0.29	-0.36	*	*	F	0.93	0.94
	Arg	191	.	.	B	B	.	.	.	-0.18	-0.06	*	*	.	0.66	0.47
	Val	192	.	.	B	B	.	.	.	0.18	0.23	.	*	.	-0.06	0.19
	Gly	193	.	.	B	B	.	.	.	-0.03	0.23	.	*	.	-0.18	0.47
35	Phe	194	.	.	B	B	.	.	.	-0.03	-0.03	.	*	.	0.64	0.37
	Leu	195	.	.	B	B	.	.	.	0.08	-0.03	.	*	.	1.13	1.00
	Lys	196	.	.	B	.	.	T	.	0.01	0.11	.	*	F	1.27	0.88
	Pro	197	.	.	B	.	.	T	.	0.87	-0.31	*	*	F	2.36	2.02
	Lys	198	.	.	.	.	T	T	.	0.87	-1.10	*	*	F	3.40	4.10
40	Phe	199	.	.	B	.	.	T	.	1.22	-1.36	*	*	F	2.66	2.03
	Lys	200	.	.	B	.	.	.	.	2.14	-0.93	*	*	F	2.12	1.30

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	Asp	201	.	.	.	.	T	T	.	1.76	-1.36	*	*	F	2.38	1.27
	Gly	202	.	.	.	.	T	T	.	1.38	-0.93	*	*	F	2.04	1.45
	Gly	203	.	.	.	.	T	T	.	1.33	-1.21	*	*	F	1.85	0.73
	Arg	204	.	.	.	.	.	T	C	2.03	-0.81	*	*	F	1.95	0.71
5	Gly	205	.	.	.	.	.	.	C	1.69	-0.81	*	.	F	2.20	1.19
	Ala	206	.	.	.	.	.	.	C	1.38	-0.86	*	.	F	2.50	1.62
	Asn	207	.	.	.	.	.	T	C	1.42	-0.80	*	.	F	3.00	1.19
	Asp	208	.	.	.	.	.	T	C	1.18	-0.41	*	.	F	2.40	1.61
	Ser	209	.	.	.	.	.	T	C	0.47	-0.34	*	.	F	2.10	1.61
10	Thr	210	.	.	.	.	.	T	C	0.60	-0.23	*	.	F	1.65	0.99
	Ser	211	.	.	.	.	.	.	C	1.19	-0.20	.	.	F	1.15	0.92
	Ala	212	.	A	.	.	.	.	C	1.19	-0.20	.	.	F	0.80	1.19
	Met	213	.	A	B	.	.	.	.	0.59	-0.19	*	.	.	0.45	1.42
	Pro	214	.	A	.	.	.	.	C	0.93	-0.06	.	*	F	0.80	1.05
15	Glu	215	A	A	.	.	.	.	.	0.54	-0.44	.	*	F	0.60	2.08
	Gln	216	A	A	.	.	.	.	.	0.84	-0.16	.	*	F	0.60	1.82
	Met	217	A	A	.	.	.	.	.	1.14	-0.37	.	*	F	0.60	2.04
	Lys	218	A	.	.	B	.	.	.	0.86	0.11	*	*	.	-0.15	1.24
	Phe	219	A	.	.	B	.	.	.	1.18	0.80	*	*	.	-0.60	0.50
20	Gln	220	.	.	B	B	.	.	.	0.32	0.40	.	*	.	-0.60	0.99
	Trp	221	.	.	B	B	.	.	.	0.37	0.43	*	*	.	-0.60	0.37
	Ile	222	.	.	B	B	.	.	.	1.08	0.43	*	.	.	-0.37	0.85
	Arg	223	.	.	B	B	.	.	.	0.72	-0.36	.	.	.	0.76	0.96
	Val	224	.	.	B	B	.	.	.	1.39	-0.27	*	.	.	1.14	1.32
25	Lys	225	.	.	.	B	T	.	.	0.53	-0.69	*	.	F	2.22	2.56
	Arg	226	.	.	.	B	T	.	.	0.61	-0.73	*	.	F	2.30	0.97
	Thr	227	.	.	.	B	T	.	.	1.54	-0.30	*	*	F	1.92	2.02
	His	228	.	.	.	B	.	.	C	1.09	-0.94	*	.	F	1.79	2.02
	Val	229	.	.	.	B	.	.	C	1.66	-0.51	.	.	F	1.56	1.02
30	Pro	230	.	.	B	.	.	T	.	0.72	0.40	.	.	F	0.18	0.74
	Lys	231	.	.	.	.	T	T	.	0.66	0.60	.	*	F	0.35	0.38
	Gly	232	.	.	.	.	T	T	.	0.62	0.10	*	*	F	0.80	1.03
	Trp	233	.	.	B	.	.	T	.	0.66	-0.11	*	*	F	0.85	0.66
	Ile	234	.	.	B	.	.	.	.	0.92	-0.14	*	*	F	0.92	0.53
35	Lys	235	.	.	B	.	.	.	.	1.13	0.36	.	*	F	0.59	0.54
	Gly	236	.	.	.	.	.	.	C	1.09	0.33	*	*	F	1.06	0.83
	Asn	237	.	.	.	.	.	T	C	0.54	-0.59	*	*	F	2.58	1.98
	Ala	238	.	.	.	.	.	T	C	0.49	-0.59	*	*	F	2.70	0.69
	Asn	239	.	.	.	.	.	T	C	0.78	-0.16	*	*	F	2.13	0.69
40	Asp	240	.	.	.	.	T	T	.	0.73	0.03	.	*	F	1.46	0.43
	Ile	241	.	.	B	.	.	.	.	0.83	-0.37	.	*	.	1.04	0.71

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	Gly	242	.	.	B	.	.	.	.	0.83	-0.11	.	*	.	0.77	0.69
	Met	243	.	.	B	.	.	.	.	1.18	-0.51	*	.	.	0.80	0.69
	Asp	244	.	.	B	.	.	T	.	0.59	0.24	*	*	.	0.25	1.54
	Tyr	245	.	.	B	.	.	T	.	-0.22	0.06	.	*	.	0.25	1.57
5	Asp	246	.	.	B	.	.	T	.	-0.14	0.31	.	*	.	0.25	1.31
	Tyr	247	.	.	B	.	.	T	.	0.20	0.39	.	.	.	0.10	0.65
	Ala	248	A	A	.	.	.	.	.	-0.01	0.39	.	*	.	-0.30	0.71
	Leu	249	A	A	.	.	.	.	.	0.03	0.31	*	.	.	-0.30	0.35
	Leu	250	A	A	.	.	.	.	.	0.32	0.31	*	.	.	-0.30	0.45
10	Glu	251	A	A	.	.	.	.	.	0.11	-0.44	*	.	.	0.30	0.89
	Leu	252	A	A	.	.	.	.	.	0.32	-0.51	*	.	F	0.90	1.67
	Lys	253	A	A	.	.	.	.	.	0.96	-0.70	*	.	F	0.90	2.76
	Lys	254	A	.	.	.	.	T	.	1.88	-1.39	*	.	F	1.30	3.18
	Pro	255	A	.	.	.	.	T	.	2.73	-1.39	*	.	F	1.30	7.56
15	His	256	A	.	.	.	.	T	.	2.03	-2.07	*	.	F	1.30	7.56
	Lys	257	A	.	.	.	.	T	.	2.24	-1.29	*	.	F	1.30	3.27
	Arg	258	A	.	.	.	.	.	.	2.24	-0.67	*	.	F	1.10	2.09
	Lys	259	.	.	B	.	.	.	.	1.31	-1.10	*	.	F	1.10	3.08
	Phe	260	.	.	B	B	.	.	.	1.18	-0.91	*	.	.	0.75	1.08
20	Met	261	.	.	B	B	.	.	.	0.36	-0.49	*	*	.	0.30	0.55
	Lys	262	.	.	B	B	.	.	.	0.01	0.16	*	*	.	-0.30	0.20
	Ile	263	.	.	B	B	.	.	.	-0.31	0.54	*	*	.	-0.60	0.31
	Gly	264	.	.	B	B	.	.	.	-0.57	0.19	*	*	.	-0.02	0.49
	Val	265	.	.	.	B	.	.	C	-0.46	0.00	*	*	F	0.61	0.38
25	Ser	266	.	.	.	B	.	.	C	0.19	0.50	.	*	F	0.59	0.55
	Pro	267	.	.	.	.	.	T	C	0.14	-0.19	.	*	F	2.32	1.10
	Pro	268	.	.	.	.	T	T	.	0.22	-0.21	.	.	F	2.80	2.57
	Ala	269	.	.	.	.	T	T	.	0.36	-0.17	*	.	F	2.52	1.58
	Lys	270	.	.	B	.	.	T	.	0.87	-0.13	*	.	F	1.84	1.58
30	Gln	271	.	.	B	.	.	.	.	0.82	-0.13	.	.	F	1.36	1.01
	Leu	272	.	.	B	.	.	T	.	1.14	-0.13	.	*	F	1.13	0.99
	Pro	273	.	.	B	.	.	T	.	0.47	-0.63	.	*	F	1.15	0.97
	Gly	274	.	.	.	.	T	T	.	1.02	0.06	.	*	F	0.65	0.39
	Gly	275	.	.	B	.	.	T	.	0.28	0.16	.	*	F	0.25	0.65
35	Arg	276	.	.	B	B	.	.	.	-0.02	0.26	.	*	F	-0.15	0.36
	Ile	277	.	.	B	B	.	.	.	0.44	0.21	.	*	.	-0.14	0.49
	His	278	.	.	B	B	.	.	.	0.41	0.21	*	*	.	0.02	0.49
	Phe	279	.	.	B	.	.	T	.	0.76	0.54	*	*	.	0.28	0.39
	Ser	280	.	.	B	.	.	T	.	1.10	0.54	.	*	.	0.44	0.94
40	Gly	281	.	.	.	.	T	T	.	0.99	0.26	*	*	F	1.60	1.11
	Tyr	282	.	.	.	.	T	T	.	1.99	-0.24	.	*	F	2.04	2.14

	Asp	283	.	.	.	.	T	.	.	1.81	-1.03	.	.	F	2.32	3.12
	Asn	284	.	.	.	.	T	.	.	2.17	-0.99	.	.	F	2.50	4.88
	Asp	285	.	.	.	.	T	.	.	2.47	-0.99	.	.	F	2.68	3.08
	Arg	286	.	.	.	.	.	T	C	2.00	-1.34	*	.	F	2.86	2.97
5	Pro	287	.	.	.	.	T	T	.	1.39	-0.66	*	.	F	3.40	1.52
	Gly	288	.	.	.	.	T	T	.	1.14	-0.41	*	.	F	2.61	0.68
	Asn	289	.	.	B	.	.	T	.	1.26	0.34	*	*	F	1.27	0.54
	Leu	290	.	.	B	B	.	.	.	0.56	0.34	*	*	.	0.38	0.69
	Val	291	.	.	B	B	.	.	.	-0.22	0.70	*	.	.	-0.26	0.60
10	Tyr	292	.	.	B	B	.	.	.	-0.01	0.84	*	*	.	-0.60	0.20
	Arg	293	.	A	B	B	.	.	.	-0.52	0.44	*	*	.	-0.60	0.40
	Phe	294	.	A	B	B	.	.	.	-0.48	0.40	*	.	.	-0.60	0.40
	Cys	295	.	A	B	B	.	.	.	0.33	-0.24	*	.	.	0.30	0.52
	Asp	296	.	A	B	B	.	.	.	1.19	-1.00	*	.	.	0.60	0.44
15	Val	297	.	A	B	.	.	.	.	1.12	-1.00	*	.	.	0.60	0.88
	Lys	298	.	A	.	.	T	.	.	0.77	-1.30	*	.	F	1.30	2.37
	Asp	299	.	A	.	.	T	.	.	1.47	-1.11	*	.	F	1.30	2.23
	Glu	300	.	A	B	.	T	.	.	1.32	-1.11	*	.	F	1.30	5.01
	Thr	301	.	A	.	B	T	.	.	0.51	-1.07	*	.	F	1.30	2.06
20	Tyr	302	.	A	.	B	T	.	.	1.12	-0.39	*	.	.	0.85	1.02
	Asp	303	.	A	B	B	.	.	.	1.08	0.37	.	.	.	-0.30	0.92
	Leu	304	.	A	B	B	.	.	.	1.08	0.77	*	.	.	-0.45	1.11
	Leu	305	.	A	B	B	.	.	.	0.41	0.69	*	.	.	-0.45	1.22
	Tyr	306	.	A	B	B	.	.	.	0.72	0.50	*	.	.	-0.60	0.39
25	Gln	307	.	A	B	B	.	.	.	0.67	0.50	.	.	.	-0.60	0.80
	Gln	308	.	A	B	B	.	.	.	0.67	0.20	.	.	F	0.00	1.29
	Cys	309	.	A	B	B	.	.	.	1.27	-0.09	.	.	F	0.60	1.43
	Asp	310	.	.	.	B	T	.	.	1.73	-0.41	.	.	F	1.25	1.28
	Ser	311	.	.	B	.	.	.	.	1.39	-0.39	.	.	F	1.15	0.73
30	Gln	312	.	.	B	.	.	T	.	1.09	-0.29	.	.	F	1.75	1.37
	Pro	313	.	.	.	.	.	T	C	0.74	-0.47	.	*	F	2.20	1.10
	Gly	314	.	.	.	.	T	T	.	1.11	-0.04	.	.	F	2.50	0.81
	Ala	315	.	.	.	.	T	T	C	0.77	-0.04	.	.	F	2.25	0.63
	Ser	316	.	.	.	.	.	T	C	0.21	-0.01	.	.	F	1.80	0.40
35	Gly	317	.	.	.	.	.	T	C	-0.03	0.20	.	.	F	0.95	0.30
	Ser	318	.	.	B	.	.	T	.	-0.68	0.53	.	*	F	0.20	0.47
	Gly	319	.	.	B	.	.	T	.	-0.22	0.67	.	*	F	-0.05	0.26
	Val	320	.	.	B	B	.	.	.	-0.23	0.29	*	*	.	-0.30	0.51
	Tyr	321	.	.	B	B	.	.	.	-0.22	0.47	*	.	.	-0.60	0.38
40	Val	322	.	.	B	B	.	.	.	0.17	1.00	*	*	.	-0.60	0.40
	Arg	323	.	.	B	B	.	.	.	0.58	0.57	*	*	.	-0.45	1.09

5	Met	324	.	.	B	B	.	.	.	0.92	-0.07	*	*	.	0.45	1.36
	Trp	325	.	.	B	B	.	.	.	1.74	-0.43	*	*	.	0.45	3.17
	Lys	326	.	.	B	B	.	.	.	1.99	-0.57	*	*	.	0.75	2.20
	Arg	327	.	A	.	.	T	.	.	2.89	-0.17	*	*	F	1.00	3.85
	Gln	328	.	A	.	.	.	.	C	2.49	-0.79	*	*	F	1.10	7.33
	His	329	.	A	.	.	.	.	C	3.09	-0.79	*	.	F	1.10	3.85
	Gln	330	.	A	.	.	.	.	C	3.49	-0.79	*	.	F	1.10	3.41
	Lys	331	.	A	.	.	T	.	.	3.49	-0.79	*	.	F	1.30	3.85
10	Trp	332	.	A	.	.	T	.	.	2.49	-1.19	*	*	F	1.30	5.66
	Glu	333	.	A	.	.	.	.	C	1.60	-1.00	*	.	F	1.10	2.29
	Arg	334	.	A	B	B	.	.	.	1.29	-0.71	*	.	F	0.75	0.80
	Lys	335	.	A	B	B	.	.	.	0.69	-0.29	*	.	.	0.30	0.76
15	Ile	336	.	A	B	B	.	.	.	-0.24	-0.59	*	.	.	0.60	0.43
	Ile	337	.	A	B	B	.	.	.	-0.26	0.10	*	.	.	-0.30	0.15
	Gly	338	.	A	B	B	.	.	.	-0.60	0.49	*	.	.	-0.60	0.10
	Met	339	.	.	B	B	.	.	.	-0.74	0.91	*	.	.	-0.60	0.15
	Ile	340	.	.	B	B	.	.	.	-0.79	0.73	.	.	.	-0.60	0.28
	Ser	341	.	.	.	.	.	T	C	-0.19	0.44	.	.	.	0.00	0.50
20	Gly	342	.	.	.	.	.	T	C	-0.16	0.93	.	.	.	0.00	0.53
	His	343	.	.	.	.	.	T	C	0.19	0.96	.	.	.	0.00	0.56
	Gln	344	.	.	B	.	.	T	.	0.19	0.27	.	*	.	0.10	0.70
	Trp	345	.	.	B	.	.	.	.	1.08	0.50	.	*	.	-0.40	0.70
25	Val	346	.	.	B	.	.	.	.	1.03	0.07	.	*	.	0.20	0.86
	Asp	347	.	.	B	.	.	T	.	1.08	0.00	.	*	.	0.70	0.49
	Met	348	.	.	.	.	T	T	.	0.90	-0.01	.	*	F	2.15	0.62
	Asp	349	.	.	.	.	T	T	.	0.90	-0.50	.	*	F	2.60	1.30
30	Gly	350	.	.	.	.	.	T	C	1.19	-0.74	.	*	F	3.00	1.35
	Ser	351	.	.	.	.	.	T	C	1.34	-0.74	.	*	F	2.70	2.35
	Pro	352	.	.	.	.	.	T	C	1.03	-0.57	*	*	F	2.40	1.22
	Gln	353	.	.	.	.	T	T	.	1.74	-0.09	*	.	F	2.25	1.78
	Glu	354	.	.	B	.	.	T	.	1.40	-0.51	*	.	F	2.10	2.60
	Phe	355	.	.	B	.	.	.	.	1.08	-0.47	*	.	F	1.55	1.67
35	Thr	356	.	.	.	.	T	T	.	1.08	-0.33	*	.	F	2.25	0.52
	Arg	357	.	.	.	.	T	T	.	1.29	-0.34	*	*	F	2.50	0.40
	Gly	358	.	.	.	.	T	T	.	0.40	-0.34	*	*	F	2.25	0.80
	Cys	359	.	.	.	.	T	T	.	0.09	-0.44	*	*	F	2.00	0.39
40	Ser	360	.	.	.	B	.	.	C	0.58	-0.44	*	.	F	1.15	0.29
	Glu	361	.	.	.	B	T	.	.	0.08	-0.01	*	*	F	1.10	0.45
	Ile	362	.	.	B	B	.	.	.	-0.03	0.24	*	*	F	-0.15	0.69
	Thr	363	.	.	B	B	.	.	.	0.07	0.07	.	.	F	-0.15	0.89
	Pro	364	.	.	B	B	.	.	.	-0.16	0.44	.	.	F	-0.45	0.80

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	Leu	365	.	.	B	B	.	.	.	-0.07	1.13	*	.	.	-0.60	0.80
	Gln	366	.	.	B	B	.	.	.	-0.07	0.87	*	.	.	-0.60	0.86
	Tyr	367	.	.	B	B	.	.	.	-0.07	0.39	*	.	.	-0.30	0.93
	Ile	368	.	.	B	B	.	.	.	-0.06	0.64	*	*	.	-0.60	0.79
5	Pro	369	.	.	B	B	.	.	.	-0.73	0.34	.	*	.	-0.30	0.61
	Asp	370	.	.	B	B	.	.	.	-0.27	0.63	*	*	F	-0.45	0.27
	Ile	371	.	.	B	B	.	.	.	-1.12	0.30	*	*	F	-0.15	0.39
	Ser	372	.	.	B	B	.	.	.	-1.27	0.26	.	*	.	-0.30	0.19
	Ile	373	.	.	B	B	.	.	.	-0.77	0.26	.	*	.	-0.30	0.14
10	Gly	374	.	.	B	B	.	.	.	-0.94	0.69	.	*	.	-0.60	0.26
	Val	375	.	.	B	B	.	.	.	-1.33	0.43	.	*	.	-0.60	0.25
	Ter	376	.	.	B	B	.	.	.	-0.83	0.47	.	*	.	-0.60	0.45

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Table X

	Res	Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
5	Met	1	.	.	B	B	.	.	.	-1.26	0.43	.	.	.	-0.60	0.37
	Ala	2	.	.	B	B	.	.	.	-1.68	0.64	.	.	.	-0.60	0.22
	Ser	3	.	.	B	B	.	.	.	-1.50	0.90	.	.	.	-0.60	0.14
	Val	4	.	.	B	B	.	.	.	-1.41	0.90	.	.	.	-0.60	0.22
	Val	5	.	.	B	B	.	.	.	-1.37	0.67	.	.	.	-0.60	0.29
10	Leu	6	.	.	B	.	.	T	.	-1.07	0.60	.	.	F	-0.05	0.21
	Pro	7	.	.	.	.	T	T	.	-0.48	0.60	.	.	F	0.35	0.39
	Ser	8	.	.	.	.	T	T	.	-0.84	0.36	.	.	F	0.65	0.90
	Gly	9	.	.	.	.	T	T	.	-0.58	0.29	.	.	F	0.65	0.58
	Ser	10	.	.	.	.	.	T	C	-0.31	0.10	.	.	F	0.45	0.38
15	Gln	11	A	.	.	.	.	T	.	-0.09	0.17	.	.	F	0.25	0.29
	Cys	12	A	.	.	.	.	T	.	-0.47	0.29	.	.	.	0.10	0.29
	Ala	13	A	.	.	.	.	T	.	-0.76	0.36	.	.	.	0.10	0.22
	Ala	14	A	A	.	.	.	.	.	-1.00	0.47	.	.	.	-0.60	0.13
	Ala	15	A	A	.	.	.	.	.	-1.29	0.57	.	.	.	-0.60	0.24
20	Ala	16	A	A	.	.	.	.	.	-1.88	0.50	.	.	.	-0.60	0.24
	Ala	17	A	A	.	.	.	.	.	-1.42	0.50	.	.	.	-0.60	0.24
	Ala	18	A	A	.	.	.	.	.	-1.04	0.43	.	.	.	-0.60	0.37
	Ala	19	A	A	.	.	.	.	.	-0.80	0.36	.	.	.	-0.30	0.57
	Ala	20	A	A	.	.	.	.	.	-1.02	0.29	*	*	.	-0.30	0.56
25	Pro	21	A	.	.	.	.	T	.	-0.32	0.47	*	*	F	-0.05	0.46
	Pro	22	A	.	.	.	.	T	.	-0.54	-0.03	.	*	F	0.85	0.89
	Gly	23	A	.	.	.	.	T	.	0.16	0.16	.	*	F	0.25	0.72
	Leu	24	A	.	.	.	.	T	.	-0.07	-0.34	.	*	.	0.70	0.92
	Arg	25	.	A	B	.	.	.	.	-0.29	-0.09	.	*	.	0.30	0.49
30	Leu	26	.	A	B	.	.	.	.	-0.89	0.17	.	*	.	-0.30	0.41
	Arg	27	.	A	B	.	.	.	.	-1.49	0.43	.	*	.	-0.60	0.41
	Leu	28	.	A	B	.	.	.	.	-1.96	0.43	.	*	.	-0.60	0.17
	Leu	29	.	A	B	.	.	.	.	-1.84	1.11	.	*	.	-0.60	0.17
	Leu	30	.	A	B	.	.	.	.	-2.26	1.21	.	*	.	-0.60	0.08
35	Leu	31	A	A	.	.	.	.	.	-2.03	1.60	*	*	.	-0.60	0.12
	Leu	32	A	A	.	.	.	.	.	-2.73	1.41	*	*	.	-0.60	0.15
	Phe	33	A	A	.	.	.	.	.	-2.51	1.23	.	.	.	-0.60	0.18
	Ser	34	A	A	.	.	.	.	.	-2.51	1.04	.	.	.	-0.60	0.23
	Ala	35	A	A	.	.	.	.	.	-2.59	1.04	.	.	.	-0.60	0.23
40	Ala	36	A	A	.	.	.	.	.	-1.99	1.04	.	.	.	-0.60	0.18

	Ala	37	A	A	.	.	.	.	-1.49	0.69	.	.	-0.60	0.21
	Leu	38	.	A	B	.	.	.	-1.13	0.79	.	.	-0.60	0.30
	Ile	39	.	A	B	.	.	.	-0.83	0.71	.	.	-0.32	0.30
	Pro	40	.	A	B	.	.	.	-0.59	0.21	.	.	F	0.41 0.49
5	Thr	41	.	.	.	.	T	.	0.00	0.14	.	.	F	1.29 0.59
	Gly	42	.	.	.	.	T	T	0.59	-0.14	.	.	F	2.52 1.45
	Asp	43	.	.	.	.	T	T	0.59	-0.43	.	.	F	2.80 1.51
	Gly	44	.	.	.	.	T	C	0.78	-0.17	.	.	F	2.17 0.86
	Gln	45	.	.	B	.	.	T	0.68	0.13	*	.	F	1.09 0.75
10	Asn	46	.	.	B	B	.	.	1.03	0.19	*	.	F	0.41 0.65
	Leu	47	.	.	B	B	.	.	1.38	0.19	*	.	F	0.28 1.32
	Phe	48	.	.	B	B	.	.	0.52	-0.24	*	.	F	0.60 1.27
	Thr	49	.	.	B	B	.	.	0.56	0.00	*	.	F	-0.15 0.59
	Lys	50	.	.	B	B	.	.	-0.30	0.09	*	.	F	0.00 1.02
15	Asp	51	.	.	B	B	.	.	-1.19	0.04	*	.	F	-0.15 0.88
	Val	52	.	.	B	B	.	.	-0.38	-0.06	*	.	.	0.30 0.43
	Thr	53	.	.	B	B	.	.	-0.02	-0.54	*	.	.	0.60 0.37
	Val	54	.	.	B	B	.	.	0.29	-0.11	*	.	.	0.30 0.22
	Ile	55	A	.	.	B	.	.	-0.61	-0.11	*	.	.	0.30 0.51
20	Glu	56	A	.	.	B	.	.	-1.20	-0.11	.	.	F	0.45 0.26
	Gly	57	A	.	.	.	.	.	-0.66	-0.10	*	.	F	0.65 0.36
	Glu	58	A	.	.	B	.	.	-1.23	-0.26	.	.	F	0.45 0.74
	Val	59	A	.	.	B	.	.	-0.68	-0.26	.	.	.	0.30 0.30
	Ala	60	A	.	.	B	.	.	-0.46	0.13	.	*	.	-0.30 0.40
25	Thr	61	A	.	.	B	.	.	-0.46	0.27	.	*	.	-0.30 0.12
	Ile	62	A	.	.	B	.	.	-0.97	0.67	.	*	.	-0.60 0.29
	Ser	63	A	.	.	B	.	.	-0.97	0.67	*	.	.	-0.60 0.21
	Cys	64	.	.	B	B	.	.	-0.07	0.57	*	*	.	-0.60 0.24
	Gln	65	.	.	B	B	.	.	0.22	0.09	.	*	.	0.04 0.68
30	Val	66	.	.	B	B	.	.	0.53	-0.21	*	*	.	0.98 0.68
	Asn	67	.	.	.	B	T	.	1.42	-0.60	*	*	F	2.32 2.12
	Lys	68	.	.	.	B	T	.	1.42	-1.17	*	.	F	2.66 2.05
	Ser	69	.	.	.	.	T	T	1.23	-1.19	*	.	F	3.40 3.69
	Asp	70	.	.	.	.	T	T	0.34	-1.19	*	.	F	3.06 1.70
35	Asp	71	.	.	B	.	.	T	1.20	-0.90	*	.	F	2.17 0.60
	Ser	72	.	.	B	.	.	T	0.39	-0.50	*	.	.	1.38 0.77
	Val	73	.	.	B	B	.	.	-0.47	-0.20	*	.	.	0.64 0.38
	Ile	74	.	.	B	B	.	.	-0.17	0.49	*	.	.	-0.60 0.19
	Gln	75	.	.	B	B	.	.	-0.38	0.89	*	.	.	-0.60 0.23
40	Leu	76	.	.	B	B	.	.	-0.38	0.93	*	.	.	-0.60 0.47
	Leu	77	.	.	B	B	.	.	0.03	0.69	*	.	.	-0.17 1.08



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	Asn	78	.	.	.	.	.	T	C	0.89	0.00	*	.	F	1.16	1.22
	Pro	79	.	.	.	.	.	T	C	1.47	0.00	*	.	F	1.44	2.56
	Asn	80	.	.	.	.	.	T	T	0.58	-0.20	*	.	F	2.52	4.49
	Arg	81	.	.	.	.	.	T	T	1.14	-0.20	*	.	F	2.80	1.96
5	Gln	82	.	.	B	B	.	.	.	1.26	0.16	.	*	F	1.12	1.98
	Thr	83	.	.	B	B	.	.	.	1.37	0.51	.	*	F	0.54	1.07
	Ile	84	.	.	B	B	.	.	.	1.58	0.11	*	*	.	0.41	1.07
	Tyr	85	.	.	B	B	.	.	.	0.88	0.11	*	*	.	0.13	1.03
	Phe	86	.	.	B	B	.	.	.	0.88	0.50	.	*	.	-0.60	0.62
10	Arg	87	.	.	B	B	.	.	.	0.67	0.01	*	.	.	-0.15	1.73
	Asp	88	.	.	B	B	.	.	.	0.17	-0.24	*	.	F	0.94	1.70
	Phe	89	.	.	B	.	.	.	.	1.10	-0.31	*	.	F	1.48	1.62
	Arg	90	.	.	.	.	.	.	C	1.34	-1.10	*	.	F	2.32	1.66
	Pro	91	.	.	.	.	.	.	C	1.74	-1.10	*	*	F	2.66	1.66
15	Leu	92	.	.	.	.	.	T	T	1.74	-0.71	*	*	F	3.40	2.56
	Lys	93	.	.	.	.	.	T	T	1.04	-1.50	.	*	F	3.06	2.56
	Asp	94	.	.	.	.	.	T	T	1.74	-0.71	*	*	F	2.72	1.44
	Ser	95	A	.	.	.	.	T	.	0.82	-0.74	*	*	F	1.98	3.01
	Arg	96	.	A	B	.	.	.	.	0.22	-0.74	.	.	F	1.24	1.24
20	Phe	97	.	A	B	.	.	.	.	1.03	-0.06	.	.	.	0.30	0.61
	Gln	98	.	A	B	.	.	.	.	0.29	0.34	.	.	.	-0.30	0.74
	Leu	99	.	A	B	.	.	.	.	-0.01	0.74	.	*	.	-0.60	0.33
	Leu	100	.	A	B	.	.	.	.	-0.01	1.13	.	*	.	-0.60	0.50
	Asn	101	.	A	.	.	.	.	C	-0.42	0.73	.	*	.	-0.40	0.39
25	Phe	102	.	A	.	.	.	.	C	0.28	0.71	*	.	F	-0.25	0.63
	Ser	103	.	.	.	.	.	T	C	-0.53	0.03	*	.	F	0.60	1.33
	Ser	104	A	.	.	.	.	T	.	0.32	0.03	*	*	F	0.25	0.68
	Ser	105	A	.	.	.	.	T	.	0.28	-0.37	.	*	F	1.00	1.58
	Glu	106	A	.	.	.	.	T	.	-0.02	-0.51	.	*	F	1.15	0.87
30	Leu	107	A	.	.	B	.	.	.	-0.13	-0.51	.	*	F	0.75	0.87
	Lys	108	A	.	.	B	.	.	.	-0.14	-0.21	.	*	F	0.45	0.54
	Val	109	A	.	.	B	.	.	.	0.16	-0.11	*	*	.	0.30	0.45
	Ser	110	.	.	B	B	.	.	.	-0.40	0.29	*	*	.	-0.30	0.87
	Leu	111	.	.	B	B	.	.	.	-0.70	0.24	.	*	.	-0.30	0.32
35	Thr	112	.	.	B	B	.	.	.	-0.78	0.63	.	*	.	-0.60	0.58
	Asn	113	.	.	B	B	.	.	.	-1.12	0.67	.	.	.	-0.60	0.31
	Val	114	.	.	B	B	.	.	.	-0.27	0.67	.	.	.	-0.60	0.50
	Ser	115	.	.	B	B	.	.	.	0.03	-0.01	.	.	.	0.64	0.58
	Ile	116	.	.	B	B	.	.	.	0.50	-0.50	.	*	F	1.13	0.62
40	Ser	117	.	.	B	.	.	T	.	0.92	-0.47	*	*	F	1.87	0.83
	Asp	118	.	.	.	.	.	T	T	0.68	-1.11	*	*	F	3.06	1.21

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	Glu	119	.	.	.	.	T	T	.	0.83	-0.74	*	*	F	3.40	2.70
	Gly	120	.	.	.	.	T	T	.	0.47	-0.64	*	*	F	3.06	1.74
	Arg	121	.	.	.	B	T	.	.	1.36	-0.46	*	*	F	1.87	0.56
	Tyr	122	.	.	.	B	T	.	.	0.84	-0.06	*	*	.	1.38	0.56
5	Phe	123	.	.	B	B	.	.	.	0.60	0.63	*	*	.	-0.26	0.47
	Cys	124	.	.	B	B	.	.	.	0.29	0.96	*	*	.	-0.60	0.37
	Gln	125	.	.	B	B	.	.	.	0.63	1.44	*	*	.	-0.60	0.34
	Leu	126	.	.	B	B	.	.	.	0.31	0.69	*	*	.	-0.60	0.66
	Tyr	127	.	.	.	.	T	.	.	0.34	0.33	*	.	.	0.79	1.91
10	Thr	128	.	.	.	.	T	.	.	1.04	0.19	*	.	F	1.28	1.71
	Asp	129	.	.	.	.	.	T	C	1.71	0.19	*	.	F	1.62	3.58
	Pro	130	.	.	.	.	.	T	C	1.41	-0.50	*	.	F	2.86	3.96
	Pro	131	.	.	.	.	T	T	.	1.98	-0.87	.	.	F	3.40	3.68
	Gln	132	.	.	.	.	T	T	.	1.91	-0.60	.	.	F	3.06	3.45
15	Glu	133	.	.	B	B	.	.	.	1.91	-0.11	*	.	F	1.62	3.22
	Ser	134	.	.	B	B	.	.	.	1.02	-0.06	*	.	F	1.28	3.01
	Tyr	135	.	.	B	B	.	.	.	0.92	0.20	.	.	F	0.34	1.22
	Thr	136	.	.	B	B	.	.	.	0.28	0.29	.	.	F	0.00	1.01
	Thr	137	.	.	B	B	.	.	.	-0.53	0.93	*	.	F	-0.45	0.56
20	Ile	138	.	.	B	B	.	.	.	-1.39	1.23	.	.	.	-0.60	0.30
	Thr	139	.	.	B	B	.	.	.	-1.30	1.11	.	.	.	-0.60	0.15
	Val	140	.	.	B	B	.	.	.	-1.27	1.06	.	*	.	-0.60	0.16
	Leu	141	.	.	B	B	.	.	.	-0.84	1.00	.	*	.	-0.60	0.36
	Val	142	.	.	B	B	.	.	.	-0.53	0.31	.	*	.	-0.30	0.49
25	Pro	143	.	.	B	.	.	T	.	-0.46	0.23	.	*	F	0.40	1.06
	Pro	144	.	.	.	.	T	T	.	-0.74	0.27	.	.	F	0.80	1.06
	Arg	145	.	.	.	.	T	T	.	-0.78	0.20	.	.	F	0.80	1.41
	Asn	146	A	.	.	.	.	T	.	0.03	0.24	.	.	.	0.10	0.64
	Leu	147	.	A	B	.	.	.	.	0.00	-0.19	*	*	.	0.30	0.69
30	Met	148	.	A	B	.	.	.	.	0.21	0.07	*	.	.	-0.30	0.25
	Ile	149	.	A	B	.	.	.	.	0.47	0.47	*	*	.	-0.60	0.27
	Asp	150	.	A	B	.	.	.	.	0.36	0.07	*	*	.	-0.30	0.64
	Ile	151	A	A	.	.	.	.	.	0.04	-0.61	*	*	.	0.75	1.09
	Gln	152	A	.	.	.	.	T	.	0.27	-0.74	.	*	F	1.30	2.24
35	Lys	153	A	.	.	.	.	T	.	0.01	-0.93	.	*	F	1.30	1.36
	Asp	154	A	.	.	.	.	T	.	0.90	-0.29	.	*	F	1.00	1.43
	Thr	155	A	.	.	.	.	T	.	0.56	-0.97	.	*	F	1.30	1.43
	Ala	156	A	A	.	.	.	.	.	1.44	-0.94	.	.	F	0.75	0.71
	Val	157	A	A	.	.	.	.	.	1.44	-0.94	.	.	F	0.75	0.74
40	Glu	158	A	A	.	.	.	.	.	0.51	-0.94	.	.	F	0.75	0.88
	Gly	159	A	A	.	.	.	.	.	0.51	-0.74	.	*	F	0.75	0.61

5	Glu	160	A	A	.	.	.	.	.	-0.03	-1.24	.	*	F	0.90	1.43
	Glu	161	A	A	.	.	.	.	.	0.56	-1.24	.	*	F	0.75	0.61
	Ile	162	A	A	.	.	.	.	.	0.74	-0.84	.	*	F	0.75	1.00
	Glu	163	A	A	.	.	.	.	.	0.43	-0.70	.	*	.	0.60	0.31
	Val	164	A	A	.	.	.	.	.	0.19	-0.21	.	*	.	0.30	0.26
10	Asn	165	A	A	.	.	.	.	.	-0.41	0.29	.	*	.	-0.30	0.37
	Cys	166	A	A	.	.	.	.	.	-1.00	0.21	.	*	.	-0.30	0.21
	Thr	167	A	A	.	.	.	.	.	-0.41	0.71	.	*	.	-0.60	0.29
	Ala	168	A	A	.	.	.	.	.	-0.37	0.46	.	*	.	-0.60	0.24
	Met	169	A	.	.	.	.	.	.	0.28	0.06	.	.	.	-0.10	0.90
15	Ala	170	A	.	.	.	.	.	.	-0.31	-0.09	*	.	.	0.50	0.96
	Ser	171	A	.	.	.	.	.	.	0.04	-0.07	.	.	F	0.65	0.96
	Lys	172	A	.	.	.	.	.	.	0.04	-0.09	*	.	F	0.80	1.40
	Pro	173	A	.	.	B	.	.	.	-0.26	-0.21	*	*	F	0.60	2.00
	Ala	174	A	.	.	B	.	.	.	0.46	-0.03	*	*	F	0.60	1.05
20	Thr	175	.	.	B	B	.	.	.	0.76	-0.41	*	*	F	0.60	1.02
	Thr	176	.	.	B	B	.	.	.	0.36	0.50	*	*	F	-0.45	0.70
	Ile	177	.	.	B	B	.	.	.	0.36	0.86	*	*	.	-0.60	0.60
	Arg	178	.	.	B	B	.	.	.	0.22	0.36	*	.	.	-0.30	0.83
	Trp	179	.	.	B	B	.	.	.	0.81	0.30	*	.	.	-0.30	0.57
25	Phe	180	.	.	.	.	.	T	C	0.81	0.21	*	*	.	0.45	1.30
	Lys	181	.	.	.	.	.	T	C	1.12	0.01	*	*	F	0.45	0.96
	Gly	182	.	.	.	.	.	T	C	1.20	0.01	*	*	F	0.60	1.58
	Asn	183	.	.	.	.	.	T	C	1.13	-0.21	*	*	F	1.20	1.50
	Thr	184	.	A	.	.	.	.	C	1.08	-1.00	.	*	F	1.40	1.50
30	Glu	185	A	A	.	.	.	.	.	1.82	-0.57	.	*	F	1.50	1.50
	Leu	186	A	A	.	.	.	.	.	1.48	-1.00	.	*	F	1.80	1.87
	Lys	187	A	A	.	.	.	.	.	1.82	-1.01	.	*	F	2.10	1.74
	Gly	188	.	.	.	.	.	T	C	0.97	-1.50	.	*	F	3.00	1.74
	Lys	189	.	.	.	.	.	T	C	1.28	-0.86	.	*	F	2.70	1.56
35	Ser	190	A	.	.	.	.	T	.	1.28	-1.54	.	*	F	2.20	1.35
	Glu	191	A	.	.	.	.	T	.	1.80	-1.54	.	*	F	1.90	2.37
	Val	192	A	.	.	.	.	.	.	1.46	-1.06	*	*	F	1.40	1.25
	Glu	193	A	.	.	.	.	.	.	1.80	-0.67	*	*	F	1.10	1.25
	Glu	194	A	.	.	.	.	.	.	1.16	-1.06	*	.	F	1.10	1.20
40	Trp	195	A	.	.	.	.	T	.	1.21	-0.44	*	.	F	1.00	1.60
	Ser	196	A	.	.	.	.	T	.	0.90	-0.33	.	.	.	0.85	1.45
	Asp	197	A	.	.	.	.	T	.	0.90	0.16	*	.	.	0.25	1.21
	Met	198	A	.	.	.	.	T	.	0.59	0.80	.	.	.	-0.20	0.85
	Tyr	199	A	.	.	B	.	.	.	0.29	0.37	.	.	.	-0.30	0.92
	Thr	200	A	.	.	B	.	.	.	0.58	0.37	*	.	.	-0.30	0.74

326

	Val	201	A	.	.	B	.	.	0.07	0.77	*	.	.	-0.45	1.29
	Thr	202	A	.	.	B	.	.	-0.53	0.84	.	.	F	-0.45	0.68
	Ser	203	A	A	.	B	.	.	-0.74	0.70	.	*	F	-0.45	0.47
	Gln	204	A	A	.	B	.	.	-0.46	0.90	*	*	F	-0.45	0.52
5	Leu	205	A	A	.	B	.	.	-1.00	0.26	.	*	.	-0.30	0.72
	Met	206	A	A	.	B	.	.	-0.18	0.41	*	*	.	-0.60	0.40
	Leu	207	A	A	.	B	.	.	0.18	0.53	*	*	.	-0.60	0.31
	Lys	208	A	A	.	B	.	.	0.48	0.13	*	*	.	-0.30	0.76
	Val	209	A	A	.	.	.	.	0.48	-0.56	*	*	.	1.09	1.32
10	His	210	A	A	.	.	.	.	1.29	-1.17	.	*	F	1.58	2.68
	Lys	211	A	A	.	.	.	.	1.54	-1.86	*	.	F	1.92	2.24
	Glu	212	A	.	.	.	.	T	1.50	-1.43	.	*	F	2.66	2.98
	Asp	213	.	.	.	.	.	T	1.24	-1.43	.	.	F	3.40	1.63
	Asp	214	.	.	.	.	.	T	1.24	-1.50	*	.	F	3.06	1.26
15	Gly	215	.	.	.	.	.	T	0.39	-0.86	.	.	F	2.57	0.54
	Val	216	.	.	B	B	.	.	-0.32	-0.17	*	.	.	0.98	0.23
	Pro	217	.	.	B	B	.	.	-0.32	0.40	*	.	.	-0.26	0.07
	Val	218	.	.	B	B	.	.	-1.18	0.80	*	.	.	-0.60	0.13
	Ile	219	.	.	B	B	.	.	-1.18	1.01	*	.	.	-0.60	0.13
20	Cys	220	.	.	B	B	.	.	-0.87	0.37	*	.	.	-0.30	0.14
	Gln	221	.	.	B	B	.	.	-0.22	0.44	*	*	.	-0.60	0.26
	Val	222	.	.	B	B	.	.	-0.60	0.23	*	.	.	-0.30	0.58
	Glu	223	.	.	B	B	.	.	-0.60	0.04	*	.	.	-0.15	1.08
	His	224	.	.	B	.	.	.	-0.02	0.11	*	.	.	-0.10	0.46
25	Pro	225	.	.	B	.	.	.	0.30	0.20	.	.	.	-0.10	0.90
	Ala	226	.	.	.	.	.	T	0.30	-0.01	.	*	.	0.90	0.52
	Val	227	.	.	.	.	.	T	0.34	0.39	.	*	.	0.50	0.61
	Thr	228	.	.	.	.	.	T	0.34	0.57	.	*	F	0.15	0.33
	Gly	229	.	.	.	.	.	T	0.07	0.54	.	*	F	0.15	0.56
30	Asn	230	.	.	.	.	.	T	0.28	0.53	.	*	F	0.30	1.09
	Leu	231	.	.	B	B	.	.	0.98	0.29	.	.	F	0.00	1.30
	Gln	232	.	.	B	B	.	.	1.59	-0.20	.	*	F	0.60	2.58
	Thr	233	.	.	B	B	.	.	1.09	0.13	*	.	F	0.00	2.51
	Gln	234	.	.	B	B	.	.	1.43	0.41	.	.	F	-0.30	2.51
35	Arg	235	.	.	B	B	.	.	0.58	-0.27	.	*	F	0.60	2.51
	Tyr	236	.	.	B	B	.	.	1.39	-0.03	.	.	.	0.45	1.29
	Leu	237	.	.	B	B	.	.	1.14	-0.11	*	*	.	0.45	1.29
	Glu	238	.	.	B	B	.	.	1.50	0.24	*	*	.	-0.15	1.03
	Val	239	.	.	B	B	.	.	1.29	0.24	*	*	.	-0.15	1.32
40	Gln	240	.	.	.	B	.	T	1.18	-0.09	*	*	.	0.85	2.47
	Tyr	241	.	.	.	B	.	T	0.57	-0.37	.	*	.	0.85	2.47

	Lys	242	.	.	.	B	.	.	C	1.34	0.27	.	*	F	0.20 2.47
	Pro	243	A	.	.	B	.	.	.	0.46	0.13	.	*	F	0.00 1.94
	Gln	244	.	.	B	B	.	.	.	1.31	0.41	.	*	.	-0.60 0.87
	Val	245	.	.	B	B	.	.	.	0.71	0.06	.	*	.	-0.30 0.75
5	His	246	.	.	B	B	.	.	.	0.64	0.67	.	*	.	-0.60 0.48
	Ile	247	.	.	B	B	.	.	.	0.36	0.73	.	*	.	-0.60 0.40
	Gln	248	.	.	B	B	.	.	.	0.36	1.09	.	*	.	-0.60 0.85
	Met	249	.	.	B	B	.	.	.	-0.46	0.87	.	*	.	-0.60 0.96
	Thr	250	.	.	B	B	.	.	.	0.40	1.06	.	*	.	-0.45 1.13
10	Tyr	251	.	.	B	.	.	T	.	0.09	0.77	.	*	.	-0.05 1.13
	Pro	252	.	.	B	.	.	T	.	0.17	0.80	.	*	.	-0.05 1.13
	Leu	253	.	.	.	.	T	T	.	-0.14	0.87	*	*	.	0.20 0.65
	Gln	254	.	.	B	.	.	T	.	0.57	0.87	*	*	.	0.06 0.60
	Gly	255	.	.	B	.	.	.	.	0.88	0.11	*	.	F	0.57 0.76
15	Leu	256	.	.	B	.	.	.	.	0.78	-0.31	*	.	F	1.58 1.59
	Thr	257	.	.	B	.	.	T	.	0.99	-0.57	*	.	F	2.19 0.91
	Arg	258	.	.	B	.	.	T	.	1.21	-0.97	*	.	F	2.60 1.53
	Glu	259	A	.	.	.	.	T	.	0.40	-0.90	*	.	F	2.34 1.87
	Gly	260	A	.	.	.	.	T	.	0.74	-0.90	*	.	F	2.08 1.07
20	Asp	261	A	A	.	.	.	.	.	0.74	-1.39	*	.	F	1.27 0.95
	Ala	262	A	A	.	.	.	.	.	0.74	-0.70	*	.	F	1.01 0.45
	Leu	263	A	A	.	.	.	.	.	-0.03	-0.21	*	.	.	0.30 0.66
	Glu	264	A	A	.	.	.	.	.	-0.03	-0.07	.	*	.	0.30 0.21
	Leu	265	A	A	.	.	.	.	.	-0.28	-0.07	*	.	.	0.30 0.36
25	Thr	266	A	A	.	.	.	.	.	-1.17	-0.07	*	.	.	0.30 0.44
	Cys	267	A	A	.	.	.	.	.	-0.92	-0.07	*	*	.	0.30 0.18
	Glu	268	A	A	.	.	.	.	.	-0.07	0.36	*	*	.	-0.10' 0.22
	Ala	269	A	A	.	.	.	.	.	-0.28	-0.33	*	*	.	0.70 0.30
	Ile	270	A	A	.	.	.	.	.	0.53	-0.39	.	*	.	0.90 0.86
30	Gly	271	.	A	.	.	T	.	.	0.63	-0.56	.	.	F	1.95 0.86
	Lys	272	.	.	.	.	.	.	C	0.44	-0.13	*	.	F	2.00 1.32
	Pro	273	.	.	.	.	.	.	C	-0.16	0.01	*	.	F	1.20 1.39
	Gln	274	.	.	.	B	.	.	C	-0.42	-0.06	.	.	F	1.40 1.39
	Pro	275	.	.	B	B	.	.	.	0.16	0.16	.	.	F	0.25 0.52
35	Val	276	.	.	B	B	.	.	.	0.21	0.64	.	.	.	-0.40 0.48
	Met	277	.	.	B	B	.	.	.	-0.69	1.13	*	.	.	-0.60 0.29
	Val	278	.	.	B	B	.	.	.	-0.37	1.37	*	*	.	-0.60 0.14
	Thr	279	.	.	B	B	.	.	.	-1.22	0.94	*	*	.	-0.60 0.37
	Trp	280	.	.	B	B	.	.	.	-1.01	0.94	*	*	.	-0.60 0.28
40	Val	281	.	.	B	B	.	.	.	-0.16	0.33	*	*	.	-0.30 0.63
	Arg	282	.	.	B	B	.	.	.	0.44	-0.31	*	*	.	0.30 0.73

5	Val	283	A	.	.	B	.	.	0.70	-0.80	*	*	.	0.75	1.19
	Asp	284	A	.	.	B	.	.	0.80	-1.10	*	*	F	0.90	1.59
	Asp	285	.	A	.	.	T	.	1.09	-1.31	*	*	F	1.30	1.26
	Glu	286	A	A	.	.	.	.	1.91	-0.91	*	*	F	0.90	2.93
	Met	287	A	A	.	.	.	.	1.21	-1.06	*	*	F	0.90	2.39
	Pro	288	A	A	.	.	.	.	1.21	-0.56	.	.	F	0.90	1.45
	Gln	289	A	A	.	B	.	.	0.40	0.09	.	.	.	-0.30	0.62
10	His	290	A	A	.	B	.	.	0.10	0.77	.	.	.	-0.60	0.52
	Ala	291	.	A	B	B	.	.	-0.24	0.54	.	.	.	-0.60	0.45
	Val	292	.	A	B	B	.	.	0.14	0.54	.	.	.	-0.60	0.26
	Leu	293	.	A	B	B	.	.	0.36	0.57	.	.	.	-0.60	0.29
	Ser	294	.	A	.	B	.	C	-0.46	0.47	*	.	F	-0.25	0.46
	Gly	295	.	.	.	.	T	C	-1.12	0.66	*	.	F	0.15	0.51
	Pro	296	.	.	.	.	T	C	-1.42	0.80	*	.	F	0.15	0.54
15	Asn	297	.	.	.	.	T	C	-0.57	0.80	*	.	F	0.15	0.28
	Leu	298	.	.	B	.	T	.	0.24	0.81	*	.	.	-0.20	0.46
	Phe	299	.	.	B	.	.	.	-0.27	0.79	*	.	.	-0.40	0.48
	Ile	300	.	.	B	.	.	.	0.08	1.04	*	.	.	-0.40	0.24
	Asn	301	.	.	B	.	.	.	0.33	1.04	*	.	.	-0.40	0.48
	Asn	302	.	.	B	.	.	.	0.02	0.36	*	.	.	0.39	1.10
	Leu	303	.	.	.	.	.	C	0.83	0.06	*	.	F	1.08	2.27
20	Asn	304	.	.	.	.	T	.	1.53	-0.63	*	.	F	2.52	2.36
	Lys	305	.	.	.	.	T	.	2.08	-0.63	*	.	F	2.86	2.36
	Thr	306	.	.	.	.	T	T	1.77	-0.60	*	.	F	3.40	2.83
	Asp	307	.	.	.	.	T	T	1.52	-0.80	*	*	F	3.06	2.54
	Asn	308	.	.	.	.	T	T	2.44	-0.44	*	*	F	2.42	1.99
	Gly	309	.	.	.	.	T	T	1.78	-0.44	*	*	F	2.08	2.70
	Thr	310	.	.	B	.	.	.	1.73	-0.36	.	*	F	0.99	0.87
30	Tyr	311	.	.	B	.	.	.	1.46	-0.36	.	*	.	0.50	0.93
	Arg	312	.	.	B	.	.	.	1.16	-0.26	.	*	.	0.50	0.95
	Cys	313	.	.	B	.	.	.	1.16	-0.30	.	*	.	0.50	0.88
	Glu	314	.	.	B	.	.	.	0.61	-0.39	.	*	.	0.50	0.91
	Ala	315	A	.	.	.	.	T	0.07	-0.46	.	*	.	0.70	0.32
	Ser	316	A	.	.	.	.	T	-0.03	0.19	.	*	.	0.10	0.45
	Asn	317	A	.	.	.	.	T	-0.10	0.04	.	*	.	0.10	0.26
35	Ile	318	A	.	.	.	.	T	-0.02	0.04	*	*	.	0.10	0.51
	Val	319	A	.	.	.	.	.	-0.06	0.04	*	.	.	0.10	0.38
	Gly	320	A	.	.	.	.	.	0.23	0.16	*	*	.	0.30	0.32
	Lys	321	A	.	.	.	.	.	0.53	0.14	*	*	.	0.50	0.62
	Ala	322	A	.	.	.	.	.	0.29	-0.54	*	*	F	1.90	1.40
	His	323	.	.	B	.	.	T	0.58	-0.43	.	*	F	2.00	2.21

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	Ser	324	.	.	B	.	.	T	.	0.62	-0.24	.	*	.	1.65	1.09
	Asp	325	.	.	B	.	.	T	.	0.72	0.44	.	*	.	0.40	0.89
	Tyr	326	.	.	B	.	.	T	.	-0.18	0.70	.	*	.	0.35	1.03
	Met	327	.	.	B	B	.	.	.	0.17	0.84	.	.	.	-0.40	0.57
5	Leu	328	.	.	B	B	.	.	.	0.20	1.21	.	.	.	-0.60	0.53
	Tyr	329	.	.	B	B	.	.	.	0.29	1.21	.	.	.	-0.60	0.57
	Val	330	.	.	B	B	.	.	.	0.08	0.89	.	.	.	-0.60	0.89
	Tyr	331	.	.	B	.	.	.	.	0.01	0.70	.	.	.	-0.25	1.67
	Asp	332	.	.	B	.	.	.	.	0.30	0.50	*	.	F	-0.10	1.54
10	Pro	333	.	.	B	.	.	T	.	0.22	0.23	.	.	F	0.40	2.99
	Pro	334	.	.	.	.	T	T	.	0.26	0.27	*	.	F	0.80	1.34
	Thr	335	.	.	.	.	T	T	.	0.90	-0.06	*	.	F	1.40	1.24
	Thr	336	.	.	B	.	.	T	.	0.93	0.37	.	.	F	0.40	1.24
	Ile	337	.	.	B	.	.	.	.	0.62	0.37	.	.	F	0.32	1.24
15	Pro	338	.	.	B	.	.	.	.	0.52	0.43	.	.	F	0.14	1.24
	Pro	339	.	.	.	.	.	T	C	0.42	0.43	.	.	F	0.66	1.24
	Pro	340	.	.	.	.	.	T	C	0.42	0.43	.	.	F	0.78	2.55
	Thr	341	.	.	.	.	.	T	C	0.42	0.23	.	.	F	1.20	2.38
	Thr	342	.	.	B	.	.	T	.	1.00	0.29	.	.	F	0.88	2.22
20	Thr	343	.	.	B	B	.	.	.	0.90	0.34	.	.	F	0.36	2.07
	Thr	344	.	.	B	B	.	.	.	0.80	0.40	.	.	F	-0.06	2.07
	Thr	345	.	.	B	B	.	.	.	0.70	0.40	.	.	F	-0.18	2.07
	Thr	346	.	.	B	B	.	.	.	0.70	0.40	.	.	F	-0.30	2.07
	Thr	347	.	.	B	B	.	.	.	0.70	0.40	.	.	F	-0.30	2.07
25	Thr	348	.	.	B	B	.	.	.	0.70	0.40	.	.	F	-0.30	2.07
	Thr	349	.	.	B	B	.	.	.	0.70	0.40	.	.	F	-0.30	2.07
	Thr	350	.	.	B	B	.	.	.	0.12	0.40	.	.	F	-0.30	2.07
	Thr	351	.	.	B	B	.	.	.	-0.38	0.60	.	.	F	-0.30	1.01
	Thr	352	.	.	B	B	.	.	.	-0.38	0.80	.	.	F	-0.45	0.57
30	Thr	353	.	.	B	B	.	.	.	-0.96	0.80	*	.	F	-0.45	0.57
	Ile	354	.	.	B	B	.	.	.	-1.53	1.00	*	.	.	-0.60	0.28
	Leu	355	.	.	B	B	.	.	.	-1.53	1.20	*	.	.	-0.60	0.14
	Thr	356	.	.	B	B	.	.	.	-1.22	1.20	*	.	.	-0.60	0.14
	Ile	357	.	.	B	B	.	.	.	-1.21	0.71	*	*	.	-0.60	0.32
35	Ile	358	.	.	B	B	.	.	.	-0.79	0.41	.	*	.	-0.26	0.53
	Thr	359	.	.	B	B	.	.	.	-0.49	-0.27	.	*	F	1.13	0.71
	Asp	360	.	.	B	.	.	T	.	0.43	-0.26	.	*	F	2.02	1.03
	Ser	361	.	.	.	.	.	T	C	0.36	-0.94	.	*	F	2.86	2.87
	Arg	362	.	.	.	.	T	T	.	0.86	-1.20	.	*	F	3.40	2.54
40	Ala	363	.	.	.	.	T	T	.	1.36	-1.26	.	*	.	2.91	1.95
	Arg	364	.	.	.	.	T	.	.	1.28	-0.83	.	*	.	2.37	1.86

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Ter	365	.	.	.	.	T	.	.	0.89	-0.79	.	*	.	2.03	1.21
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Table XI

	Res Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
5	Met 1	A	.	.	.	.	.	.	0.14	0.06	.	.	.	-0.10	0.89
	Ser 2	A	.	.	.	.	T	.	-0.28	0.01	.	.	.	0.10	0.94
	Ser 3	A	.	.	.	.	T	.	0.16	0.27	.	.	.	0.10	0.60
	Ser 4	A	.	.	.	.	T	.	0.51	-0.16	*	.	.	0.85	1.22
	Ser 5	A	.	.	.	.	T	.	0.09	-0.27	*	.	F	1.00	1.24
10	Leu 6	A	A	.	.	.	.	.	-0.12	0.03	*	.	F	-0.15	0.76
	Lys 7	A	A	.	.	.	.	.	-0.49	0.33	*	.	F	-0.15	0.47
	His 8	A	A	.	.	.	.	.	-0.79	0.51	*	.	.	-0.60	0.19
	Leu 9	A	A	.	.	.	.	.	-1.08	0.74	*	.	.	-0.60	0.23
	Leu 10	A	A	.	.	.	.	.	-1.59	0.56	*	*	.	-0.60	0.11
15	Cys 11	A	A	.	.	.	.	.	-1.08	1.24	*	*	.	-0.60	0.07
	Met 12	A	A	.	.	.	.	.	-1.41	1.13	*	.	.	-0.60	0.11
	Ala 13	A	A	.	.	.	.	.	-2.08	1.36	*	.	.	-0.60	0.14
	Leu 14	A	A	.	.	.	.	.	-1.57	1.46	*	.	.	-0.60	0.23
	Ser 15	A	.	.	B	.	.	.	-1.06	1.27	*	.	.	-0.60	0.31
20	Trp 16	A	.	.	B	.	.	.	-1.09	1.04	*	.	.	-0.60	0.41
	Phe 17	A	.	.	B	.	.	.	-1.38	1.33	*	.	.	-0.60	0.43
	Ser 18	.	.	.	B	.	.	C	-1.09	1.33	*	.	.	-0.40	0.23
	Ser 19	.	.	.	B	.	.	C	-0.62	1.33	*	.	.	-0.40	0.29
	Phe 20	.	.	.	B	.	.	C	-0.32	0.84	.	.	.	-0.40	0.33
25	Ile 21	.	.	.	B	.	.	C	-0.34	0.06	.	.	.	-0.10	0.43
	Ser 22	.	.	.	B	.	.	C	0.06	0.16	*	*	F	0.05	0.46
	Gly 23	.	.	.	.	.	.	C	-0.34	0.16	.	*	F	0.25	0.71
	Glu 24	.	.	.	.	.	.	C	-0.34	0.16	.	*	F	0.25	0.88
	Thr 25	.	.	.	.	.	.	C	-0.46	-0.14	.	*	F	0.85	0.88
30	Ser 26	.	.	.	.	.	.	C	-0.38	0.16	.	*	F	0.25	0.73
	Phe 27	A	.	.	.	.	.	.	-0.08	0.41	*	*	.	-0.40	0.35
	Ser 28	A	.	.	.	.	.	.	-0.03	0.81	*	*	.	-0.40	0.39
	Leu 29	.	.	.	.	.	.	C	-0.73	0.71	*	.	.	-0.20	0.39
	Leu 30	.	.	.	.	.	.	C	-1.12	1.11	.	.	.	-0.20	0.39
35	Asn 31	.	.	.	.	T	T	.	-1.63	1.11	.	.	.	0.20	0.25
	Ser 32	.	.	.	.	T	T	.	-1.14	1.41	*	.	.	0.20	0.25
	Phe 33	.	.	.	.	T	T	.	-1.09	1.16	.	.	.	0.20	0.47
	Phe 34	.	.	B	.	.	T	.	-0.49	1.23	.	.	.	-0.20	0.46
	Leu 35	.	.	.	.	.	.	C	0.02	1.26	.	.	.	-0.20	0.53
40	Pro 36	.	.	.	.	T	.	.	-0.28	1.26	.	.	.	0.00	0.82

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	Tyr	37	.	.	.	.	T	T	.	0.13	0.86	.	*	F	0.67	1.27
	Pro	38	.	.	.	.	T	T	.	0.17	0.07	.	.	F	1.14	3.02
	Ser	39	.	.	.	.	T	T	.	0.20	-0.04	.	*	F	1.91	1.05
	Ser	40	.	.	.	.	T	T	.	0.34	0.10	.	.	F	1.33	0.36
5	Arg	41	.	.	.	B	T	.	.	-0.14	-0.09	.	.	F	1.70	0.12
	Cys	42	.	.	.	B	T	.	.	-0.20	0.27	.	.	.	0.78	0.08
	Cys	43	.	.	.	B	T	.	.	-0.84	0.27	.	*	.	0.61	0.08
	Cys	44	.	.	.	B	T	.	.	-0.54	0.53	.	*	.	0.14	0.03
	Phe	45	.	.	.	B	T	.	.	-0.91	0.93	.	*	.	-0.03	0.10
10	Ser	46	.	.	.	B	T	.	.	-1.32	0.93	.	*	.	-0.20	0.10
	Val	47	.	.	.	B	T	.	.	-1.54	0.74	.	*	.	-0.20	0.25
	Gln	48	.	.	.	B	T	.	.	-1.69	0.86	.	*	.	-0.20	0.20
	Cys	49	.	.	.	B	T	.	.	-1.02	0.76	.	*	.	-0.20	0.12
	Ser	50	.	.	.	B	T	.	.	-0.53	0.37	*	*	.	0.10	0.28
15	Ile	51	.	.	.	B	T	.	.	-0.93	0.16	*	*	.	0.10	0.25
	Leu	52	.	.	.	B	T	.	.	-0.38	0.54	*	*	.	-0.20	0.40
	Asp	53	.	.	.	.	.	T	C	-1.04	0.36	.	.	.	0.30	0.40
	Pro	54	.	.	.	.	T	T	.	-0.38	0.54	*	.	F	0.35	0.30
	Phe	55	.	.	.	.	T	T	.	-0.38	0.26	.	.	.	0.50	0.59
20	Ser	56	.	.	.	.	T	T	.	-0.09	-0.04	*	.	.	1.10	0.48
	Cys	57	.	.	.	.	T	T	.	0.83	0.57	*	*	.	0.20	0.30
	Asn	58	.	.	.	.	T	T	.	0.13	0.14	*	*	.	0.50	0.69
	Ser	59	.	.	.	.	T	T	.	0.13	0.14	*	*	.	0.50	0.44
	Met	60	.	.	.	.	T	T	.	0.54	0.19	*	*	.	0.86	1.28
25	Arg	61	.	.	.	.	.	.	C	0.84	0.53	*	*	.	0.22	0.84
	Phe	62	.	.	.	.	.	.	C	1.51	0.13	*	*	.	0.88	1.08
	Pro	63	.	.	.	.	T	.	.	1.12	0.14	*	*	.	1.29	1.76
	Trp	64	.	.	.	.	T	.	.	1.03	-0.04	.	*	.	2.10	1.15
	Glu	65	A	.	.	.	.	.	.	1.24	0.39	.	*	.	0.89	1.70
30	Asn	66	.	.	.	.	T	.	.	0.74	0.03	.	*	.	1.08	1.40
	Ter	67	.	.	.	.	T	.	.	1.06	0.03	.	.	.	0.87	1.70

Table XII

	Res	Position	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
5	Met	1	.	.	B	.	.	.	.	0.97	-0.71	*	.	.	1.64	1.91
	Ser	2	.	.	B	.	.	T	.	0.76	-0.76	.	.	.	2.07	2.00
	Arg	3	.	.	B	.	.	T	.	0.33	-0.57	.	.	.	2.30	1.55
	Arg	4	.	.	B	.	.	T	.	-0.09	-0.31	.	.	.	1.77	1.29
	Ser	5	.	.	B	.	.	T	.	-0.29	-0.24	.	.	.	1.39	0.79
10	Met	6	.	A	B	.	.	.	.	0.02	-0.13	.	.	.	0.76	0.41
	Leu	7	.	A	B	.	.	.	.	-0.27	0.79	.	.	.	-0.37	0.22
	Leu	8	.	A	B	.	.	.	.	-1.19	1.29	.	.	.	-0.60	0.17
	Ala	9	.	A	B	.	.	.	.	-1.51	1.59	.	.	.	-0.60	0.14
	Trp	10	.	A	B	.	.	.	.	-1.51	1.40	.	.	.	-0.60	0.26
15	Ala	11	.	A	B	.	.	.	.	-1.72	1.10	.	.	.	-0.60	0.42
	Leu	12	.	.	B	.	.	T	.	-1.72	1.10	*	*	.	-0.20	0.34
	Pro	13	.	.	B	.	.	T	.	-0.80	1.29	*	*	.	-0.20	0.27
	Ser	14	.	.	B	.	.	T	.	-1.02	0.37	*	*	.	0.10	0.52
	Leu	15	.	.	B	.	.	T	.	-1.08	0.56	*	*	.	-0.20	0.52
20	Leu	16	.	A	B	.	.	.	.	-1.08	0.30	*	*	.	-0.30	0.33
	Arg	17	.	A	B	.	.	.	.	-0.86	0.37	*	*	.	-0.30	0.25
	Leu	18	.	A	B	.	.	.	.	-0.64	0.49	.	*	.	-0.60	0.31
	Gly	19	.	A	.	.	.	.	C	-0.34	0.20	.	*	.	-0.10	0.65
	Ala	20	.	A	.	.	.	.	C	0.16	-0.49	.	*	.	0.50	0.57
25	Ala	21	.	A	.	.	.	.	C	0.97	0.00	.	*	.	0.65	1.00
	Gln	22	.	A	B	.	.	.	.	0.86	-0.69	.	*	F	1.21	1.75
	Glu	23	.	A	B	.	.	.	.	1.46	-1.11	.	.	F	1.52	2.90
	Thr	24	.	A	.	.	T	.	.	1.21	-1.19	.	.	F	2.23	4.44
	Glu	25	.	A	.	.	T	.	.	1.13	-1.19	.	.	F	2.54	2.59
30	Asp	26	.	.	.	.	T	T	.	1.06	-1.01	.	.	F	3.10	0.80
	Pro	27	.	.	.	.	T	T	.	0.76	-0.44	.	.	F	2.49	0.30
	Ala	28	.	.	.	.	T	T	.	0.54	-0.54	.	.	.	2.33	0.23
	Cys	29	.	.	.	.	T	T	.	-0.03	-0.11	.	.	.	1.72	0.21
	Cys	30	.	.	B	B	.	.	.	-0.89	0.57	.	.	.	-0.29	0.10
35	Ser	31	.	.	B	B	.	.	.	-1.10	0.79	.	.	.	-0.60	0.07
	Pro	32	.	.	B	B	.	.	.	-0.78	0.71	.	.	.	-0.60	0.20
	Ile	33	.	.	B	B	.	.	.	-0.19	0.14	.	.	.	0.00	0.75
	Val	34	.	.	B	.	.	T	.	0.48	-0.03	.	*	F	1.45	0.90
	Pro	35	.	.	B	.	.	T	.	0.86	-0.41	.	*	F	1.90	1.01
40	Arg	36	.	.	.	.	T	T	.	1.20	0.07	.	*	F	2.00	1.51

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5	Asn	37	.	.	.	.	.	T	C	0.82	-0.61	*	*	F	3.00	4.07
	Glu	38	.	A	.	.	.	T	.	0.90	-0.76	*	*	F	2.50	2.66
	Trp	39	.	A	.	.	.	T	.	1.17	-0.50	*	*	F	2.20	1.12
	Lys	40	.	A	.	.	.	.	C	1.08	0.00	*	*	.	1.10	0.70
	Ala	41	.	A	.	.	.	.	C	0.97	-0.01	*	*	.	0.80	0.54
10	Leu	42	.	A	.	.	.	.	C	0.30	-0.01	*	.	.	0.50	0.90
	Ala	43	A	A	.	.	.	.	.	-0.29	-0.36	*	*	.	0.30	0.24
	Ser	44	A	A	.	.	.	.	.	0.00	0.14	*	.	.	-0.30	0.24
	Glu	45	A	A	.	.	.	.	.	-0.08	0.04	*	.	.	-0.30	0.50
	Cys	46	A	A	.	.	.	.	.	-0.30	-0.14	*	.	.	0.30	0.68
15	Ala	47	A	A	.	.	.	.	.	0.21	0.04	.	.	.	-0.30	0.42
	Gln	48	.	A	B	.	.	.	.	-0.01	0.04	.	.	.	-0.30	0.32
	His	49	.	A	B	.	.	.	.	0.08	0.73	*	*	.	-0.60	0.50
	Leu	50	.	A	B	.	.	.	.	-0.73	0.59	*	*	.	-0.60	0.76
	Ser	51	.	A	B	.	.	.	.	0.04	0.77	*	*	.	-0.60	0.36
20	Leu	52	.	.	B	.	.	.	.	0.39	0.37	*	*	.	-0.10	0.52
	Pro	53	.	.	B	B	.	.	.	-0.47	0.63	*	*	.	-0.60	0.99
	Leu	54	.	.	B	B	.	.	.	-1.29	0.59	.	*	.	-0.60	0.55
	Arg	55	.	.	B	B	.	.	.	-1.33	0.84	.	*	.	-0.60	0.49
	Tyr	56	.	.	B	B	.	.	.	-1.33	0.80	.	*	.	-0.60	0.24
25	Val	57	.	.	B	B	.	.	.	-0.56	0.76	.	*	.	-0.60	0.39
	Val	58	.	.	B	B	.	.	.	-0.66	0.57	.	*	.	-0.60	0.27
	Val	59	.	.	B	B	.	.	.	-0.43	1.06	.	*	.	-0.60	0.25
	Ser	60	.	.	B	.	.	.	.	-0.89	0.80	.	.	.	-0.40	0.34
	His	61	.	.	B	.	.	.	.	-0.94	0.59	.	.	.	-0.40	0.45
30	Thr	62	.	.	B	.	.	.	.	-0.39	0.33	.	.	.	-0.10	0.81
	Ala	63	.	.	.	.	.	T	.	-0.20	0.07	.	.	F	0.45	0.81
	Gly	64	.	.	.	.	.	T	T	0.66	0.26	.	.	F	0.65	0.32
	Ser	65	.	.	.	.	.	T	T	0.64	0.16	.	.	F	0.65	0.35
	Ser	66	.	.	.	.	.	T	T	0.47	0.16	.	.	F	0.65	0.51
35	Cys	67	.	.	.	.	.	T	T	0.19	0.09	.	.	F	0.65	0.79
	Asn	68	.	.	.	.	.	T	.	0.48	0.16	.	.	F	0.45	0.60
	Thr	69	.	.	.	.	.	.	C	0.16	0.16	.	.	F	0.25	0.60
	Pro	70	.	.	.	.	.	T	T	0.46	0.34	.	.	F	0.65	0.60
	Ala	71	.	.	.	.	.	T	T	0.76	0.17	.	*	F	0.65	0.64
40	Ser	72	.	.	B	.	.	.	T	1.42	0.17	.	*	F	0.25	0.77
	Cys	73	.	.	B	.	.	.	T	0.83	0.09	*	*	F	0.25	0.86
	Gln	74	.	A	B	.	.	.	.	1.26	0.16	.	*	F	-0.15	0.86
	Gln	75	.	A	B	.	.	.	.	1.47	-0.34	*	*	F	0.60	1.26
	Gln	76	.	A	B	.	.	.	.	1.20	-0.33	*	*	F	0.60	3.79
	Ala	77	.	A	B	.	.	.	.	1.50	-0.26	*	.	F	0.60	1.62

	Arg	78	.	A	B	.	.	.	.	2.13	-0.26	*	.	F	0.60	1.62
	Asn	79	.	A	B	.	.	.	.	1.89	-0.16	*	.	.	0.45	1.28
	Val	80	.	A	B	.	.	.	.	1.86	0.20	*	.	.	-0.15	1.98
	Gln	81	.	A	B	.	.	.	.	1.26	0.20	*	*	.	-0.15	1.37
5	His	82	.	A	B	.	.	.	.	1.89	0.81	*	*	.	-0.60	0.85
	Tyr	83	.	.	B	.	.	.	.	1.47	0.41	*	.	.	-0.25	2.28
	His	84	.	.	B	.	.	.	.	0.66	0.26	.	.	.	0.05	1.90
	Met	85	.	.	B	B	.	.	.	1.17	0.54	.	.	.	-0.45	1.15
	Lys	86	.	.	B	B	.	.	.	0.88	0.47	.	.	.	-0.60	0.73
10	Thr	87	.	.	.	B	T	.	.	0.24	0.63	.	.	.	-0.20	0.56
	Leu	88	.	.	.	B	T	.	.	0.49	0.70	.	*	.	-0.20	0.30
	Gly	89	.	.	.	B	T	.	.	-0.33	0.09	.	.	.	0.10	0.25
	Trp	90	.	.	B	B	.	.	.	-0.08	0.73	.	.	.	-0.60	0.13
	Cys	91	.	.	B	B	.	.	.	-0.37	0.67	.	.	.	-0.60	0.16
15	Asp	92	.	.	B	.	.	T	.	-0.06	0.74	.	*	.	-0.20	0.25
	Val	93	.	.	B	.	.	T	.	0.06	0.71	*	.	.	-0.20	0.38
	Gly	94	.	.	B	.	.	T	.	-0.41	0.59	.	*	.	-0.20	0.61
	Tyr	95	.	.	B	.	.	T	.	-1.01	0.70	.	*	.	-0.20	0.30
	Asn	96	.	.	B	B	.	.	.	-0.69	1.39	.	*	.	-0.60	0.29
20	Phe	97	.	.	B	B	.	.	.	-0.69	1.17	.	*	.	-0.60	0.29
	Leu	98	.	.	B	B	.	.	.	0.17	0.74	.	*	.	-0.60	0.32
	Ile	99	.	.	B	B	.	.	.	0.17	-0.01	.	.	.	0.30	0.33
	Gly	100	.	.	B	.	.	T	.	-0.40	0.01	.	.	.	0.10	0.38
	Glu	101	.	.	B	.	.	T	.	-1.26	-0.09	.	.	F	0.85	0.38
25	Asp	102	.	.	.	.	T	T	.	-0.80	-0.13	.	.	F	1.25	0.40
	Gly	103	.	.	.	.	.	T	C	0.01	-0.06	.	.	F	1.05	0.63
	Leu	104	.	.	B	.	.	.	.	0.56	-0.49	*	*	.	0.50	0.63
	Val	105	.	.	B	.	.	.	.	1.01	-0.06	*	*	.	0.78	0.37
	Tyr	106	.	.	B	.	.	.	.	0.67	-0.06	*	*	.	1.06	0.74
30	Glu	107	.	.	B	.	.	.	.	0.38	-0.06	*	.	F	1.49	0.89
	Gly	108	.	.	.	.	T	T	.	0.72	0.17	.	.	F	1.92	1.25
	Arg	109	.	.	.	.	T	T	.	0.83	-0.07	.	*	F	2.80	1.29
	Gly	110	.	.	.	.	T	T	.	1.38	-0.04	.	.	F	2.37	0.64
	Trp	111	.	.	.	.	T	T	.	1.28	0.44	.	*	.	1.04	0.94
35	Asn	112	.	.	.	.	.	.	C	0.69	0.44	.	.	.	0.36	0.47
	Phe	113	.	.	B	.	.	.	.	1.00	0.94	.	.	.	-0.12	0.48
	Thr	114	.	.	.	.	.	.	C	0.59	1.01	.	.	.	-0.20	0.63
	Gly	115	.	.	.	.	.	.	C	0.59	0.49	.	*	.	-0.20	0.52
	Ala	116	.	.	.	.	.	.	C	0.84	0.51	.	*	.	-0.20	0.60
40	His	117	.	.	.	.	.	T	C	0.03	0.23	.	.	.	0.30	0.56
	Ser	118	.	.	.	.	.	T	C	0.44	0.43	.	.	.	0.00	0.47

	Gly	119	.	.	.	.	T	C	0.76	0.91	.	.	.	0.00	0.49
	His	120	.	.	.	.	T	C	0.89	0.81	.	.	.	0.00	0.58
	Leu	121	.	.	.	.	T	.	0.88	0.74	.	.	.	0.00	0.67
	Trp	122	.	.	.	.	.	C	0.61	0.97	.	.	.	-0.20	0.67
5	Asn	123	.	.	.	.	.	C	0.02	0.93	.	.	.	-0.20	0.66
	Pro	124	.	.	B	B	.	.	0.02	1.11	.	*	.	-0.60	0.56
	Met	125	.	.	.	B	T	.	-0.83	0.86	*	*	.	-0.20	0.52
	Ser	126	.	.	B	B	.	.	-0.32	0.63	.	*	.	-0.60	0.23
	Ile	127	.	.	B	B	.	.	-0.73	0.61	.	*	.	-0.60	0.20
10	Gly	128	.	.	B	B	.	.	-1.33	0.97	.	*	.	-0.60	0.17
	Ile	129	.	.	B	B	.	.	-1.47	0.97	.	*	.	-0.60	0.13
	Ser	130	.	.	B	B	.	.	-0.87	1.01	.	*	.	-0.60	0.18
	Phe	131	.	.	B	B	.	.	-0.81	0.73	.	*	.	-0.60	0.29
	Met	132	.	.	B	.	T	.	-0.52	1.06	.	*	.	-0.20	0.66
15	Gly	133	.	.	.	.	T	T	-0.18	0.99	*	*	.	0.20	0.48
	Asn	134	.	.	.	.	T	T	0.82	0.60	*	*	.	0.20	0.93
	Tyr	135	.	.	.	.	T	T	0.27	-0.19	*	*	.	1.25	1.85
	Met	136	.	.	.	.	T	.	0.76	-0.16	*	*	.	1.31	1.39
	Asp	137	.	.	.	.	T	.	1.04	-0.16	*	*	.	1.57	1.33
20	Arg	138	.	.	B	.	.	.	1.18	-0.07	*	*	F	1.58	1.23
	Val	139	.	.	B	.	T	.	1.18	-0.40	*	.	F	2.04	1.92
	Pro	140	.	.	B	.	T	.	0.83	-0.61	.	.	F	2.60	1.99
	Thr	141	.	.	.	.	T	C	0.54	-0.11	.	*	F	2.24	1.03
	Pro	142	.	.	B	.	T	.	0.66	0.57	.	*	F	0.73	0.97
25	Gln	143	.	A	B	.	.	.	-0.04	-0.07	*	*	F	1.12	1.23
	Ala	144	.	A	B	.	.	.	0.22	0.00	*	.	.	0.56	0.86
	Ile	145	.	A	B	.	.	.	0.43	0.01	*	.	.	-0.30	0.56
	Arg	146	.	A	B	.	.	.	0.40	-0.01	*	.	.	0.30	0.56
	Ala	147	.	A	B	.	.	.	-0.20	0.01	*	.	.	-0.30	0.55
30	Ala	148	.	A	B	.	.	.	-1.01	0.20	*	.	.	-0.30	0.65
	Gln	149	.	A	B	.	.	.	-1.01	0.20	*	*	.	-0.30	0.27
	Gly	150	.	A	B	.	.	.	-0.79	0.70	*	*	.	-0.60	0.27
	Leu	151	.	A	B	.	.	.	-1.24	0.77	*	.	.	-0.60	0.14
	Leu	152	.	A	B	.	.	.	-1.51	0.70	.	.	.	-0.60	0.08
35	Ala	153	.	A	B	.	.	.	-1.51	0.94	.	.	.	-0.60	0.06
	Cys	154	.	A	B	.	.	.	-1.51	1.01	.	.	.	-0.60	0.08
	Gly	155	.	A	B	.	.	.	-1.51	0.73	.	.	.	-0.60	0.16
	Val	156	.	A	B	.	.	.	-1.29	0.47	.	.	.	-0.60	0.16
	Ala	157	.	A	B	.	.	.	-1.29	0.47	*	*	.	-0.60	0.29
40	Gln	158	.	A	B	.	.	.	-0.59	0.59	*	*	.	-0.60	0.25
	Gly	159	.	A	B	.	.	.	-0.22	0.16	*	*	.	-0.30	0.65

	Ala	160	.	A	B	.	.	.	0.12	-0.10	*	*	F	0.45	0.86
	Leu	161	.	A	B	.	.	.	0.73	-0.20	*	*	F	0.45	0.80
	Arg	162	.	.	B	.	.	T	0.47	0.16	*	*	F	0.40	1.26
	Ser	163	.	.	B	.	.	T	-0.34	0.37	*	*	F	0.25	0.93
5	Asn	164	.	.	B	.	.	T	0.04	0.56	.	*	F	-0.05	0.93
	Tyr	165	.	.	B	.	.	T	0.29	-0.13	.	*	.	0.70	0.95
	Val	166	.	.	B	B	.	.	1.07	0.30	.	*	.	-0.12	0.70
	Leu	167	.	.	B	B	.	.	1.07	0.41	*	*	.	-0.24	0.59
	Lys	168	.	.	B	B	.	.	1.37	0.01	*	.	F	0.39	0.74
10	Gly	169	.	.	B	.	.	.	0.51	-0.74	*	*	F	1.82	1.67
	His	170	.	.	B	B	.	.	0.76	-0.74	*	.	F	1.80	1.50
	Arg	171	.	.	B	B	.	.	1.72	-1.03	*	.	F	1.62	1.30
	Asp	172	.	.	B	B	.	.	2.22	-1.03	*	.	F	1.44	2.57
	Val	173	.	.	B	B	.	.	1.37	-0.97	*	.	F	1.26	2.72
15	Gln	174	.	.	B	B	.	.	1.41	-0.79	*	.	F	1.08	1.15
	Arg	175	.	.	B	B	.	.	1.23	-0.40	*	.	F	0.57	0.92
	Thr	176	.	.	B	B	.	.	0.78	0.03	*	.	F	0.24	1.92
	Leu	177	.	.	.	B	.	C	0.78	-0.19	*	.	F	1.16	1.10
	Ser	178	.	.	.	.	T	C	1.63	-0.19	*	.	F	1.53	0.90
20	Pro	179	.	.	.	.	T	C	0.82	0.21	*	.	F	1.20	1.08
	Gly	180	.	.	.	.	T	T	0.47	0.41	*	.	F	0.98	1.08
	Asn	181	.	.	.	.	T	T	0.74	0.49	.	.	F	0.86	1.26
	Gln	182	.	A	B	.	.	.	0.74	0.60	*	.	F	-0.06	1.11
	Leu	183	.	A	B	.	.	.	0.16	0.86	*	.	.	-0.48	0.93
25	Tyr	184	.	A	B	.	.	.	0.37	1.11	*	.	.	-0.60	0.40
	His	185	.	A	B	.	.	.	0.71	1.11	*	.	.	-0.60	0.40
	Leu	186	.	A	B	.	.	.	0.42	1.11	*	.	.	-0.60	0.79
	Ile	187	.	A	B	.	.	.	0.21	1.34	*	.	.	-0.60	0.53
	Gln	188	.	A	B	.	.	.	0.99	1.01	*	.	.	-0.60	0.60
30	Asn	189	.	A	.	.	T	.	0.99	1.01	.	*	.	-0.20	0.99
	Trp	190	.	.	.	.	T	C	1.13	1.09	.	*	.	0.15	2.21
	Pro	191	.	.	.	.	T	C	1.64	0.40	.	*	.	0.45	2.50
	His	192	.	.	.	.	T	T	2.32	0.39	.	*	.	0.86	2.09
	Tyr	193	.	.	.	.	T	T	1.93	0.41	.	.	.	0.77	3.07
35	Arg	194	.	.	.	.	T	.	1.54	-0.07	.	.	.	1.68	2.54
	Ser	195	.	.	.	.	.	C	1.44	-0.07	.	.	.	1.69	2.38
	Pro	196	.	.	.	.	T	.	1.27	-0.14	.	*	.	2.10	1.94

Table XIII

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
1	HAOAB64	203484 11/17/98	pSport1	11	2609	1	2609	599	599	29	1	30	31	529
2	HOHCH55	203484 11/17/98	pCMV/Sport 2.0	12	2499	1	2499	221	221	30	1	23	24	494
2	HOHCH55	203484 11/17/98	pCMV/Sport 2.0	23	2522	1	2522	230	230	41	1	23	24	469
3	HTLEW81	203484 11/17/98	Uni-ZAP XR	13	1339	1	1339	37	37	31	1	27	28	148
4	HARAO44	203484 11/17/98	pBluescript SK-	14	1389	1	1389	125	125	32	1	21	22	332
5	HDPCL05	203484 11/17/98	pCMV/Sport 3.0	15	2295	1	2295	58	58	33	1	16	17	639
5	HDPCL05	203484 11/17/98	pCMV/Sport 3.0	24	1344	1	1344	52	52	42	1	16	17	127
6	HDPW68	203484 11/17/98	pCMV/Sport 3.0	16	1748	1	1748	40	40	34	1	18	19	467
7	HOHBY69	203484 11/17/98	pCMV/Sport 2.0	17	4995	1	4995	82	82	35	1	22	23	1189



Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
7	HOHBY69	203484 11/17/98	pCMV Sport 2.0	25	4631	1	4631	84	84	43	1	22	23	1034
8	HCDDP40	203484 11/17/98	Uni-ZAP XR	18	726	1	726	32	32	36	1	21	22	196
9	HTTDB46	203484 11/17/98	Uni-ZAP XR	19	3059	1	3059	55	55	37	1	17	18	318
9	HTTDB46	203484 11/17/98	Uni-ZAP XR	26	2008	215	2008	153	153	44	1	17	18	461
10	HUSAQ05	203484 11/17/98	Lambda ZAP II	20	1699	1	1699	115	115	38	1	19	20	375
10	HUSAQ05	203484 11/17/98	Lambda ZAP II	27	1654	1	1654	115	115	45	1	19	20	383
11	HOUDJ81	203484 11/17/98	Uni-ZAP XR	21	1520	1	1520	26	26	39	1	44	45	364
11	HOUDJ81	203484 11/17/98	Uni-ZAP XR	28	1508	19	1508	454	454	46	1	30	31	229
12	HPWCM76	203484 11/17/98	Uni-ZAP XR	22	807	1	807	582	582	40	1	23	24	66

Table XIII summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table XIII and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X (where X may be any of the polynucleotide sequences disclosed in the sequence listing) and the translated SEQ ID NO:Y (where Y may be any of the polypeptide sequences disclosed in the sequence listing) are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below.

5 For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used, for

10 example, to generate antibodies which bind specifically to proteins containing the polypeptides and the secreted proteins encoded by the cDNA clones identified in Table XIII.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or

15 deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in

20 an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a

25 human cDNA of the invention deposited with the ATCC, as set forth in Table XIII. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein

encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X,  
5 SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are allelic variants, orthologs, and/or species  
10 homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or a deposited clone, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by  
15 making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a  
20 combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or  
25 leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a

polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using  
5 techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the secreted protein.

The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or a cDNA contained in ATCC deposit Z. The present invention also provides a polypeptide comprising, or  
10 alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y and/or a polypeptide encoded by the cDNA contained in ATCC deposit Z. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of the polypeptide sequence of SEQ ID NO:Y and/or a polypeptide sequence encoded by the cDNA contained in ATCC deposit Z are also encompassed by the invention.

#### 15 **Signal Sequences**

The present invention also encompasses mature forms of the polypeptide having the polypeptide sequence of SEQ ID NO:Y and/or the polypeptide sequence encoded by the cDNA in a deposited clone. Polynucleotides encoding the mature forms (such as, for example, the polynucleotide sequence in SEQ ID NO:X and/or the polynucleotide  
20 sequence contained in the cDNA of a deposited clone) are also encompassed by the invention. According to the signal hypothesis, proteins secreted by mammalian cells have a signal or secretary leader sequence which is cleaved from the mature protein once export of the growing protein chain across the rough endoplasmic reticulum has been initiated. Most mammalian cells and even insect cells cleave secreted proteins with the same  
25 specificity. However, in some cases, cleavage of a secreted protein is not entirely uniform, which results in two or more mature species of the protein. Further, it has long been known that cleavage specificity of a secreted protein is ultimately determined by the

primary structure of the complete protein, that is, it is inherent in the amino acid sequence of the polypeptide.

Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, 5 Virus Res. 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, Nucleic Acids Res. 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of 10 known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, supra.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., Protein 15 Engineering 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results shown in Table XIII.

20 As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., + or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of 25 the signal sequence from a secreted protein is not entirely uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. Nonetheless, the present invention provides the mature protein produced by expression of the polynucleotide sequence of SEQ ID NO:X and/or the polynucleotide sequence contained in the cDNA of a deposited clone, in a mammalian cell (e.g., COS cells, as described below). These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

#### **Polynucleotide and Polypeptide Variants**

The present invention is directed to variants of the polynucleotide sequence disclosed in SEQ ID NO:X, the complementary strand thereto, and/or the cDNA sequence contained in a deposited clone.

The present invention also encompasses variants of the polypeptide sequence disclosed in SEQ ID NO:Y and/or encoded by a deposited clone.

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

The present invention is also directed to nucleic acid molecules which comprise, or alternatively consist of, a nucleotide sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for example, the nucleotide coding sequence in SEQ ID NO:X or the complementary strand thereto, the nucleotide coding sequence contained in a deposited cDNA clone or the complementary strand thereto, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding the polypeptide encoded by the cDNA contained in a deposited clone, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein).

Polynucleotides which hybridize to these nucleic acid molecules under stringent hybridization conditions or lower stringency conditions are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

The present invention is also directed to polypeptides which comprise, or  
5 alternatively consist of, an amino acid sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% identical to, for example, the polypeptide sequence shown in SEQ ID NO:Y, the polypeptide sequence encoded by the cDNA contained in a deposited clone, and/or polypeptide fragments of any of these polypeptides (e.g., those fragments described herein).

10 By a nucleic acid having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the nucleic acid is identical to the reference sequence except that the nucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other  
15 words, to obtain a nucleic acid having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence shown in Table XIII, the ORF (open  
20 reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a  
25 query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245(1990)). In a sequence alignment the query and subject sequences are both DNA sequences. An



RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff  
5 Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations  
10 of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the  
15 FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the  
20 query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases  
25 at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another

example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, an amino acid sequences shown in Table XIII (SEQ ID NO:Y) or to the amino acid sequence encoded by cDNA contained in a deposited clone can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245(1990)). In a sequence alignment the query and subject sequences are either both nucleotide sequences

or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are:

Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap  
5 Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal  
10 truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence.

15 Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which  
20 are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-  
25 terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the

percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level and are included in the present invention. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological

function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie et al., Science 247:1306-1310 (1990), wherein the

authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where

the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as, for example, an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of the present invention having an amino acid sequence which contains at least one amino acid substitution, but not more than 50 amino acid substitutions, even more preferably, not more than 40 amino acid substitutions, still more preferably, not more than 30 amino acid substitutions, and still even more preferably, not more than 20 amino acid substitutions. Of course, in order of ever-increasing preference, it is highly preferable for a peptide or polypeptide to have an amino acid sequence which comprises the amino acid sequence of the present invention, which contains at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 amino acid substitutions. In specific embodiments, the number of additions, substitutions, and/or deletions in the amino acid sequence of the present invention or fragments thereof (e.g., the mature form and/or other fragments described herein), is 1-5, 5-10, 5-25, 5-50, 10-50 or 50-150, conservative amino acid substitutions are preferable.

**Polynucleotide and Polypeptide Fragments**

The present invention is also directed to polynucleotide fragments of the polynucleotides of the invention.

5        In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence which: is a portion of that contained in a deposited clone, or encoding the polypeptide encoded by the cDNA in a deposited clone; is a portion of that shown in SEQ ID NO:X or the complementary strand thereto, or is a portion of a polynucleotide sequence encoding the polypeptide of SEQ ID NO:Y. The  
10        nucleotide fragments of the invention are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt, at least about 50 nt, at least about 75 nt, or at least about 150 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in a deposited clone or  
15        the nucleotide sequence shown in SEQ ID NO:X. In this context "about" includes the particularly recited value, a value larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. These nucleotide fragments have uses that include, but are not limited to, as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

20        Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250,  
25        1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, or 2001 to the end of SEQ ID NO:X, or the complementary strand thereto, or the cDNA contained in a deposited clone. In this context "about" includes the particularly recited



ranges, and ranges larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity. More preferably, these polynucleotides can be used as probes or primers as discussed herein. Polynucleotides which hybridize to these nucleic acid  
5 molecules under stringent hybridization conditions or lower stringency conditions are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

In the present invention, a "polypeptide fragment" refers to an amino acid sequence which is a portion of that contained in SEQ ID NO:Y or encoded by the cDNA contained in a deposited clone. Protein (polypeptide) fragments may be "free-standing," or  
10 comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide  
15 fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges or values, and ranges or values larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes. Polynucleotides encoding these polypeptides are also encompassed by the invention.

20 Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form.  
25 Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotides encoding these polypeptide fragments are also preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha  
5 amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotides encoding these domains are also contemplated.

Other preferred polypeptide fragments are biologically active fragments.

10 Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity. Polynucleotides encoding these polypeptide fragments are also encompassed by the invention.

15 Preferably, the polynucleotide fragments of the invention encode a polypeptide which demonstrates a functional activity. By a polypeptide demonstrating a "functional activity" is meant, a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) polypeptide of invention protein. Such functional activities include, but are not limited to, biological activity, antigenicity [ability  
20 to bind (or compete with a polypeptide of the invention for binding) to an antibody to the polypeptide of the invention], immunogenicity (ability to generate antibody which binds to a polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide of the invention.

The functional activity of polypeptides of the invention, and fragments, variants  
25 derivatives, and analogs thereof, can be assayed by various methods.

For example, in one embodiment where one is assaying for the ability to bind or compete with full-length polypeptide of the invention for binding to an antibody of the polypeptide of the invention, various immunoassays known in the art can be used,

including but not limited to, competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

In another embodiment, where a ligand for a polypeptide of the invention identified, or the ability of a polypeptide fragment, variant or derivative of the invention to multimerize is being evaluated, binding can be assayed, e.g., by means well-known in the art, such as, for example, reducing and non-reducing gel chromatography, protein affinity chromatography, and affinity blotting. See generally, Phizicky, E., et al., 1995, Microbiol. Rev. 59:94-123. In another embodiment, physiological correlates of binding of a polypeptide of the invention to its substrates (signal transduction) can be assayed.

In addition, assays described herein (see Examples) and otherwise known in the art may routinely be applied to measure the ability of polypeptides of the invention and fragments, variants derivatives and analogs thereof to elicit related biological activity related to that of the polypeptide of the invention (either in vitro or in vivo). Other methods will be known to the skilled artisan and are within the scope of the invention.

### **Epitopes & Antibodies**

The present invention is also directed to polypeptide fragments comprising, or alternatively consisting of, an epitope of the polypeptide sequence shown in SEQ ID

NO:Y, or the polypeptide sequence encoded by the cDNA contained in a deposited clone. Polynucleotides encoding these epitopes (such as, for example, the sequence disclosed in SEQ ID NO:X) are also encompassed by the invention, as is the nucleotide sequences of the complementary strand of the polynucleotides encoding these epitopes. And

5 polynucleotides which hybridize to the complementary strand under stringent hybridization conditions or lower stringency conditions.

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as  
10 the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983).)

Fragments which function as epitopes may be produced by any conventional  
15 means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, and most preferably between about 15 to about 30 amino acids.  
20 Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues in length. Antigenic epitopes are useful, for example, to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe et al., Science 219:660-666 (1983).)

25 Similarly, immunogenic epitopes can be used, for example, to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle et al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the

secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise  
5 antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

Epitope-bearing polypeptides of the present invention may be used to induce antibodies according to methods well known in the art including, but not limited to, *in vivo* immunization, *in vitro* immunization, and phage display methods. See, e.g., Sutcliffe et  
10 al., supra; Wilson et al., supra, and Bittle et al., J. Gen. Virol., 66:2347-2354 (1985). If *in vivo* immunization is used, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine residues may be coupled to a carrier using a linker such as  
15 -maleimidobenzoyl- N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carriers using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100  $\mu$ gs of peptide or carrier protein and Freund's adjuvant. Several booster injections  
20 may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies  
25 according to methods well known in the art.

As one of skill in the art will appreciate, and discussed above, the polypeptides of the present invention comprising an immunogenic or antigenic epitope can be fused to heterologous polypeptide sequences. For example, the polypeptides of the present

invention may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, any combination thereof including both entire domains and portions thereof) resulting in chimeric polypeptides. These fusion proteins facilitate purification, and show an increased half-life *in vivo*. This has been shown, *e.g.*,  
5 for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. See, *e.g.*, EPA 0,394,827; Traunecker et al., *Nature*, 331:84-86 (1988). Fusion proteins that have a disulfide-linked dimeric structure due to the IgG portion can also be more efficient in binding and neutralizing other molecules than monomeric  
10 polypeptides or fragments thereof alone. See, *e.g.*, Fountoulakis et al., *J. Biochem.*, 270:3958-3964 (1995). Nucleic acids encoding the above epitopes can also be recombined with a gene of interest as an epitope tag to aid in detection and purification of the expressed polypeptide.

Additional fusion proteins of the invention may be generated through the  
15 techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling may be employed to modulate the activities of polypeptides corresponding to SEQ ID NO:Y thereby effectively generating agonists and antagonists of the polypeptides. See, generally, U.S. Patent Nos. 5,605,793, 5,811,238, 5,830,721, 5,834,252, and 5,837,458, and Patten, P.A., et al., *Curr.*  
20 *Opinion Biotechnol.* 8:724-33 (1997); Harayama, S., *Trends Biotechnol.* 16(2):76-82 (1998); Hansson, L.O., et al., *J. Mol. Biol.* 287:265-76 (1999); and Lorenzo, M. M. and Blasco, R., *Biotechniques* 24(2):308-13 (1998) (each of these patents and publications are hereby incorporated by reference). In one embodiment, alteration of polynucleotides corresponding to SEQ ID NO:X and corresponding polypeptides may be achieved by DNA  
25 shuffling. DNA shuffling involves the assembly of two or more DNA segments into a desired molecule corresponding to SEQ ID NO:X polynucleotides of the invention by homologous, or site-specific, recombination. In another embodiment, polynucleotides corresponding to SEQ ID NO:X and corresponding polypeptides may be altered by being

subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of coding polynucleotide corresponding to SEQ ID NO:X, or the polypeptide encoded thereby may be recombined with one or more  
5 components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.

### Antibodies

The present invention further relates to antibodies and T-cell antigen receptors  
10 (TCR) which specifically bind the polypeptides of the present invention. The antibodies of the present invention include IgG (including IgG1, IgG2, IgG3, and IgG4), IgA (including IgA1 and IgA2), IgD, IgE, or IgM, and IgY. As used herein, the term "antibody" (Ab) is meant to include whole antibodies, including single-chain whole antibodies, and antigen-binding fragments thereof. Most preferably the antibodies are human antigen binding  
15 antibody fragments of the present invention and include, but are not limited to, Fab, Fab' and F(ab')<sub>2</sub>, Fd, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a V<sub>L</sub> or V<sub>H</sub> domain. The antibodies may be from any animal origin including birds and mammals. Preferably, the antibodies are human, murine, rabbit, goat, guinea pig, camel, horse, or chicken.

20 Antigen-binding antibody fragments, including single-chain antibodies, may comprise the variable region(s) alone or in combination with the entire or partial of the following: hinge region, CH1, CH2, and CH3 domains. Also included in the invention are any combinations of variable region(s) and hinge region, CH1, CH2, and CH3 domains. The present invention further includes monoclonal, polyclonal, chimeric, humanized, and  
25 human monoclonal and human polyclonal antibodies which specifically bind the polypeptides of the present invention. The present invention further includes antibodies which are anti-idiotypic to the antibodies of the present invention.

The antibodies of the present invention may be monospecific, bispecific, trispecific

or of greater multispecificity. Multispecific antibodies may be specific for different epitopes of a polypeptide of the present invention or may be specific for both a polypeptide of the present invention as well as for heterologous compositions, such as a heterologous polypeptide or solid support material. *See, e.g.*, WO 93/17715; WO 92/08802; WO 91/00360; WO 92/05793; Tutt, et al., J. Immunol. 147:60-69 (1991); US Patents 5,573,920, 4,474,893, 5,601,819, 4,714,681, 4,925,648; Kostelny et al., J. Immunol. 148:1547-1553 (1992).

Antibodies of the present invention may be described or specified in terms of the epitope(s) or portion(s) of a polypeptide of the present invention which are recognized or specifically bound by the antibody. The epitope(s) or polypeptide portion(s) may be specified as described herein, *e.g.*, by N-terminal and C-terminal positions, by size in contiguous amino acid residues, or listed in the Tables and Figures. Antibodies which specifically bind any epitope or polypeptide of the present invention may also be excluded. Therefore, the present invention includes antibodies that specifically bind polypeptides of the present invention, and allows for the exclusion of the same.

Antibodies of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies that do not bind any other analog, ortholog, or homolog of the polypeptides of the present invention are included. Antibodies that do not bind polypeptides with less than 95%, less than 90%, less than 85%, less than 80%, less than 75%, less than 70%, less than 65%, less than 60%, less than 55%, and less than 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. Further included in the present invention are antibodies which only bind polypeptides encoded by polynucleotides which hybridize to a polynucleotide of the present invention under stringent hybridization conditions (as described herein). Antibodies of the present invention may also be described or specified in terms of their binding affinity. Preferred binding affinities include those with a dissociation constant or  $K_d$  less than  $5 \times 10^{-6}M$ ,  $10^{-6}M$ ,  $5 \times 10^{-7}M$ ,  $10^{-7}M$ ,  $5 \times 10^{-8}M$ ,  $10^{-8}M$ ,  $5 \times 10^{-9}M$ ,  $10^{-9}M$ ,  $5 \times 10^{-10}M$ ,  $10^{-10}M$ ,  $5 \times 10^{-11}M$ ,  $10^{-11}M$ .



$^{11}\text{M}$ ,  $5 \times 10^{-12}\text{M}$ ,  $10^{-12}\text{M}$ ,  $5 \times 10^{-13}\text{M}$ ,  $10^{-13}\text{M}$ ,  $5 \times 10^{-14}\text{M}$ ,  $10^{-14}\text{M}$ ,  $5 \times 10^{-15}\text{M}$ , and  $10^{-15}\text{M}$ .

Antibodies of the present invention have uses that include, but are not limited to, methods known in the art to purify, detect, and target the polypeptides of the present invention including both *in vitro* and *in vivo* diagnostic and therapeutic methods. For example, the antibodies have use in immunoassays for qualitatively and quantitatively measuring levels of the polypeptides of the present invention in biological samples. See, e.g., Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988) (incorporated by reference in the entirety).

The antibodies of the present invention may be used either alone or in combination with other compositions. The antibodies may further be recombinantly fused to a heterologous polypeptide at the N- or C-terminus or chemically conjugated (including covalently and non-covalently conjugations) to polypeptides or other compositions. For example, antibodies of the present invention may be recombinantly fused or conjugated to molecules useful as labels in detection assays and effector molecules such as heterologous polypeptides, drugs, or toxins. See, e.g., WO 92/08495; WO 91/14438; WO 89/12624; US Patent 5,314,995; and EP 0 396 387.

The antibodies of the present invention may be prepared by any suitable method known in the art. For example, a polypeptide of the present invention or an antigenic fragment thereof can be administered to an animal in order to induce the production of sera containing polyclonal antibodies. The term "monoclonal antibody" is not limited to antibodies produced through hybridoma technology. The term "monoclonal antibody" refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced. Monoclonal antibodies can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display technology.

Hybridoma techniques include those known in the art and taught in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: MONOCLONAL ANTIBODIES AND T-CELL

HYBRIDOMAS 563-681 (Elsevier, N.Y., 1981) (said references incorporated by reference in their entireties). Fab and F(ab')<sub>2</sub> fragments may be produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')<sub>2</sub> fragments).

5           Alternatively, antibodies of the present invention can be produced through the application of recombinant DNA and phage display technology or through synthetic chemistry using methods known in the art. For example, the antibodies of the present invention can be prepared using various phage display methods known in the art. In phage display methods, functional antibody domains are displayed on the surface of a phage  
10   particle which carries polynucleotide sequences encoding them. Phage with a desired binding property are selected from a repertoire or combinatorial antibody library (e.g. human or murine) by selecting directly with antigen, typically antigen bound or captured to a solid surface or bead. Phage used in these methods are typically filamentous phage including fd and M13 with Fab, Fv or disulfide stabilized Fv antibody domains  
15   recombinantly fused to either the phage gene III or gene VIII protein. Examples of phage display methods that can be used to make the antibodies of the present invention include those disclosed in Brinkman et al., J. Immunol. Methods 182:41-50 (1995); Ames et al., J. Immunol. Methods 184:177-186 (1995); Kettleborough et al., Eur. J. Immunol. 24:952-958 (1994); Persic et al., Gene 187 9-18 (1997); Burton et al., Advances in Immunology  
20   57:191-280 (1994); PCT/GB91/01134; WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and US Patents 5,698,426, 5,223,409, 5,403,484, 5,580,717, 5,427,908, 5,750,753, 5,821,047, 5,571,698, 5,427,908, 5,516,637, 5,780,225, 5,658,727 and 5,733,743 (said references incorporated by reference in their entireties).

25           As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host including mammalian cells, insect cells, plant cells, yeast, and bacteria. For

example, techniques to recombinantly produce Fab, Fab' and F(ab')<sub>2</sub> fragments can also be employed using methods known in the art such as those disclosed in WO 92/22324; Mullinax et al., BioTechniques 12(6):864-869 (1992); and Sawai et al., AJRI 34:26-34 (1995); and Better et al., Science 240:1041-1043 (1988) (said references incorporated by  
5 reference in their entirety).

Examples of techniques which can be used to produce single-chain Fvs and antibodies include those described in U.S. Patents 4,946,778 and 5,258,498; Huston et al., Methods in Enzymology 203:46-88 (1991); Shu, L. et al., PNAS 90:7995-7999 (1993); and Skerra et al., Science 240:1038-1040 (1988). For some uses, including *in vivo* use of  
10 antibodies in humans and *in vitro* detection assays, it may be preferable to use chimeric, humanized, or human antibodies. Methods for producing chimeric antibodies are known in the art. See e.g., Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Gillies et al., (1989) J. Immunol. Methods 125:191-202; and US Patent 5,807,715. Antibodies can be humanized using a variety of techniques including CDR-grafting (EP 0  
15 239 400; WO 91/09967; US Patent 5,530,101; and 5,585,089), veneering or resurfacing (EP 0 592 106; EP 0 519 596; Padlan E.A., Molecular Immunology 28(4/5):489-498 (1991); Studnicka et al., Protein Engineering 7(6):805-814 (1994); Roguska. et al., PNAS 91:969-973 (1994)), and chain shuffling (US Patent 5,565,332). Human antibodies can be made by a variety of methods known in the art including phage display methods described  
20 above. See also, US Patents 4,444,887, 4,716,111, 5,545,806, and 5,814,318; and WO 98/46645, WO 98/50433, WO 98/24893, WO 98/16654, WO 96/34096, WO 96/33735, and WO 91/10741 (said references incorporated by reference in their entirety).

Further included in the present invention are antibodies recombinantly fused or chemically conjugated (including both covalently and non-covalently conjugations) to a  
25 polypeptide of the present invention. The antibodies may be specific for antigens other than polypeptides of the present invention. For example, antibodies may be used to target the polypeptides of the present invention to particular cell types, either *in vitro* or *in vivo*, by fusing or conjugating the polypeptides of the present invention to antibodies specific for

particular cell surface receptors. Antibodies fused or conjugated to the polypeptides of the present invention may also be used in *in vitro* immunoassays and purification methods using methods known in the art. See e.g., Harbor et al. *supra* and WO 93/21232; EP 0 439 095; Naramura et al., Immunol. Lett. 39:91-99 (1994); US Patent 5,474,981; Gillies et al.,  
5 PNAS 89:1428-1432 (1992); Fell et al., J. Immunol. 146:2446-2452 (1991) (said references incorporated by reference in their entireties).

The present invention further includes compositions comprising the polypeptides of the present invention fused or conjugated to antibody domains other than the variable regions. For example, the polypeptides of the present invention may be fused or  
10 conjugated to an antibody Fc region, or portion thereof. The antibody portion fused to a polypeptide of the present invention may comprise the hinge region, CH1 domain, CH2 domain, and CH3 domain or any combination of whole domains or portions thereof. The polypeptides of the present invention may be fused or conjugated to the above antibody portions to increase the *in vivo* half life of the polypeptides or for use in immunoassays  
15 using methods known in the art. The polypeptides may also be fused or conjugated to the above antibody portions to form multimers. For example, Fc portions fused to the polypeptides of the present invention can form dimers through disulfide bonding between the Fc portions. Higher multimeric forms can be made by fusing the polypeptides to portions of IgA and IgM. Methods for fusing or conjugating the polypeptides of the present  
20 invention to antibody portions are known in the art. See e.g., US Patents 5,336,603, 5,622,929, 5,359,046, 5,349,053, 5,447,851, 5,112,946; EP 0 307 434, EP 0 367 166; WO 96/04388, WO 91/06570; Ashkenazi et al., PNAS 88:10535-10539 (1991); Zheng et al., J. Immunol. 154:5590-5600 (1995); and Vil et al., PNAS 89:11337-11341 (1992) (said references incorporated by reference in their entireties).

25 The invention further relates to antibodies which act as agonists or antagonists of the polypeptides of the present invention. For example, the present invention includes antibodies which disrupt the receptor/ligand interactions with the polypeptides of the invention either partially or fully. Included are both receptor-specific antibodies and

ligand-specific antibodies. Included are receptor-specific antibodies which do not prevent ligand binding but prevent receptor activation. Receptor activation (i.e., signaling) may be determined by techniques described herein or otherwise known in the art. Also included are receptor-specific antibodies which both prevent ligand binding and receptor activation.

5 Likewise, included are neutralizing antibodies which bind the ligand and prevent binding of the ligand to the receptor, as well as antibodies which bind the ligand, thereby preventing receptor activation, but do not prevent the ligand from binding the receptor. Further included are antibodies which activate the receptor. These antibodies may act as agonists for either all or less than all of the biological activities affected by ligand-

10 mediated receptor activation. The antibodies may be specified as agonists or antagonists for biological activities comprising specific activities disclosed herein. The above antibody agonists can be made using methods known in the art. See e.g., WO 96/40281; US Patent 5,811,097; Deng et al., *Blood* 92(6):1981-1988 (1998); Chen, et al., *Cancer Res.* 58(16):3668-3678 (1998); Harrop et al., *J. Immunol.* 161(4):1786-1794 (1998); Zhu et al.,

15 *Cancer Res.* 58(15):3209-3214 (1998); Yoon, et al., *J. Immunol.* 160(7):3170-3179 (1998); Prat et al., *J. Cell. Sci.* 111(Pt2):237-247 (1998); Pitard et al., *J. Immunol. Methods* 205(2):177-190 (1997); Liautard et al., *Cytokine* 9(4):233-241 (1997); Carlson et al., *J. Biol. Chem.* 272(17):11295-11301 (1997); Taryman et al., *Neuron* 14(4):755-762 (1995); Muller et al., *Structure* 6(9):1153-1167 (1998); Bartunek et al., *Cytokine* 8(1):14-20 (1996)

20 (said references incorporated by reference in their entireties).

As discussed above, antibodies to the polypeptides of the invention can, in turn, be utilized to generate anti-idiotypic antibodies that "mimic" polypeptides of the invention using techniques well known to those skilled in the art. (See, e.g., Greenspan & Bona, *FASEB J.* 7(5):437-444; (1989) and Nissinoff, *J. Immunol.* 147(8):2429-2438 (1991)).

25 For example, antibodies which bind to and competitively inhibit polypeptide multimerization and/or binding of a polypeptide of the invention to ligand can be used to generate anti-idiotypes that "mimic" the polypeptide multimerization and/or binding domain and, as a consequence, bind to and neutralize polypeptide and/or its ligand. Such

neutralizing anti-idiotypes or Fab fragments of such anti-idiotypes can be used in therapeutic regimens to neutralize polypeptide ligand. For example, such anti-idiotypic antibodies can be used to bind a polypeptide of the invention and/or to bind its ligands/receptors, and thereby block its biological activity.

5           The invention further relates to a diagnostic kit for use in screening serum containing antibodies specific against proliferative and/or cancerous polynucleotides and polypeptides. Such a kit may include a substantially isolated polypeptide antigen comprising an epitope which is specifically immunoreactive with at least one anti-polypeptide antigen antibody. Such a kit also includes means for detecting the binding of  
10   said antibody to the antigen. In specific embodiments, the kit may include a recombinantly produced or chemically synthesized polypeptide antigen. The polypeptide antigen of the kit may also be attached to a solid support.

          In a more specific embodiment the detecting means of the above-described kit includes a solid support to which said polypeptide antigen is attached. Such a kit may also  
15   include a non-attached reporter-labelled anti-human antibody. In this embodiment, binding of the antibody to the polypeptide antigen can be detected by binding of the said reporter-labelled antibody.

          The invention further includes a method of detecting proliferative and/or cancerous disorders and conditions in a test subject. This detection method includes reacting serum  
20   from a test subject (e.g. one in which proliferative and/or cancerous cells or tissues may be present) with a substantially isolated polypeptide and/or polynucleotide antigen, and examining the antigen for the presence of bound antibody. In a specific embodiment, the method includes a polypeptide antigen attached to a solid support, and the serum is reacted with the support. Subsequently, the support is reacted with a reporter labelled anti-human  
25   antibody. The solid support is then examined for the presence of reporter-labelled antibody.

          Additionally, the invention includes a proliferative condition vaccine composition. The composition includes a substantially isolated polypeptide and/or polynucleotide

antigen, where the antigen includes an epitope which is specifically immunoreactive with at least antibody specific for the epitope. The peptide and/or polynucleotide antigen may be produced according to methods known in the art, including recombinant expression or chemical synthesis. The peptide antigen is preferably present in a pharmacologically effective dose in a pharmaceutically acceptable carrier.

Further, the invention includes a monoclonal antibody that is specifically immunoreactive with polypeptide and/or polynucleotide epitopes. The invention includes a substantially isolated preparation of polyclonal antibodies specifically immunoreactive with polynucleotides and/or polypeptides of the present invention. In a more specific embodiment, such polyclonal antibodies are prepared by affinity chromatography, in addition to, other methods known in the art.

In another embodiment, the invention includes a method for producing antibodies to polypeptide and/or polynucleotide antigens. The method includes administering to a test subject a substantially isolated polypeptide and/or polynucleotide antigen, where the antigen includes an epitope which is specifically immunoreactive with at least one anti-polypeptide and/or polynucleotide antibody. The antigen is administered in an amount sufficient to produce an immune response in the subject.

In an additional embodiment, the invention includes a diagnostic kit for use in screening serum containing antigens of the polypeptide of the invention. The diagnostic kit includes a substantially isolated antibody specifically immunoreactive with polypeptide or polynucleotide antigens, and means for detecting the binding of the polynucleotide or polypeptide antigen to the antibody. In one embodiment, the antibody is attached to a solid support. In a specific embodiment, the antibody may be a monoclonal antibody. The detecting means of the kit may include a second, labelled monoclonal antibody. Alternatively, or in addition, the detecting means may include a labelled, competing antigen.

In one diagnostic configuration, test serum is reacted with a solid phase reagent having a surface-bound antigen obtained by the methods of the present invention. After

binding with specific antigen antibody to the reagent and removing unbound serum components by washing, the reagent is reacted with reporter-labelled anti-human antibody to bind reporter to the reagent in proportion to the amount of bound anti-antigen antibody on the solid support. The reagent is again washed to remove unbound labelled antibody, and the amount of reporter associated with the reagent is determined. Typically, the reporter is an enzyme which is detected by incubating the solid phase in the presence of a suitable fluorometric or colorimetric substrate (Sigma, St. Louis, MO).

The solid surface reagent in the above assay is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plate or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or covalent attachment of the protein, typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

Thus, the invention provides an assay system or kit for carrying out this diagnostic method. The kit generally includes a support with surface-bound recombinant antigens, and a reporter-labelled anti-human antibody for detecting surface-bound anti-antigen antibody.

## **Fusion Proteins**

Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.



Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

5           Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate  
10           purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

          Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of  
15           immunoglobulins (IgA, IgE, IgG, IgM) or portions thereof (CH1, CH2, CH3, and any combination thereof, including both entire domains and portions thereof), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions  
20           of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

25           Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved

pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have  
5 been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In  
10 preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for  
15 purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

20

### **Vectors, Host Cells, and Protein Production**

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant  
25 techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then  
5 transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will  
10 further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

15 As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella  
20 typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9,  
25 available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available

from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, 5 electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant 10 cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

15 Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells.

20 Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is 25 removed with high efficiency from any protein after translation in all eukaryotic cells.

While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or replace endogenous genetic material (e.g., coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with the polynucleotides of the invention, and which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous polynucleotide sequences via homologous recombination (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; International Publication No. WO 96/29411, published September 26, 1996; International Publication No. WO 94/12650, published August 4, 1994; Koller et al., *Proc. Natl. Acad. Sci. USA* 86:8932-8935 (1989); and Zijlstra et al., *Nature* 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entirety).

In addition, polypeptides of the invention can be chemically synthesized using techniques known in the art (e.g., see Creighton, 1983, *Proteins: Structures and Molecular Principles*, W.H. Freeman & Co., N.Y., and Hunkapiller et al., *Nature*, 310:105-111 (1984)). For example, a polypeptide corresponding to a fragment of a polypeptide sequence of the invention can be synthesized by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the polypeptide sequence. Non-classical amino acids include, but are not limited to, to the D-isomers of the common amino acids, 2,4-diaminobutyric acid,  $\alpha$ -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid,  $\gamma$ -Abu,  $\epsilon$ -Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine,  $\beta$ -alanine, fluoro-amino acids, designer amino acids such as  $\beta$ -methyl amino acids,  $\alpha$ -methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the amino

acid can be D (dextrorotary) or L (levorotary).

The invention encompasses polypeptides which are differentially modified during or after translation, *e.g.*, by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH<sub>4</sub>; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; etc.

Additional post-translational modifications encompassed by the invention include, for example, *e.g.*, N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of procaryotic host cell expression. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein.

Also provided by the invention are chemically modified derivatives of the polypeptides of the invention which may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent NO: 4,179,337). The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between about 1 kDa and about 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some

molecules will weigh more, some less, than the stated molecular weight) for ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein or analog).

The polyethylene glycol molecules (or other chemical moieties) should be attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art, e.g., EP 0 401 384, herein incorporated by reference (coupling PEG to G-CSF), see also Malik et al., Exp. Hematol. 20:1028-1035 (1992) (reporting pegylation of GM-CSF using tresyl chloride). For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as, a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residues; those having a free carboxyl group may include aspartic acid residues glutamic acid residues and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecules. Preferred for therapeutic purposes is attachment at an amino group, such as attachment at the N-terminus or lysine group.

One may specifically desire proteins chemically modified at the N-terminus. Using polyethylene glycol as an illustration of the present composition, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (polypeptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective proteins chemically modified at the

N-terminus modification may be accomplished by reductive alkylation which exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus  
5 with a carbonyl group containing polymer is achieved.

The polypeptides of the invention may be in monomers or multimers (i.e., dimers, trimers, tetramers and higher multimers). Accordingly, the present invention relates to monomers and multimers of the polypeptides of the invention, their preparation, and compositions (preferably, *Therapeutics*) containing them. In specific embodiments, the  
10 polypeptides of the invention are monomers, dimers, trimers or tetramers. In additional embodiments, the multimers of the invention are at least dimers, at least trimers, or at least tetramers.

Multimers encompassed by the invention may be homomers or heteromers. As used herein, the term homomer, refers to a multimer containing only polypeptides  
15 corresponding to the amino acid sequence of SEQ ID NO:Y or encoded by the cDNA contained in a deposited clone (including fragments, variants, splice variants, and fusion proteins, corresponding to these polypeptides as described herein). These homomers may contain polypeptides having identical or different amino acid sequences. In a specific embodiment, a homomer of the invention is a multimer containing only polypeptides  
20 having an identical amino acid sequence. In another specific embodiment, a homomer of the invention is a multimer containing polypeptides having different amino acid sequences. In specific embodiments, the multimer of the invention is a homodimer (*e.g.*, containing polypeptides having identical or different amino acid sequences) or a homotrimer (*e.g.*, containing polypeptides having identical and/or different amino acid sequences). In  
25 additional embodiments, the homomeric multimer of the invention is at least a homodimer, at least a homotrimer, or at least a homotetramer.

As used herein, the term heteromer refers to a multimer containing one or more heterologous polypeptides (*i.e.*, polypeptides of different proteins) in addition to the



polypeptides of the invention. In a specific embodiment, the multimer of the invention is a heterodimer, a heterotrimer, or a heterotetramer. In additional embodiments, the heteromeric multimer of the invention is at least a heterodimer, at least a heterotrimer, or at least a heterotetramer.

5           Multimers of the invention may be the result of hydrophobic, hydrophilic, ionic and/or covalent associations and/or may be indirectly linked, by for example, liposome formation. Thus, in one embodiment, multimers of the invention, such as, for example, homodimers or homotrimers, are formed when polypeptides of the invention contact one another in solution. In another embodiment, heteromultimers of the invention, such as, for  
10           example, heterotrimers or heterotetramers, are formed when polypeptides of the invention contact antibodies to the polypeptides of the invention (including antibodies to the heterologous polypeptide sequence in a fusion protein of the invention) in solution. In other embodiments, multimers of the invention are formed by covalent associations with and/or between the polypeptides of the invention. Such covalent associations may involve  
15           one or more amino acid residues contained in the polypeptide sequence ( e.g., that recited in the sequence listing, or contained in the polypeptide encoded by a deposited clone). In one instance, the covalent associations are cross-linking between cysteine residues located within the polypeptide sequences which interact in the native (i.e., naturally occurring) polypeptide. In another instance, the covalent associations are the consequence of  
20           chemical or recombinant manipulation. Alternatively, such covalent associations may involve one or more amino acid residues contained in the heterologous polypeptide sequence in a fusion protein of the invention.

          In one example, covalent associations are between the heterologous sequence contained in a fusion protein of the invention (see, e.g., US Patent Number 5,478,925). In  
25           a specific example, the covalent associations are between the heterologous sequence contained in an Fc fusion protein of the invention (as described herein). In another specific example, covalent associations of fusion proteins of the invention are between heterologous polypeptide sequence from another protein that is capable of forming

covalently associated multimers, such as for example, osteoprotegerin (see, e.g., International Publication NO: WO 98/49305, the contents of which are herein incorporated by reference in its entirety). In another embodiment, two or more polypeptides of the invention are joined through peptide linkers. Examples include those peptide linkers  
5 described in U.S. Pat. No. 5,073,627 (hereby incorporated by reference). Proteins comprising multiple polypeptides of the invention separated by peptide linkers may be produced using conventional recombinant DNA technology.

Another method for preparing multimer polypeptides of the invention involves use of polypeptides of the invention fused to a leucine zipper or isoleucine zipper polypeptide  
10 sequence. Leucine zipper and isoleucine zipper domains are polypeptides that promote multimerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., Science 240:1759, (1988)), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize.  
15 Examples of leucine zipper domains suitable for producing soluble multimeric proteins of the invention are those described in PCT application WO 94/10308, hereby incorporated by reference. Recombinant fusion proteins comprising a polypeptide of the invention fused to a polypeptide sequence that dimerizes or trimerizes in solution are expressed in suitable host cells, and the resulting soluble multimeric fusion protein is recovered from  
20 the culture supernatant using techniques known in the art.

Trimeric polypeptides of the invention may offer the advantage of enhanced biological activity. Preferred leucine zipper moieties and isoleucine moieties are those that preferentially form trimers. One example is a leucine zipper derived from lung surfactant protein D (SPD), as described in Hoppe et al. (FEBS Letters 344:191, (1994)) and in U.S.  
25 patent application Ser. No. 08/446,922, hereby incorporated by reference. Other peptides derived from naturally occurring trimeric proteins may be employed in preparing trimeric polypeptides of the invention.

In another example, proteins of the invention are associated by interactions between Flag® polypeptide sequence contained in fusion proteins of the invention containing Flag® polypeptide sequence. In a further embodiment, associations proteins of the invention are associated by interactions between heterologous polypeptide sequence  
5 contained in Flag® fusion proteins of the invention and anti-Flag® antibody.

The multimers of the invention may be generated using chemical techniques known in the art. For example, polypeptides desired to be contained in the multimers of the invention may be chemically cross-linked using linker molecules and linker molecule length optimization techniques known in the art (see, e.g., US Patent Number 5,478,925,  
10 which is herein incorporated by reference in its entirety). Additionally, multimers of the invention may be generated using techniques known in the art to form one or more inter-molecule cross-links between the cysteine residues located within the sequence of the polypeptides desired to be contained in the multimer (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Further, polypeptides  
15 of the invention may be routinely modified by the addition of cysteine or biotin to the C terminus or N-terminus of the polypeptide and techniques known in the art may be applied to generate multimers containing one or more of these modified polypeptides (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).  
Additionally, techniques known in the art may be applied to generate liposomes containing  
20 the polypeptide components desired to be contained in the multimer of the invention (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

Alternatively, multimers of the invention may be generated using genetic engineering techniques known in the art. In one embodiment, polypeptides contained in  
25 multimers of the invention are produced recombinantly using fusion protein technology described herein or otherwise known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In a specific embodiment, polynucleotides coding for a homodimer of the invention are generated by ligating a

polynucleotide sequence encoding a polypeptide of the invention to a sequence encoding a linker polypeptide and then further to a synthetic polynucleotide encoding the translated product of the polypeptide in the reverse orientation from the original C-terminus to the N-terminus (lacking the leader sequence) (see, e.g., US Patent Number 5,478,925, which is  
5 herein incorporated by reference in its entirety). In another embodiment, recombinant techniques described herein or otherwise known in the art are applied to generate recombinant polypeptides of the invention which contain a transmembrane domain (or hydrophobic or signal peptide) and which can be incorporated by membrane reconstitution techniques into liposomes (see, e.g., US Patent Number 5,478,925, which is herein  
10 incorporated by reference in its entirety).

#### **Uses of the Polynucleotides**

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known  
15 techniques.

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each polynucleotide of the present invention can  
20 be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell  
25 hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day

using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA  
5 libraries.

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human  
10 Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved  
15 within gene families, thus increasing the chance of cross hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage analysis establishes coinheritance between a chromosomal location and presentation of a particular  
20 disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library) .) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

25 Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined. First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the

presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a  
5 polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or  
10 mutation) can be used as a diagnostic or prognostic marker.

Thus, the invention also provides a diagnostic method useful during diagnosis of a disorder, involving measuring the expression level of polynucleotides of the present invention in cells or body fluid from an individual and comparing the measured gene expression level with a standard level of polynucleotide expression level, whereby an  
15 increase or decrease in the gene expression level compared to the standard is indicative of a disorder.

In still another embodiment, the invention includes a kit for analyzing samples for the presence of proliferative and/or cancerous polynucleotides derived from a test subject. In a general embodiment, the kit includes at least one polynucleotide probe containing a  
20 nucleotide sequence that will specifically hybridize with a polynucleotide of the present invention and a suitable container. In a specific embodiment, the kit includes two polynucleotide probes defining an internal region of the polynucleotide of the present invention, where each probe has one strand containing a 31' mer-end internal to the region. In a further embodiment, the probes may be useful as primers for polymerase chain  
25 reaction amplification.

Where a diagnosis of a disorder, has already been made according to conventional methods, the present invention is useful as a prognostic indicator, whereby patients exhibiting enhanced or depressed polynucleotide of the present invention expression will

experience a worse clinical outcome relative to patients expressing the gene at a level nearer the standard level.

By "measuring the expression level of polynucleotide of the present invention" is intended qualitatively or quantitatively measuring or estimating the level of the polypeptide of the present invention or the level of the mRNA encoding the polypeptide in a first biological sample either directly (e.g., by determining or estimating absolute protein level or mRNA level) or relatively (e.g., by comparing to the polypeptide level or mRNA level in a second biological sample). Preferably, the polypeptide level or mRNA level in the first biological sample is measured or estimated and compared to a standard polypeptide level or mRNA level, the standard being taken from a second biological sample obtained from an individual not having the disorder or being determined by averaging levels from a population of individuals not having a disorder. As will be appreciated in the art, once a standard polypeptide level or mRNA level is known, it can be used repeatedly as a standard for comparison.

By "biological sample" is intended any biological sample obtained from an individual, body fluid, cell line, tissue culture, or other source which contains the polypeptide of the present invention or mRNA. As indicated, biological samples include body fluids (such as semen, lymph, sera, plasma, urine, synovial fluid and spinal fluid) which contain the polypeptide of the present invention, and other tissue sources found to express the polypeptide of the present invention. Methods for obtaining tissue biopsies and body fluids from mammals are well known in the art. Where the biological sample is to include mRNA, a tissue biopsy is the preferred source.

The method(s) provided above may preferably be applied in a diagnostic method and/or kits in which polynucleotides and/or polypeptides are attached to a solid support. In one exemplary method, the support may be a "gene chip" or a "biological chip" as described in US Patents 5,837,832, 5,874,219, and 5,856,174. Further, such a gene chip with polynucleotides of the present invention attached may be used to identify polymorphisms between the polynucleotide sequences, with polynucleotides isolated from

a test subject. The knowledge of such polymorphisms (i.e. their location, as well as, their existence) would be beneficial in identifying disease loci for many disorders, including cancerous diseases and conditions. Such a method is described in US Patents 5,858,659 and 5,856,104. The US Patents referenced supra are hereby incorporated by reference in  
5 their entirety herein.

The present invention encompasses polynucleotides of the present invention that are chemically synthesized, or reproduced as peptide nucleic acids (PNA), or according to other methods known in the art. The use of PNAs would serve as the preferred form if the polynucleotides are incorporated onto a solid support, or gene chip. For the purposes of the  
10 present invention, a peptide nucleic acid (PNA) is a polyamide type of DNA analog and the monomeric units for adenine, guanine, thymine and cytosine are available commercially (Perceptive Biosystems). Certain components of DNA, such as phosphorus, phosphorus oxides, or deoxyribose derivatives, are not present in PNAs. As disclosed by P. E. Nielsen, M. Egholm, R. H. Berg and O. Buchardt, Science 254, 1497 (1991); and M.  
15 Egholm, O. Buchardt, L.Christensen, C. Behrens, S. M. Freier, D. A. Driver, R. H. Berg, S. K. Kim, B. Norden, and P. E. Nielsen, Nature 365, 666 (1993), PNAs bind specifically and tightly to complementary DNA strands and are not degraded by nucleases. In fact, PNA binds more strongly to DNA than DNA itself does. This is probably because there is no electrostatic repulsion between the two strands, and also the polyamide backbone is  
20 more flexible. Because of this, PNA/DNA duplexes bind under a wider range of stringency conditions than DNA/DNA duplexes, making it easier to perform multiplex hybridization. Smaller probes can be used than with DNA due to the strong binding. In addition, it is more likely that single base mismatches can be determined with PNA/DNA hybridization because a single mismatch in a PNA/DNA 15-mer lowers the melting point ( $T_{sub.m}$ ) by  
25  $8^{\circ}$ - $20^{\circ}$  C, vs.  $4^{\circ}$ - $16^{\circ}$  C for the DNA/DNA 15-mer duplex. Also, the absence of charge groups in PNA means that hybridization can be done at low ionic strengths and reduce possible interference by salt during the analysis.



The present invention is useful for detecting cancer in mammals. In particular the invention is useful during diagnosis of pathological cell proliferative neoplasias which include, but are not limited to: acute myelogenous leukemias including acute monocytic leukemia, acute myeloblastic leukemia, acute promyelocytic leukemia, acute  
5 myelomonocytic leukemia, acute erythroleukemia, acute megakaryocytic leukemia, and acute undifferentiated leukemia, etc.; and chronic myelogenous leukemias including chronic myelomonocytic leukemia, chronic granulocytic leukemia, etc. Preferred mammals include monkeys, apes, cats, dogs, cows, pigs, horses, rabbits and humans. Particularly preferred are humans.

10 Pathological cell proliferative disorders are often associated with inappropriate activation of proto-oncogenes. (Germann, E. P. et al., "The Etiology of Acute Leukemia: Molecular Genetics and Viral Oncology," in Neoplastic Diseases of the Blood, Vol 1., Wiernik, P. H. et al. eds., 161-182 (1985)). Neoplasias are now believed to result from the  
15 qualitative alteration of a normal cellular gene product, or from the quantitative modification of gene expression by insertion into the chromosome of a viral sequence, by chromosomal translocation of a gene to a more actively transcribed region, or by some other mechanism. (Germann et al., supra) It is likely that mutated or altered expression of specific genes is involved in the pathogenesis of some leukemias, among other tissues and cell types. (Germann et al., supra) Indeed, the human counterparts of the oncogenes  
20 involved in some animal neoplasias have been amplified or translocated in some cases of human leukemia and carcinoma. (Germann et al., supra)

For example, c-myc expression is highly amplified in the non-lymphocytic leukemia cell line HL-60. When HL-60 cells are chemically induced to stop proliferation, the level of c-myc is found to be downregulated. (International Publication Number WO 91/15580)  
25 However, it has been shown that exposure of HL-60 cells to a DNA construct that is complementary to the 5' end of c-myc or c-myb blocks translation of the corresponding mRNAs which downregulates expression of the c-myc or c-myb proteins and causes arrest of cell proliferation and differentiation of the treated cells. (International Publication

Number WO 91/15580; Wickstrom et al., Proc. Natl. Acad. Sci. 85:1028 (1988); Anfossi et al., Proc. Natl. Acad. Sci. 86:3379 (1989)). However, the skilled artisan would appreciate the present invention's usefulness would not be limited to treatment of proliferative disorders of hematopoietic cells and tissues, in light of the numerous cells and  
5 cell types of varying origins which are known to exhibit proliferative phenotypes.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Antisense techniques are discussed, for example, in Okano, J. Neurochem. 56: 560 (1991); "Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca  
10 Raton, FL (1988). Triple helix formation is discussed in, for instance Lee et al., Nucleic Acids Research 6: 3073 (1979); Cooney et al., Science 241: 456 (1988); and Dervan et al., Science 251: 1360 (1991). Both methods rely on binding of the polynucleotide to a complementary DNA or RNA. For these techniques, preferred polynucleotides are usually oligonucleotides 20 to 40 bases in length and complementary to either the region of the  
15 gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991) ) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from  
20 DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal  
25 of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal

is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of  
5 restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the  
10 present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique,  
15 individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as  
20 disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, synovial fluid, amniotic fluid, breast milk, lymph, pulmonary sputum or surfactant, urine, fecal matter, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify  
25 individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to

the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

#### **Uses of the Polypeptides**

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell . Biol. 105:3087-3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and technetium (99mTc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example,  $^{131}\text{I}$ ,  $^{112}\text{In}$ ,  $^{99\text{m}}\text{Tc}$ ), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of  $^{99\text{m}}\text{Tc}$ . The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments," (Chapter 13 in *Tumor Imaging: The Radiochemical Detection of Cancer*, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder. With respect to cancer, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical

symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Moreover, polypeptides of the present invention can be used to treat disease. For  
5 example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B, SOD, catalase, DNA repair proteins), to inhibit the activity of a polypeptide (e.g., an oncogene or tumor suppressor), to activate the activity of a polypeptide (e.g., by binding to a  
10 receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth inhibition, enhancement of the immune response to proliferative cells or tissues).

Similarly, antibodies directed to a polypeptide of the present invention can also be  
15 used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as  
20 molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

25

**Gene Therapy Methods**

Another aspect of the present invention is to gene therapy methods for treating disorders, diseases and conditions. The gene therapy methods relate to the introduction of nucleic acid (DNA, RNA and antisense DNA or RNA) sequences into an animal to achieve  
5 expression of a polypeptide of the present invention. This method requires a polynucleotide which codes for a polypeptide of the invention that operatively linked to a promoter and any other genetic elements necessary for the expression of the polypeptide by the target tissue. Such gene therapy and delivery techniques are known in the art, see, for example, WO90/11092, which is herein incorporated by reference.

10 Thus, for example, cells from a patient may be engineered with a polynucleotide (DNA or RNA) comprising a promoter operably linked to a polynucleotide of the invention *ex vivo*, with the engineered cells then being provided to a patient to be treated with the polypeptide. Such methods are well-known in the art. For example, see  
15 Belldegrün et al., J. Natl. Cancer Inst., 85:207-216 (1993); Ferrantini et al., Cancer Research, 53:107-1112 (1993); Ferrantini et al., J. Immunology 153: 4604-4615 (1994); Kaido, T., et al., Int. J. Cancer 60: 221-229 (1995); Ogura et al., Cancer Research 50: 5102-5106 (1990); Santodonato, et al., Human Gene Therapy 7:1-10 (1996); Santodonato, et al., Gene Therapy 4:1246-1255 (1997); and Zhang, et al., Cancer Gene Therapy 3: 31-38 (1996)), which are herein incorporated by reference. In one embodiment, the cells which  
20 are engineered are arterial cells. The arterial cells may be reintroduced into the patient through direct injection to the artery, the tissues surrounding the artery, or through catheter injection.

As discussed in more detail below, the polynucleotide constructs can be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection  
25 into the interstitial space of tissues (heart, muscle, skin, lung, liver, and the like). The polynucleotide constructs may be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

In one embodiment, the polynucleotide of the invention is delivered as a naked polynucleotide. The term "naked" polynucleotide, DNA or RNA refers to sequences that are free from any delivery vehicle that acts to assist, promote or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotides of the invention can also be delivered in liposome formulations and lipofectin formulations and the like can be prepared by methods well known to those skilled in the art. Such methods are described, for example, in U.S. Patent Nos. 5,593,972, 5,589,466, and 5,580,859, which are herein incorporated by reference.

The polynucleotide vector constructs of the invention used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Appropriate vectors include pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; pSVK3, pBPV, pMSG and pSVL available from Pharmacia; and pEF1/V5, pcDNA3.1, and pRc/CMV2 available from Invitrogen. Other suitable vectors will be readily apparent to the skilled artisan.

Any strong promoter known to those skilled in the art can be used for driving the expression of polynucleotide sequence of the invention. Suitable promoters include adenoviral promoters, such as the adenoviral major late promoter; or heterologous promoters, such as the cytomegalovirus (CMV) promoter; the respiratory syncytial virus (RSV) promoter; inducible promoters, such as the MMT promoter, the metallothionein promoter; heat shock promoters; the albumin promoter; the ApoAI promoter; human globin promoters; viral thymidine kinase promoters, such as the Herpes Simplex thymidine kinase promoter; retroviral LTRs; the b-actin promoter; and human growth hormone promoters. The promoter also may be the native promoter for the polynucleotides of the invention.

Unlike other gene therapy techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be



introduced into cells to provide production of the desired polypeptide for periods of up to six months.

The polynucleotide construct of the invention can be delivered to the interstitial space of tissues within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular, fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. *In vivo* muscle cells are particularly competent in their ability to take up and express polynucleotides.

For the naked *nucleic acid* sequence injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 mg/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration.

The preferred route of administration is by the parenteral route of injection into the interstitial space of tissues. However, other parenteral routes may also be used, such as,

inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked DNA constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

The naked polynucleotides are delivered by any method known in the art, including, but not limited to, direct needle injection at the delivery site, intravenous injection, topical administration, catheter infusion, and so-called "gene guns". These delivery methods are known in the art.

The constructs may also be delivered with delivery vehicles such as viral sequences, viral particles, liposome formulations, lipofectin, precipitating agents, etc. Such methods of delivery are known in the art.

In certain embodiments, the polynucleotide constructs of the invention are complexed in a liposome preparation. Liposomal preparations for use in the instant invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. However, cationic liposomes are particularly preferred because a tight charge complex can be formed between the cationic liposome and the polyanionic nucleic acid. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner et al., Proc. Natl. Acad. Sci. USA , 84:7413-7416 (1987), which is herein incorporated by reference); mRNA (Malone et al., Proc. Natl. Acad. Sci. USA , 86:6077-6081 (1989), which is herein incorporated by reference); and purified transcription factors (Debs et al., J. Biol. Chem., 265:10189-10192 (1990), which is herein incorporated by reference), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are particularly useful and are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, N.Y. (See, also, Felgner et al., Proc. Natl Acad. Sci. USA , 84:7413-7416 (1987), which is herein incorporated by reference). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer).

Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, e.g. PCT Publication NO: WO 90/11092 (which is herein incorporated by reference) for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes. Preparation of DOTMA liposomes is explained in the literature, see, e.g., Felgner et al., Proc. Natl. Acad. Sci. USA, 84:7413-7417, which is herein incorporated by reference. Similar methods can be used to prepare liposomes from other cationic lipid materials.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, Ala.), or can be easily prepared using readily available materials. Such materials include phosphatidyl, choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

For example, commercially dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), and dioleoylphosphatidyl ethanolamine (DOPE) can be used in various combinations to make conventional liposomes, with or without the addition of cholesterol. Thus, for example, DOPG/DOPC vesicles can be prepared by drying 50 mg each of DOPG and DOPC under a stream of nitrogen gas into a sonication vial. The sample is placed under a vacuum pump overnight and is hydrated the following day with deionized water. The sample is then sonicated for 2 hours in a capped vial, using a Heat Systems model 350 sonicator equipped with an inverted cup (bath type) probe at the maximum setting while the bath is circulated at 15EC. Alternatively, negatively charged vesicles can be prepared without sonication to produce multilamellar vesicles or by extrusion through nucleopore membranes to produce unilamellar vesicles of discrete size. Other methods are known and available to those of skill in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs), with SUVs being preferred. The

various liposome-nucleic acid complexes are prepared using methods well known in the art. See, e.g., Straubinger et al., *Methods of Immunology* , 101:512-527 (1983), which is herein incorporated by reference. For example, MLVs containing nucleic acid can be prepared by depositing a thin film of phospholipid on the walls of a glass tube and subsequently hydrating with a solution of the material to be encapsulated. SUVs are prepared by extended sonication of MLVs to produce a homogeneous population of unilamellar liposomes. The material to be entrapped is added to a suspension of preformed MLVs and then sonicated. When using liposomes containing cationic lipids, the dried lipid film is resuspended in an appropriate solution such as sterile water or an isotonic buffer solution such as 10 mM Tris/NaCl, sonicated, and then the preformed liposomes are mixed directly with the DNA. The liposome and DNA form a very stable complex due to binding of the positively charged liposomes to the cationic DNA. SUVs find use with small nucleic acid fragments. LUVs are prepared by a number of methods, well known in the art. Commonly used methods include  $\text{Ca}^{2+}$ -EDTA chelation (Papahadjopoulos et al., *Biochim. Biophys. Acta*, 394:483 (1975); Wilson et al., *Cell* , 17:77 (1979)); ether injection (Deamer et al., *Biochim. Biophys. Acta*, 443:629 (1976); Ostro et al., *Biochem. Biophys. Res. Commun.*, 76:836 (1977); Fraley et al., *Proc. Natl. Acad. Sci. USA*, 76:3348 (1979)); detergent dialysis (Enoch et al., *Proc. Natl. Acad. Sci. USA* , 76:145 (1979)); and reverse-phase evaporation (REV) (Fraley et al., *J. Biol. Chem.*, 255:10431 (1980); Szoka et al., *Proc. Natl. Acad. Sci. USA* , 75:145 (1978); Schaefer-Ridder et al., *Science*, 215:166 (1982)), which are herein incorporated by reference.

Generally, the ratio of DNA to liposomes will be from about 10:1 to about 1:10. Preferably, the ration will be from about 5:1 to about 1:5. More preferably, the ration will be about 3:1 to about 1:3. Still more preferably, the ratio will be about 1:1.

U.S. Patent NO: 5,676,954 (which is herein incorporated by reference) reports on the injection of genetic material, complexed with cationic liposomes carriers, into mice. U.S. Patent Nos. 4,897,355, 4,946,787, 5,049,386, 5,459,127, 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication NO: WO 94/9469 (which are herein

incorporated by reference) provide cationic lipids for use in transfecting DNA into cells and mammals. U.S. Patent Nos. 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication NO: WO 94/9469 (which are herein incorporated by reference) provide methods for delivering DNA-cationic lipid complexes to mammals.

5 In certain embodiments, cells are engineered, *ex vivo* or *in vivo*, using a retroviral particle containing RNA which comprises a sequence encoding polypeptides of the invention. Retroviruses from which the retroviral plasmid vectors may be derived include, but are not limited to, Moloney Murine Leukemia Virus, spleen necrosis virus, Rous sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, gibbon ape leukemia virus,  
10 human immunodeficiency virus, Myeloproliferative Sarcoma Virus, and mammary tumor virus.

The retroviral plasmid vector is employed to transduce packaging cell lines to form producer cell lines. Examples of packaging cells which may be transduced include, but are not limited to, the PE501, PA317, R-2, R-AM, PA12, T19-14X, VT-19-17-H2, RCRE,  
15 RCRIP, GP+E-86, GP+envAm12, and DAN cell lines as described in Miller, Human Gene Therapy, 1:5-14 (1990), which is incorporated herein by reference in its entirety. The vector may transduce the packaging cells through any means known in the art. Such means include, but are not limited to, electroporation, the use of liposomes, and CaPO<sub>4</sub> precipitation. In one alternative, the retroviral plasmid vector may be encapsulated into a  
20 liposome, or coupled to a lipid, and then administered to a host.

The producer cell line generates infectious retroviral vector particles which include polynucleotide encoding polypeptides of the invention. Such retroviral vector particles then may be employed, to transduce eukaryotic cells, either *in vitro* or *in vivo*. The transduced eukaryotic cells will express polypeptides of the invention.

25 In certain other embodiments, cells are engineered, *ex vivo* or *in vivo*, with polynucleotides of the invention contained in an adenovirus vector. Adenovirus can be manipulated such that it encodes and expresses polypeptides of the invention, and at the same time is inactivated in terms of its ability to replicate in a normal lytic viral life cycle.

Adenovirus expression is achieved without integration of the viral DNA into the host cell chromosome, thereby alleviating concerns about insertional mutagenesis. Furthermore, adenoviruses have been used as live enteric vaccines for many years with an excellent safety profile (Schwartz et al., Am. Rev. Respir. Dis., 109:233-238 (1974)). Finally, adenovirus mediated gene transfer has been demonstrated in a number of instances including transfer of alpha-1-antitrypsin and CFTR to the lungs of cotton rats (Rosenfeld et al., Science, 252:431-434 (1991); Rosenfeld et al., Cell, 68:143-155 (1992)). Furthermore, extensive studies to attempt to establish adenovirus as a causative agent in human cancer were uniformly negative (Green et al. Proc. Natl. Acad. Sci. USA, 76:6606 (1979)).

Suitable adenoviral vectors useful in the present invention are described, for example, in Kozarsky and Wilson, Curr. Opin. Genet. Devel., 3:499-503 (1993); Rosenfeld et al., Cell, 68:143-155 (1992); Engelhardt et al., Human Genet. Ther., 4:759-769 (1993); Yang et al., Nature Genet., 7:362-369 (1994); Wilson et al., Nature, 365:691-692 (1993); and U.S. Patent NO: 5,652,224, which are herein incorporated by reference. For example, the adenovirus vector Ad2 is useful and can be grown in human 293 cells. These cells contain the E1 region of adenovirus and constitutively express E1a and E1b, which complement the defective adenoviruses by providing the products of the genes deleted from the vector. In addition to Ad2, other varieties of adenovirus (e.g., Ad3, Ad5, and Ad7) are also useful in the present invention.

Preferably, the adenoviruses used in the present invention are replication deficient. Replication deficient adenoviruses require the aid of a helper virus and/or packaging cell line to form infectious particles. The resulting virus is capable of infecting cells and can express a polynucleotide of interest which is operably linked to a promoter, but cannot replicate in most cells. Replication deficient adenoviruses may be deleted in one or more of all or a portion of the following genes: E1a, E1b, E3, E4, E2a, or L1 through L5.

In certain other embodiments, the cells are engineered, *ex vivo* or *in vivo*, using an adeno-associated virus (AAV). AAVs are naturally occurring defective viruses that require helper viruses to produce infectious particles (Muzyczka, Curr. Topics in

Microbiol. Immunol., 158:97 (1992)). It is also one of the few viruses that may integrate its DNA into non-dividing cells. Vectors containing as little as 300 base pairs of AAV can be packaged and can integrate, but space for exogenous DNA is limited to about 4.5 kb. Methods for producing and using such AAVs are known in the art. See, for example, U.S. Patent Nos. 5,139,941, 5,173,414, 5,354,678, 5,436,146, 5,474,935, 5,478,745, and 5,589,377.

For example, an appropriate AAV vector for use in the present invention will include all the sequences necessary for DNA replication, encapsidation, and host-cell integration. The polynucleotide construct containing polynucleotides of the invention is inserted into the AAV vector using standard cloning methods, such as those found in Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press (1989). The recombinant AAV vector is then transfected into packaging cells which are infected with a helper virus, using any standard technique, including lipofection, electroporation, calcium phosphate precipitation, etc. Appropriate helper viruses include adenoviruses, cytomegaloviruses, vaccinia viruses, or herpes viruses. Once the packaging cells are transfected and infected, they will produce infectious AAV viral particles which contain the polynucleotide construct of the invention. These viral particles are then used to transduce eukaryotic cells, either *ex vivo* or *in vivo*. The transduced cells will contain the polynucleotide construct integrated into its genome, and will express the desired gene product.

Another method of gene therapy involves operably associating heterologous control regions and endogenous polynucleotide sequences (e.g. encoding the polypeptide sequence of interest) via homologous recombination (see, e.g., U.S. Patent NO: 5,641,670, issued June 24, 1997; International Publication NO: WO 96/29411, published September 26, 1996; International Publication NO: WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA, 86:8932-8935 (1989); and Zijlstra et al., Nature, 342:435-438 (1989). This method involves the activation of a gene which is present in the

target cells, but which is not normally expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made, using standard techniques known in the art, which contain the promoter with targeting sequences flanking the promoter. Suitable  
5 promoters are described herein. The targeting sequence is sufficiently complementary to an endogenous sequence to permit homologous recombination of the promoter-targeting sequence with the endogenous sequence. The targeting sequence will be sufficiently near the 5' end of the desired endogenous polynucleotide sequence so the promoter will be operably linked to the endogenous sequence upon homologous recombination.

10 The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence contains the same restriction site as the 3' end of the amplified promoter. The  
15 amplified promoter and targeting sequences are digested and ligated together.

The promoter-targeting sequence construct is delivered to the cells, either as naked polynucleotide, or in conjunction with transfection-facilitating agents, such as liposomes, viral sequences, viral particles, whole viruses, lipofection, precipitating agents, etc., described in more detail above. The P promoter-targeting sequence can be delivered by  
20 any method, included direct needle injection, intravenous injection, topical administration, catheter infusion, particle accelerators, etc. The methods are described in more detail below.

The promoter-targeting sequence construct is taken up by cells. Homologous recombination between the construct and the endogenous sequence takes place, such that  
25 an endogenous sequence is placed under the control of the promoter. The promoter then drives the expression of the endogenous sequence.

The polynucleotides encoding polypeptides of the present invention may be administered along with other polynucleotides encoding other angiogenic proteins.



Angiogenic proteins include, but are not limited to, acidic and basic fibroblast growth factors, VEGF-1, VEGF-2 (VEGF-C), VEGF-3 (VEGF-B), epidermal growth factor alpha and beta, platelet-derived endothelial cell growth factor, platelet-derived growth factor, tumor necrosis factor alpha, hepatocyte growth factor, insulin like growth factor, colony  
5 stimulating factor, macrophage colony stimulating factor, granulocyte/macrophage colony stimulating factor, and nitric oxide synthase.

Preferably, the polynucleotide encoding a polypeptide of the invention contains a secretory signal sequence that facilitates secretion of the protein. Typically, the signal sequence is positioned in the coding region of the polynucleotide to be expressed towards  
10 or at the 5' end of the coding region. The signal sequence may be homologous or heterologous to the polynucleotide of interest and may be homologous or heterologous to the cells to be transfected. Additionally, the signal sequence may be chemically synthesized using methods known in the art.

Any mode of administration of any of the above-described polynucleotides  
15 constructs can be used so long as the mode results in the expression of one or more molecules in an amount sufficient to provide a therapeutic effect. This includes direct needle injection, systemic injection, catheter infusion, biolistic injectors, particle accelerators (i.e., "gene guns"), gelfoam sponge depots, other commercially available depot materials, osmotic pumps (e.g., Alza minipumps), oral or suppository solid (tablet  
20 or pill) pharmaceutical formulations, and decanting or topical applications during surgery. For example, direct injection of naked calcium phosphate-precipitated plasmid into rat liver and rat spleen or a protein-coated plasmid into the portal vein has resulted in gene expression of the foreign gene in the rat livers. (Kaneda et al., Science, 243:375 (1989)).

A preferred method of local administration is by direct injection. Preferably, a  
25 recombinant molecule of the present invention complexed with a delivery vehicle is administered by direct injection into or locally within the area of arteries. Administration of a composition locally within the area of arteries refers to injecting the composition centimeters and preferably, millimeters within arteries.

Another method of local administration is to contact a polynucleotide construct of the present invention in or around a surgical wound. For example, a patient can undergo surgery and the polynucleotide construct can be coated on the surface of tissue inside the wound or the construct can be injected into areas of tissue inside the wound.

5           Therapeutic compositions useful in systemic administration, include recombinant molecules of the present invention complexed to a targeted delivery vehicle of the present invention. Suitable delivery vehicles for use with systemic administration comprise liposomes comprising ligands for targeting the vehicle to a particular site.

Preferred methods of systemic administration, include intravenous injection,  
10   aerosol, oral and percutaneous (topical) delivery. Intravenous injections can be performed using methods standard in the art. Aerosol delivery can also be performed using methods standard in the art (see, for example, Stribling et al., Proc. Natl. Acad. Sci. USA , 189:11277-11281 (1992), which is incorporated herein by reference). Oral delivery can be performed by complexing a polynucleotide construct of the present invention to a carrier  
15   capable of withstanding degradation by digestive enzymes in the gut of an animal. Examples of such carriers, include plastic capsules or tablets, such as those known in the art. Topical delivery can be performed by mixing a polynucleotide construct of the present invention with a lipophilic reagent (e.g., DMSO) that is capable of passing into the skin.

Determining an effective amount of substance to be delivered can depend upon a  
20   number of factors including, for example, the chemical structure and biological activity of the substance, the age and weight of the animal, the precise condition requiring treatment and its severity, and the route of administration. The frequency of treatments depends upon a number of factors, such as the amount of polynucleotide constructs administered per dose, as well as the health and history of the subject. The precise amount, number of  
25   doses, and timing of doses will be determined by the attending physician or veterinarian. Therapeutic compositions of the present invention can be administered to any animal, preferably to mammals and birds. Preferred mammals include humans, dogs, cats, mice, rats, rabbits sheep, cattle, horses and pigs, with humans being particularly

**Biological Activities**

The polynucleotides or polypeptides, or agonists or antagonists of the present invention can be used in assays to test for one or more biological activities. If these  
5 polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides or polypeptides, or agonists or antagonists could be used to treat the associated disease.

**Immune Activity**

The polynucleotides or polypeptides, or agonists or antagonists of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing  
15 myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotides or polypeptides, or agonists or antagonists of the present invention can be used as a marker or  
20 detector of a particular immune system disease or disorder.

A polynucleotides or polypeptides, or agonists or antagonists of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. A polynucleotides or polypeptides, or agonists or antagonists of the present invention could be used to increase differentiation and proliferation of hematopoietic cells,  
25 including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable

immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

5           Moreover, a polynucleotides or polypeptides, or agonists or antagonists of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotides or polypeptides, or agonists or antagonists of the present invention could be used to treat blood coagulation disorders (e.g., afibrinogenemia,  
10   factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotides or polypeptides, or agonists or antagonists of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

15           A polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polynucleotides or  
20   polypeptides, or agonists or antagonists of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

          Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia,  
25   antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune

Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic  
5 asthma) or other respiratory problems, may also be treated by a polynucleotides or polypeptides, or agonists or antagonists of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

A polynucleotides or polypeptides, or agonists or antagonists of the present  
10 invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of a polynucleotides or polypeptides, or agonists or antagonists  
15 of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be used to modulate inflammation. For example, the  
20 polypeptide or polynucleotide or agonists or antagonist may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin  
25 lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

**Hyperproliferative Disorders**

A polynucleotides or polypeptides, or agonists or antagonists of the invention can be used to treat or detect hyperproliferative disorders, including neoplasms. A polynucleotides or polypeptides, or agonists or antagonists of the present invention may  
5 inhibit the proliferation of the disorder through direct or indirect interactions.

Alternatively, a polynucleotides or polypeptides, or agonists or antagonists of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or  
10 mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by a  
15 polynucleotides or polypeptides, or agonists or antagonists of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

20 Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotides or polypeptides, or agonists or antagonists of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstrom's Macroglobulinemia, Gaucher's Disease,  
25 histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

One preferred embodiment utilizes polynucleotides of the present invention to inhibit aberrant cellular division, by gene therapy using the present invention, and/or protein fusions or fragments thereof.

Thus, the present invention provides a method for treating cell proliferative disorders by inserting into an abnormally proliferating cell a polynucleotide of the present invention, wherein said polynucleotide represses said expression.

Another embodiment of the present invention provides a method of treating cell-proliferative disorders in individuals comprising administration of one or more active gene copies of the present invention to an abnormally proliferating cell or cells. In a preferred embodiment, polynucleotides of the present invention is a DNA construct comprising a recombinant expression vector effective in expressing a DNA sequence encoding said polynucleotides. In another preferred embodiment of the present invention, the DNA construct encoding the polynucleotides of the present invention is inserted into cells to be treated utilizing a retrovirus, or more preferably an adenoviral vector (See G J. Nabel, et al., PNAS 1999 96: 324-326, which is hereby incorporated by reference). In a most preferred embodiment, the viral vector is defective and will not transform non-proliferating cells, only proliferating cells. Moreover, in a preferred embodiment, the polynucleotides of the present invention inserted into proliferating cells either alone, or in combination with or fused to other polynucleotides, can then be modulated via an external stimulus (i.e. magnetic, specific small molecule, chemical, or drug administration, etc.), which acts upon the promoter upstream of said polynucleotides to induce expression of the encoded protein product. As such the beneficial therapeutic affect of the present invention may be expressly modulated (i.e. to increase, decrease, or inhibit expression of the present invention) based upon said external stimulus.

Polynucleotides of the present invention may be useful in repressing expression of oncogenic genes or antigens. By "repressing expression of the oncogenic genes " is intended the suppression of the transcription of the gene, the degradation of the gene transcript (pre-message RNA), the inhibition of splicing, the destruction of the messenger

RNA, the prevention of the post-translational modifications of the protein, the destruction of the protein, or the inhibition of the normal function of the protein.

For local administration to abnormally proliferating cells, polynucleotides of the present invention may be administered by any method known to those of skill in the art including, but not limited to transfection, electroporation, microinjection of cells, or in vehicles such as liposomes, lipofectin, or as naked polynucleotides, or any other method described throughout the specification. The polynucleotide of the present invention may be delivered by known gene delivery systems such as, but not limited to, retroviral vectors (Gilboa, J. Virology 44:845 (1982); Hocke, Nature 320:275 (1986); Wilson, et al., Proc. Natl. Acad. Sci. U.S.A. 85:3014), vaccinia virus system (Chakrabarty et al., Mol. Cell Biol. 5:3403 (1985) or other efficient DNA delivery systems (Yates et al., Nature 313:812 (1985)) known to those skilled in the art. These references are exemplary only and are hereby incorporated by reference. In order to specifically deliver or transfect cells which are abnormally proliferating and spare non-dividing cells, it is preferable to utilize a retrovirus, or adenoviral (as described in the art and elsewhere herein) delivery system known to those of skill in the art. Since host DNA replication is required for retroviral DNA to integrate and the retrovirus will be unable to self replicate due to the lack of the retrovirus genes needed for its life cycle. Utilizing such a retroviral delivery system for polynucleotides of the present invention will target said gene and constructs to abnormally proliferating cells and will spare the non-dividing normal cells.

The polynucleotides of the present invention may be delivered directly to cell proliferative disorder/disease sites in internal organs, body cavities and the like by use of imaging devices used to guide an injecting needle directly to the disease site. The polynucleotides of the present invention may also be administered to disease sites at the time of surgical intervention.

By "cell proliferative disease" is meant any human or animal disease or disorder, affecting any one or any combination of organs, cavities, or body parts, which is



characterized by single or multiple local abnormal proliferations of cells, groups of cells, or tissues, whether benign or malignant.

Any amount of the polynucleotides of the present invention may be administered as long as it has a biologically inhibiting effect on the proliferation of the treated cells.

5 Moreover, it is possible to administer more than one of the polynucleotide of the present invention simultaneously to the same site. By "biologically inhibiting" is meant partial or total growth inhibition as well as decreases in the rate of proliferation or growth of the cells. The biologically inhibitory dose may be determined by assessing the effects of the polynucleotides of the present invention on target malignant or abnormally proliferating

10 cell growth in tissue culture, tumor growth in animals and cell cultures, or any other method known to one of ordinary skill in the art.

The present invention is further directed to antibody-based therapies which involve administering of anti-polypeptides and anti-polynucleotide antibodies to a mammalian, preferably human, patient for treating one or more of the described disorders. Methods for

15 producing anti-polypeptides and anti-polynucleotide antibodies polyclonal and monoclonal antibodies are described in detail elsewhere herein. Such antibodies may be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the present

20 invention locally or systemically in the body or by direct cytotoxicity of the antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC). Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the art will know how to use the antibodies of the present invention for diagnostic, monitoring or therapeutic purposes without undue experimentation.

25 In particular, the antibodies, fragments and derivatives of the present invention are useful for treating a subject having or developing cell proliferative and/or differentiation disorders as described herein. Such treatment comprises administering a single or multiple doses of the antibody, or a fragment, derivative, or a conjugate thereof.

The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or hematopoietic growth factors, for example, which serve to increase the number or activity of effector cells which interact with the antibodies.

5 It is preferred to use high affinity and/or potent in vivo inhibiting and/or neutralizing antibodies against polypeptides or polynucleotides of the present invention, fragments or regions thereof, for both immunoassays directed to and therapy of disorders related to polynucleotides or polypeptides, including fragments thereof, of the present invention. Such antibodies, fragments, or regions, will preferably have an affinity for  
10 polynucleotides or polypeptides, including fragments thereof. Preferred binding affinities include those with a dissociation constant or  $K_d$  less than  $5 \times 10^{-6}M$ ,  $10^{-6}M$ ,  $5 \times 10^{-7}M$ ,  $10^{-7}M$ ,  $5 \times 10^{-8}M$ ,  $10^{-8}M$ ,  $5 \times 10^{-9}M$ ,  $10^{-9}M$ ,  $5 \times 10^{-10}M$ ,  $10^{-10}M$ ,  $5 \times 10^{-11}M$ ,  $10^{-11}M$ ,  $5 \times 10^{-12}M$ ,  $10^{-12}M$ ,  $5 \times 10^{-13}M$ ,  $10^{-13}M$ ,  $5 \times 10^{-14}M$ ,  $10^{-14}M$ ,  $5 \times 10^{-15}M$ , and  $10^{-15}M$ .

Moreover, polypeptides of the present invention are useful in inhibiting the  
15 angiogenesis of proliferative cells or tissues, either alone, as a protein fusion, or in combination with other polypeptides directly or indirectly, as described elsewhere herein. In a most preferred embodiment, said anti-angiogenesis effect may be achieved indirectly, for example, through the inhibition of hematopoietic, tumor-specific cells, such as tumor-associated macrophages (See Joseph IB, et al. J Natl Cancer Inst, 90(21):1648-53 (1998),  
20 which is hereby incorporated by reference). Antibodies directed to polypeptides or polynucleotides of the present invention may also result in inhibition of angiogenesis directly, or indirectly (See Witte L, et al., Cancer Metastasis Rev. 17(2):155-61 (1998), which is hereby incorporated by reference)).

Polypeptides, including protein fusions, of the present invention, or fragments  
25 thereof may be useful in inhibiting proliferative cells or tissues through the induction of apoptosis. Said polypeptides may act either directly, or indirectly to induce apoptosis of proliferative cells and tissues, for example in the activation of a death-domain receptor, such as tumor necrosis factor (TNF) receptor-1, CD95 (Fas/APO-1), TNF-receptor-related

apoptosis-mediated protein (TRAMP) and TNF-related apoptosis-inducing ligand (TRAIL) receptor-1 and -2 (See Schulze-Osthoff K, et.al., Eur J Biochem 254(3):439-59 (1998), which is hereby incorporated by reference). Moreover, in another preferred embodiment of the present invention, said polypeptides may induce apoptosis through other  
5 mechanisms, such as in the activation of other proteins which will activate apoptosis, or through stimulating the expression of said proteins, either alone or in combination with small molecule drugs or adjuvants, such as apoptonin, galectins, thioredoxins, antiinflammatory proteins (See for example, Mutat Res 400(1-2):447-55 (1998), Med Hypotheses.50(5):423-33 (1998), Chem Biol Interact. Apr 24;111-112:23-34 (1998), J Mol  
10 Med.76(6):402-12 (1998), Int J Tissue React;20(1):3-15 (1998), which are all hereby incorporated by reference).

Polypeptides, including protein fusions to, or fragments thereof, of the present invention are useful in inhibiting the metastasis of proliferative cells or tissues. Inhibition may occur as a direct result of administering polypeptides, or antibodies directed to said  
15 polypeptides as described elsewhere herein, or indirectly, such as activating the expression of proteins known to inhibit metastasis, for example alpha 4 integrins, (See, e.g., Curr Top Microbiol Immunol 1998;231:125-41, which is hereby incorporated by reference). Such therapeutic affects of the present invention may be achieved either alone, or in combination with small molecule drugs or adjuvants.

20 In another embodiment, the invention provides a method of delivering compositions containing the polypeptides of the invention (e.g., compositions containing polypeptides or polypeptide antibodies associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs) to targeted cells expressing the polypeptide of the present invention. Polypeptides or polypeptide antibodies of the invention may be  
25 associated with with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs via hydrophobic, hydrophilic, ionic and/or covalent interactions.

Polypeptides, protein fusions to, or fragments thereof, of the present invention are useful in enhancing the immunogenicity and/or antigenicity of proliferating cells or tissues, either

directly, such as would occur if the polypeptides of the present invention 'vaccinated' the immune response to respond to proliferative antigens and immunogens, or indirectly, such as in activating the expression of proteins known to enhance the immune response (e.g. chemokines), to said antigens and immunogens.

5

### **Cardiovascular Disorders**

Polynucleotides or polypeptides, or agonists or antagonists of the invention may be used to treat cardiovascular disorders, including peripheral artery disease, such as limb ischemia.

10 Cardiovascular disorders include cardiovascular abnormalities, such as arterio-arterial fistula, arteriovenous fistula, cerebral arteriovenous malformations, congenital heart defects, pulmonary atresia, and Scimitar Syndrome. Congenital heart defects include aortic coarctation, cor triatriatum, coronary vessel anomalies, crisscross heart, dextrocardia, patent ductus arteriosus, Ebstein's anomaly, Eisenmenger complex,  
15 hypoplastic left heart syndrome, levocardia, tetralogy of fallot, transposition of great vessels, double outlet right ventricle, tricuspid atresia, persistent truncus arteriosus, and heart septal defects, such as aortopulmonary septal defect, endocardial cushion defects, Lutembacher's Syndrome, trilogly of Fallot, ventricular heart septal defects.

Cardiovascular disorders also include heart disease, such as arrhythmias, carcinoid  
20 heart disease, high cardiac output, low cardiac output, cardiac tamponade, endocarditis (including bacterial), heart aneurysm, cardiac arrest, congestive heart failure, congestive cardiomyopathy, paroxysmal dyspnea, cardiac edema, heart hypertrophy, congestive cardiomyopathy, left ventricular hypertrophy, right ventricular hypertrophy, post-infarction heart rupture, ventricular septal rupture, heart valve diseases, myocardial diseases,  
25 myocardial ischemia, pericardial effusion, pericarditis (including constrictive and tuberculous), pneumopericardium, postpericardiotomy syndrome, pulmonary heart disease, rheumatic heart disease, ventricular dysfunction, hyperemia, cardiovascular pregnancy

complications, Scimitar Syndrome, cardiovascular syphilis, and cardiovascular tuberculosis.

Arrhythmias include sinus arrhythmia, atrial fibrillation, atrial flutter, bradycardia, extrasystole, Adams-Stokes Syndrome, bundle-branch block, sinoatrial block, long QT  
5 syndrome, parasystole, Lown-Ganong-Levine Syndrome, Mahaim-type pre-excitation syndrome, Wolff-Parkinson-White syndrome, sick sinus syndrome, tachycardias, and ventricular fibrillation. Tachycardias include paroxysmal tachycardia, supraventricular tachycardia, accelerated idioventricular rhythm, atrioventricular nodal reentry tachycardia, ectopic atrial tachycardia, ectopic junctional tachycardia, sinoatrial nodal reentry  
10 tachycardia, sinus tachycardia, Torsades de Pointes, and ventricular tachycardia.

Heart valve disease include aortic valve insufficiency, aortic valve stenosis, heart murmurs, aortic valve prolapse, mitral valve prolapse, tricuspid valve prolapse, mitral valve insufficiency, mitral valve stenosis, pulmonary atresia, pulmonary valve insufficiency, pulmonary valve stenosis, tricuspid atresia, tricuspid valve insufficiency, and  
15 tricuspid valve stenosis.

Myocardial diseases include alcoholic cardiomyopathy, congestive cardiomyopathy, hypertrophic cardiomyopathy, aortic subvalvular stenosis, pulmonary subvalvular stenosis, restrictive cardiomyopathy, Chagas cardiomyopathy, endocardial fibroelastosis, endomyocardial fibrosis, Kearns Syndrome, myocardial reperfusion injury,  
20 and myocarditis.

Myocardial ischemias include coronary disease, such as angina pectoris, coronary aneurysm, coronary arteriosclerosis, coronary thrombosis, coronary vasospasm, myocardial infarction and myocardial stunning.

Cardiovascular diseases also include vascular diseases such as aneurysms,  
25 angiodyplasia, angiomatosis, bacillary angiomatosis, Hippel-Lindau Disease, Klippel-Trenaunay-Weber Syndrome, Sturge-Weber Syndrome, angioneurotic edema, aortic diseases, Takayasu's Arteritis, aortitis, Leriche's Syndrome, arterial occlusive diseases, arteritis, enarteritis, polyarteritis nodosa, cerebrovascular disorders, diabetic angiopathies,

diabetic retinopathy, embolisms, thrombosis, erythromelalgia, hemorrhoids, hepatic veno-occlusive disease, hypertension, hypotension, ischemia, peripheral vascular diseases, phlebitis, pulmonary veno-occlusive disease, Raynaud's disease, CREST syndrome, retinal vein occlusion, Scimitar syndrome, superior vena cava syndrome, telangiectasia, atacia  
5 telangiectasia, hereditary hemorrhagic telangiectasia, varicocele, varicose veins, varicose ulcer, vasculitis, and venous insufficiency.

Aneurysms include dissecting aneurysms, false aneurysms, infected aneurysms, ruptured aneurysms, aortic aneurysms, cerebral aneurysms, coronary aneurysms, heart aneurysms, and iliac aneurysms.

10 Arterial occlusive diseases include arteriosclerosis, intermittent claudication, carotid stenosis, fibromuscular dysplasias, mesenteric vascular occlusion, Moyamoya disease, renal artery obstruction, retinal artery occlusion, and thromboangiitis obliterans.

Cerebrovascular disorders include carotid artery diseases, cerebral amyloid angiopathy, cerebral aneurysm, cerebral anoxia, cerebral arteriosclerosis, cerebral  
15 arteriovenous malformation, cerebral artery diseases, cerebral embolism and thrombosis, carotid artery thrombosis, sinus thrombosis, Wallenberg's syndrome, cerebral hemorrhage, epidural hematoma, subdural hematoma, subarachnoid hemorrhage, cerebral infarction, cerebral ischemia (including transient), subclavian steal syndrome, periventricular leukomalacia, vascular headache, cluster headache, migraine, and vertebrobasilar  
20 insufficiency.

Embolisms include air embolisms, amniotic fluid embolisms, cholesterol embolisms, blue toe syndrome, fat embolisms, pulmonary embolisms, and thromboembolisms. Thrombosis include coronary thrombosis, hepatic vein thrombosis, retinal vein occlusion, carotid artery thrombosis, sinus thrombosis, Wallenberg's syndrome,  
25 and thrombophlebitis.

Ischemia includes cerebral ischemia, ischemic colitis, compartment syndromes, anterior compartment syndrome, myocardial ischemia, reperfusion injuries, and peripheral limb ischemia. Vasculitis includes aortitis, arteritis, Behcet's Syndrome, Churg-Strauss

Syndrome, mucocutaneous lymph node syndrome, thromboangiitis obliterans, hypersensitivity vasculitis, Schoenlein-Henoch purpura, allergic cutaneous vasculitis, and Wegener's granulomatosis.

Polynucleotides or polypeptides, or agonists or antagonists of the invention, are especially effective for the treatment of critical limb ischemia and coronary disease.

Polypeptides may be administered using any method known in the art, including, but not limited to, direct needle injection at the delivery site, intravenous injection, topical administration, catheter infusion, biolistic injectors, particle accelerators, gelfoam sponge depots, other commercially available depot materials, osmotic pumps, oral or suppositorial solid pharmaceutical formulations, decanting or topical applications during surgery, aerosol delivery. Such methods are known in the art. Polypeptides of the invention may be administered as part of a *Therapeutic*, described in more detail below. Methods of delivering polynucleotides of the invention are described in more detail herein.

### **Anti-Angiogenesis Activity**

The naturally occurring balance between endogenous stimulators and inhibitors of angiogenesis is one in which inhibitory influences predominate. Rastinejad *et al.*, *Cell* 56:345-355 (1989). In those rare instances in which neovascularization occurs under normal physiological conditions, such as wound healing, organ regeneration, embryonic development, and female reproductive processes, angiogenesis is stringently regulated and spatially and temporally delimited. Under conditions of pathological angiogenesis such as that characterizing solid tumor growth, these regulatory controls fail. Unregulated angiogenesis becomes pathologic and sustains progression of many neoplastic and non-neoplastic diseases. A number of serious diseases are dominated by abnormal neovascularization including solid tumor growth and metastases, arthritis, some types of eye disorders, and psoriasis. See, e.g., reviews by Moses *et al.*, *Biotech.* 9:630-634 (1991); Folkman *et al.*, *N. Engl. J. Med.*, 333:1757-1763 (1995); Auerbach *et al.*, *J. Microvasc. Res.* 29:401-411 (1985); Folkman, *Advances in Cancer Research*, eds. Klein and

Weinhouse, Academic Press, New York, pp. 175-203 (1985); Patz, *Am. J. Ophthalmol.* 94:715-743 (1982); and Folkman *et al.*, *Science* 221:719-725 (1983). In a number of pathological conditions, the process of angiogenesis contributes to the disease state. For example, significant data have accumulated which suggest that the growth of solid tumors  
5 is dependent on angiogenesis. Folkman and Klagsbrun, *Science* 235:442-447 (1987).

The present invention provides for treatment of diseases or disorders associated with neovascularization by administration of the polynucleotides and/or polypeptides of the invention, as well as agonists or antagonists of the present invention. Malignant and metastatic conditions which can be treated with the polynucleotides and polypeptides, or  
10 agonists or antagonists of the invention include, but are not limited to, malignancies, solid tumors, and cancers described herein and otherwise known in the art (for a review of such disorders, see Fishman *et al.*, *Medicine*, 2d Ed., J. B. Lippincott Co., Philadelphia (1985)). Thus, the present invention provides a method of treating an angiogenesis-related disease and/or disorder, comprising administering to an individual in need thereof a  
15 therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist of the invention. For example, polynucleotides, polypeptides, antagonists and/or agonists may be utilized in a variety of additional methods in order to therapeutically treat a cancer or tumor. Cancers which may be treated with polynucleotides, polypeptides, antagonists and/or agonists include, but are not limited to solid tumors, including prostate,  
20 lung, breast, ovarian, stomach, pancreas, larynx, esophagus, testes, liver, parotid, biliary tract, colon, rectum, cervix, uterus, endometrium, kidney, bladder, thyroid cancer; primary tumors and metastases; melanomas; glioblastoma; Kaposi's sarcoma; leiomyosarcoma; non-small cell lung cancer; colorectal cancer; advanced malignancies; and blood born tumors such as leukemias. For example, polynucleotides, polypeptides, antagonists and/or  
25 agonists may be delivered topically, in order to treat cancers such as skin cancer, head and neck tumors, breast tumors, and Kaposi's sarcoma.

Within yet other aspects, polynucleotides, polypeptides, antagonists and/or agonists may be utilized to treat superficial forms of bladder cancer by, for example, intravesical



administration. Polynucleotides, polypeptides, antagonists and/or agonists may be delivered directly into the tumor, or near the tumor site, via injection or a catheter. Of course, as the artisan of ordinary skill will appreciate, the appropriate mode of administration will vary according to the cancer to be treated. Other modes of delivery are  
5 discussed herein.

Polynucleotides, polypeptides, antagonists and/or agonists may be useful in treating other disorders, besides cancers, which involve angiogenesis. These disorders include, but are not limited to: benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas; arteriosclerotic plaques; ocular  
10 angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, retinoblastoma, uveitis and Pterygia (abnormal blood vessel growth) of the eye; rheumatoid arthritis; psoriasis; delayed wound healing; endometriosis; vasculogenesis; granulations; hypertrophic scars (keloids); nonunion fractures; scleroderma; trachoma;  
15 vascular adhesions; myocardial angiogenesis; coronary collaterals; cerebral collaterals; arteriovenous malformations; ischemic limb angiogenesis; Osler-Webber Syndrome; plaque neovascularization; telangiectasia; hemophilic joints; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; and atherosclerosis.

For example, within one aspect of the present invention methods are provided for  
20 treating hypertrophic scars and keloids, comprising the step of administering a polynucleotide, polypeptide, antagonist and/or agonist of the invention to a hypertrophic scar or keloid.

Within one embodiment of the present invention polynucleotides, polypeptides, antagonists and/or agonists are directly injected into a hypertrophic scar or keloid, in order  
25 to prevent the progression of these lesions. This therapy is of particular value in the prophylactic treatment of conditions which are known to result in the development of hypertrophic scars and keloids (e.g., burns), and is preferably initiated after the proliferative phase has had time to progress (approximately 14 days after the initial injury),

but before hypertrophic scar or keloid development. As noted above, the present invention also provides methods for treating neovascular diseases of the eye, including for example, corneal neovascularization, neovascular glaucoma, proliferative diabetic retinopathy, retrolental fibroplasia and macular degeneration.

5           Moreover, Ocular disorders associated with neovascularization which can be treated with the polynucleotides and polypeptides of the present invention (including agonists and/or antagonists) include, but are not limited to: neovascular glaucoma, diabetic retinopathy, retinoblastoma, retrolental fibroplasia, uveitis, retinopathy of prematurity  
10       macular degeneration, corneal graft neovascularization, as well as other eye inflammatory diseases, ocular tumors and diseases associated with choroidal or iris neovascularization. See, e.g., reviews by Waltman *et al.*, *Am. J. Ophthalmol.* 85:704-710 (1978) and Gartner *et al.*, *Surv. Ophthalmol.* 22:291-312 (1978).

          Thus, within one aspect of the present invention methods are provided for treating neovascular diseases of the eye such as corneal neovascularization (including corneal graft  
15       neovascularization), comprising the step of administering to a patient a therapeutically effective amount of a compound (as described above) to the cornea, such that the formation of blood vessels is inhibited. Briefly, the cornea is a tissue which normally lacks blood vessels. In certain pathological conditions however, capillaries may extend into the cornea from the pericorneal vascular plexus of the limbus. When the cornea becomes  
20       vascularized, it also becomes clouded, resulting in a decline in the patient's visual acuity. Visual loss may become complete if the cornea completely opacitates. A wide variety of disorders can result in corneal neovascularization, including for example, corneal infections (e.g., trachoma, herpes simplex keratitis, leishmaniasis and onchocerciasis), immunological processes (e.g., graft rejection and Stevens-Johnson's syndrome), alkali  
25       burns, trauma, inflammation (of any cause), toxic and nutritional deficiency states, and as a complication of wearing contact lenses.

          Within particularly preferred embodiments of the invention, may be prepared for topical administration in saline (combined with any of the preservatives and antimicrobial

agents commonly used in ocular preparations), and administered in eyedrop form. The solution or suspension may be prepared in its pure form and administered several times daily. Alternatively, anti-angiogenic compositions, prepared as described above, may also be administered directly to the cornea. Within preferred embodiments, the anti-angiogenic composition is prepared with a muco-adhesive polymer which binds to cornea. Within further embodiments, the anti-angiogenic factors or anti-angiogenic compositions may be utilized as an adjunct to conventional steroid therapy. Topical therapy may also be useful prophylactically in corneal lesions which are known to have a high probability of inducing an angiogenic response (such as chemical burns). In these instances the treatment, likely in combination with steroids, may be instituted immediately to help prevent subsequent complications.

Within other embodiments, the compounds described above may be injected directly into the corneal stroma by an ophthalmologist under microscopic guidance. The preferred site of injection may vary with the morphology of the individual lesion, but the goal of the administration would be to place the composition at the advancing front of the vasculature (i.e., interspersed between the blood vessels and the normal cornea). In most cases this would involve perilimbic corneal injection to "protect" the cornea from the advancing blood vessels. This method may also be utilized shortly after a corneal insult in order to prophylactically prevent corneal neovascularization. In this situation the material could be injected in the perilimbic cornea interspersed between the corneal lesion and its undesired potential limbic blood supply. Such methods may also be utilized in a similar fashion to prevent capillary invasion of transplanted corneas. In a sustained-release form injections might only be required 2-3 times per year. A steroid could also be added to the injection solution to reduce inflammation resulting from the injection itself.

Within another aspect of the present invention, methods are provided for treating neovascular glaucoma, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eye, such that the formation of blood vessels is inhibited. In one embodiment, the compound

may be administered topically to the eye in order to treat early forms of neovascular glaucoma. Within other embodiments, the compound may be implanted by injection into the region of the anterior chamber angle. Within other embodiments, the compound may also be placed in any location such that the compound is continuously released into the aqueous humor. Within another aspect of the present invention, methods are provided for  
5 treating proliferative diabetic retinopathy, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eyes, such that the formation of blood vessels is inhibited.

Within particularly preferred embodiments of the invention, proliferative diabetic  
10 retinopathy may be treated by injection into the aqueous humor or the vitreous, in order to increase the local concentration of the polynucleotide, polypeptide, antagonist and/or agonist in the retina. Preferably, this treatment should be initiated prior to the acquisition of severe disease requiring photocoagulation.

Within another aspect of the present invention, methods are provided for treating  
15 retrolental fibroplasia, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eye, such that the formation of blood vessels is inhibited. The compound may be administered topically, via intravitreal injection and/or via intraocular implants.

Additionally, disorders which can be treated with the polynucleotides,  
20 polypeptides, agonists and/or antagonists include, but are not limited to, hemangioma, arthritis, psoriasis, angiofibroma, atherosclerotic plaques, delayed wound healing, granulations, hemophilic joints, hypertrophic scars, nonunion fractures, Osler-Weber syndrome, pyogenic granuloma, scleroderma, trachoma, and vascular adhesions.

Moreover, disorders and/or states, which can be treated with the the  
25 polynucleotides, polypeptides, agonists and/or antagonists include, but are not limited to, solid tumors, blood born tumors such as leukemias, tumor metastasis, Kaposi's sarcoma, benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases, for

example, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, retinoblastoma, and uveitis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars (keloids), nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial  
5 angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemic limb angiogenesis, Osler-Webber Syndrome, plaque neovascularization, telangiectasia, hemophilic joints, angiofibroma fibromuscular dysplasia, wound granulation, Crohn's disease, atherosclerosis, birth control agent by preventing vascularization required for embryo implantation controlling menstruation, diseases that  
10 have angiogenesis as a pathologic consequence such as cat scratch disease (Rochelominalia quintosa), ulcers (*Helicobacter pylori*), Bartonellosis and bacillary angiomatosis.

In one aspect of the birth control method, an amount of the compound sufficient to block embryo implantation is administered before or after intercourse and fertilization have occurred, thus providing an effective method of birth control, possibly a "morning after"  
15 method. Polynucleotides, polypeptides, agonists and/or antagonists may also be used in controlling menstruation or administered as either a peritoneal lavage fluid or for peritoneal implantation in the treatment of endometriosis.

Polynucleotides, polypeptides, agonists and/or antagonists of the present invention may be incorporated into surgical sutures in order to prevent stitch granulomas.

20 Polynucleotides, polypeptides, agonists and/or antagonists may be utilized in a wide variety of surgical procedures. For example, within one aspect of the present invention a composition (in the form of, for example, a spray or film) may be utilized to coat or spray an area prior to removal of a tumor, in order to isolate normal surrounding tissues from malignant tissue, and/or to prevent the spread of disease to surrounding tissues. Within  
25 other aspects of the present invention, compositions (e.g., in the form of a spray) may be delivered via endoscopic procedures in order to coat tumors, or inhibit angiogenesis in a desired locale. Within yet other aspects of the present invention, surgical meshes which have been coated with anti-angiogenic compositions of the present invention may be

utilized in any procedure wherein a surgical mesh might be utilized. For example, within one embodiment of the invention a surgical mesh laden with an anti-angiogenic composition may be utilized during abdominal cancer resection surgery (e.g., subsequent to colon resection) in order to provide support to the structure, and to release an amount of  
5 the anti-angiogenic factor.

Within further aspects of the present invention, methods are provided for treating tumor excision sites, comprising administering a polynucleotide, polypeptide, agonist and/or agonist to the resection margins of a tumor subsequent to excision, such that the local recurrence of cancer and the formation of new blood vessels at the site is inhibited.  
10 Within one embodiment of the invention, the anti-angiogenic compound is administered directly to the tumor excision site (e.g., applied by swabbing, brushing or otherwise coating the resection margins of the tumor with the anti-angiogenic compound). Alternatively, the anti-angiogenic compounds may be incorporated into known surgical pastes prior to administration. Within particularly preferred embodiments of the invention,  
15 the anti-angiogenic compounds are applied after hepatic resections for malignancy, and after neurosurgical operations.

Within one aspect of the present invention, polynucleotides, polypeptides, agonists and/or agonists may be administered to the resection margin of a wide variety of tumors, including for example, breast, colon, brain and hepatic tumors. For example, within one  
20 embodiment of the invention, anti-angiogenic compounds may be administered to the site of a neurological tumor subsequent to excision, such that the formation of new blood vessels at the site are inhibited.

The polynucleotides, polypeptides, agonists and/or agonists of the present invention may also be administered along with other anti-angiogenic factors. Representative  
25 examples of other anti-angiogenic factors include: Anti-Invasive Factor, retinoic acid and derivatives thereof, paclitaxel, Suramin, Tissue Inhibitor of Metalloproteinase-1, Tissue Inhibitor of Metalloproteinase-2, Plasminogen Activator Inhibitor-1, Plasminogen Activator Inhibitor-2, and various forms of the lighter "d group" transition metals.

Lighter "d group" transition metals include, for example, vanadium, molybdenum, tungsten, titanium, niobium, and tantalum species. Such transition metal species may form transition metal complexes. Suitable complexes of the above-mentioned transition metal species include oxo transition metal complexes.

5        Representative examples of vanadium complexes include oxo vanadium complexes such as vanadate and vanadyl complexes. Suitable vanadate complexes include metavanadate and orthovanadate complexes such as, for example, ammonium metavanadate, sodium metavanadate, and sodium orthovanadate. Suitable vanadyl complexes include, for example, vanadyl acetylacetonate and vanadyl sulfate including  
10       vanadyl sulfate hydrates such as vanadyl sulfate mono- and trihydrates.

      Representative examples of tungsten and molybdenum complexes also include oxo complexes. Suitable oxo tungsten complexes include tungstate and tungsten oxide complexes. Suitable tungstate complexes include ammonium tungstate, calcium tungstate, sodium tungstate dihydrate, and tungstic acid. Suitable tungsten oxides include tungsten  
15       (IV) oxide and tungsten (VI) oxide. Suitable oxo molybdenum complexes include molybdate, molybdenum oxide, and molybdenyl complexes. Suitable molybdate complexes include ammonium molybdate and its hydrates, sodium molybdate and its hydrates, and potassium molybdate and its hydrates. Suitable molybdenum oxides include  
20       molybdenum (VI) oxide, molybdenum (VI) oxide, and molybdic acid. Suitable molybdenyl complexes include, for example, molybdenyl acetylacetonate. Other suitable tungsten and molybdenum complexes include hydroxo derivatives derived from, for example, glycerol, tartaric acid, and sugars.

      A wide variety of other anti-angiogenic factors may also be utilized within the context of the present invention. Representative examples include platelet factor 4;  
25       protamine sulphate; sulphated chitin derivatives (prepared from queen crab shells), (Murata et al., Cancer Res. 51:22-26, 1991); Sulphated Polysaccharide Peptidoglycan Complex (SP- PG) (the function of this compound may be enhanced by the presence of steroids such as estrogen, and tamoxifen citrate); Staurosporine; modulators of matrix

metabolism, including for example, proline analogs, cishydroxyproline, d,L-3,4-dehydroproline, Thiaproline, alpha,alpha-dipyridyl, aminopropionitrile fumarate; 4-propyl-5-(4-pyridinyl)-2(3H)-oxazolone; Methotrexate; Mitoxantrone; Heparin; Interferons; 2 Macroglobulin-serum; ChIMP-3 (Pavloff et al., J. Bio. Chem. 267:17321-17326, 1992);

5 Chymostatin (Tomkinson et al., Biochem J. 286:475-480, 1992); Cyclodextrin Tetradasulfate; Eponemycin; Camptothecin; Fumagillin (Ingber et al., Nature 348:555-557, 1990); Gold Sodium Thiomalate ("GST"; Matsubara and Ziff, J. Clin. Invest. 79:1440-1446, 1987); anticollagenase-serum; alpha2-antiplasmin (Holmes et al., J. Biol. Chem. 262(4):1659-1664, 1987); Bisantrone (National Cancer Institute); Lobenzarit

10 disodium (N-(2)-carboxyphenyl-4- chloroanthronilic acid disodium or "CCA"; Takeuchi et al., Agents Actions 36:312-316, 1992); Thalidomide; Angostatic steroid; AGM-1470; carboxynaminolimidazole; and metalloproteinase inhibitors such as BB94.

#### **Diseases at the Cellular Level**

15 Diseases associated with increased cell survival or the inhibition of apoptosis that could be treated or detected by the polynucleotides or polypeptides and/or antagonists or agonists of the invention, include cancers (such as follicular lymphomas, carcinomas with p53 mutations, and hormone-dependent tumors, including, but not limited to colon cancer, cardiac tumors, pancreatic cancer, melanoma, retinoblastoma, glioblastoma, lung cancer,

20 intestinal cancer, testicular cancer, stomach cancer, neuroblastoma, myxoma, myoma, lymphoma, endothelioma, osteoblastoma, osteoclastoma, osteosarcoma, chondrosarcoma, adenoma, breast cancer, prostate cancer, Kaposi's sarcoma and ovarian cancer); autoimmune disorders (such as, multiple sclerosis, Sjogren's syndrome, Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic

25 lupus erythematosus and immune-related glomerulonephritis and rheumatoid arthritis) and viral infections (such as herpes viruses, pox viruses and adenoviruses), inflammation, graft v. host disease, acute graft rejection, and chronic graft rejection. In preferred embodiments, the polynucleotides or polypeptides, and/or agonists or antagonists of the



invention are used to inhibit growth, progression, and/or metasis of cancers, in particular those listed above.

Additional diseases or conditions associated with increased cell survival that could be treated or detected by the polynucleotides or polypeptides, or agonists or antagonists of the invention, include, but are not limited to, progression, and/or metastases of malignancies and related disorders such as leukemia (including acute leukemias (e.g., acute lymphocytic leukemia, acute myelocytic leukemia (including myeloblastic, promyelocytic, myelomonocytic, monocytic, and erythroleukemia)) and chronic leukemias (e.g., chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia)), polycythemia vera, lymphomas (e.g., Hodgkin's disease and non-Hodgkin's disease), multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, and solid tumors including, but not limited to, sarcomas and carcinomas such as fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilm's tumor, cervical cancer, testicular tumor, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma, melanoma, neuroblastoma, and retinoblastoma.

Diseases associated with increased apoptosis that could be treated or detected by the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, include AIDS; neurodegenerative disorders (such as Alzheimer's disease, Parkinson's disease, Amyotrophic lateral sclerosis, Retinitis pigmentosa, Cerebellar degeneration and

brain tumor or prior associated disease); autoimmune disorders (such as, multiple sclerosis, Sjogren's syndrome, Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic lupus erythematosus and immune-related glomerulonephritis and rheumatoid arthritis) myelodysplastic syndromes (such as aplastic  
5 anemia), graft v. host disease, ischemic injury (such as that caused by myocardial infarction, stroke and reperfusion injury), liver injury (e.g., hepatitis related liver injury, ischemia/reperfusion injury, cholestasis (bile duct injury) and liver cancer); toxin-induced liver disease (such as that caused by alcohol), septic shock, cachexia and anorexia.

#### 10 Wound Healing and Epithelial Cell Proliferation

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, for therapeutic purposes, for example, to stimulate epithelial cell proliferation and basal keratinocytes for the purpose of wound healing, and to stimulate  
15 hair follicle production and healing of dermal wounds. Polynucleotides or polypeptides, as well as agonists or antagonists of the invention, may be clinically useful in stimulating wound healing including surgical wounds, excisional wounds, deep wounds involving damage of the dermis and epidermis, eye tissue wounds, dental tissue wounds, oral cavity wounds, diabetic ulcers, dermal ulcers, cubitus ulcers, arterial ulcers, venous stasis ulcers,  
20 burns resulting from heat exposure or chemicals, and other abnormal wound healing conditions such as uremia, malnutrition, vitamin deficiencies and complications associated with systemic treatment with steroids, radiation therapy and antineoplastic drugs and antimetabolites. Polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to promote dermal reestablishment subsequent to dermal loss

25 The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to increase the adherence of skin grafts to a wound bed and to stimulate re-epithelialization from the wound bed. The following are a non-exhaustive list of grafts that polynucleotides or polypeptides, agonists or antagonists of the invention,

could be used to increase adherence to a wound bed: autografts, artificial skin, allografts, autodermic graft, autoepidermic grafts, avascular grafts, Blair-Brown grafts, bone graft, brephoplastic grafts, cutis graft, delayed graft, dermic graft, epidermic graft, fascia graft, full thickness graft, heterologous graft, xenograft, homologous graft, hyperplastic graft, lamellar graft, mesh graft, mucosal graft, Ollier-Thiersch graft, omentoplastic graft, patch graft, pedicle graft, penetrating graft, split skin graft, thick split graft. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, can be used to promote skin strength and to improve the appearance of aged skin.

It is believed that the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, will also produce changes in hepatocyte proliferation, and epithelial cell proliferation in the lung, breast, pancreas, stomach, small intestine, and large intestine. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could promote proliferation of epithelial cells such as sebocytes, hair follicles, hepatocytes, type II pneumocytes, mucin-producing goblet cells, and other epithelial cells and their progenitors contained within the skin, lung, liver, and gastrointestinal tract. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, may promote proliferation of endothelial cells, keratinocytes, and basal keratinocytes.

The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could also be used to reduce the side effects of gut toxicity that result from radiation, chemotherapy treatments or viral infections. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, may have a cytoprotective effect on the small intestine mucosa. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, may also stimulate healing of mucositis (mouth ulcers) that result from chemotherapy and viral infections.

The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could further be used in full regeneration of skin in full and partial thickness skin defects, including burns, (i.e., repopulation of hair follicles, sweat glands, and sebaceous glands), treatment of other skin defects such as psoriasis. The polynucleotides or

polypeptides, and/or agonists or antagonists of the invention, could be used to treat epidermolysis bullosa, a defect in adherence of the epidermis to the underlying dermis which results in frequent, open and painful blisters by accelerating reepithelialization of these lesions. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could also be used to treat gastric and duodenal ulcers and help heal by scar formation of the mucosal lining and regeneration of glandular mucosa and duodenal mucosal lining more rapidly. Inflammatory bowel diseases, such as Crohn's disease and ulcerative colitis, are diseases which result in destruction of the mucosal surface of the small or large intestine, respectively. Thus, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to promote the resurfacing of the mucosal surface to aid more rapid healing and to prevent progression of inflammatory bowel disease. Treatment with the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, is expected to have a significant effect on the production of mucus throughout the gastrointestinal tract and could be used to protect the intestinal mucosa from injurious substances that are ingested or following surgery. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to treat diseases associated with the under expression of the polynucleotides of the invention.

Moreover, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to prevent and heal damage to the lungs due to various pathological states. A growth factor such as the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, which could stimulate proliferation and differentiation and promote the repair of alveoli and bronchiolar epithelium to prevent or treat acute or chronic lung damage. For example, emphysema, which results in the progressive loss of alveoli, and inhalation injuries, i.e., resulting from smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli could be effectively treated using the polynucleotides or polypeptides, and/or agonists or antagonists of the invention. Also, the polynucleotides or polypeptides, and/or agonists or antagonists of the

invention, could be used to stimulate the proliferation of and differentiation of type II pneumocytes, which may help treat or prevent disease such as hyaline membrane diseases, such as infant respiratory distress syndrome and bronchopulmonary dysplasia, in premature infants.

5           The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could stimulate the proliferation and differentiation of hepatocytes and, thus, could be used to alleviate or treat liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances (i.e., acetaminophen, carbon tetrachloride and other hepatotoxins known in the art).

10           In addition, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to treat or prevent the onset of diabetes mellitus. In patients with newly diagnosed Types I and II diabetes, where some islet cell function remains, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to maintain the islet function so as to alleviate, delay or prevent permanent  
15           manifestation of the disease. Also, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used as an auxiliary in islet cell transplantation to improve or promote islet cell function.

### **Infectious Disease**

20           A polypeptide or polynucleotide and/or agonist or antagonist of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response.

25           Alternatively, polypeptide or polynucleotide and/or agonist or antagonist of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention. Examples of viruses, include, but are not limited to Examples of viruses, include, but are not limited to the following DNA and RNA viruses and viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Dengue, EBV, HIV, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza A, Influenza B, and parainfluenza), Papiloma virus, Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiollitis, respiratory syncytial virus, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), Japanese B encephalitis, Junin, Chikungunya, Rift Valley fever, yellow fever, meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used to treat or detect any of these symptoms or diseases. In specific embodiments, polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat: meningitis, Dengue, EBV, and/or hepatitis (e.g., hepatitis B). In an additional specific embodiment polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat patients nonresponsive to one or more other commercially available hepatitis vaccines. In a further specific embodiment polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat AIDS.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention include, but not limited to, include, but not limited to, the following Gram-Negative and Gram-positive bacteria and bacterial families and fungi:

- 5 Actinomycetales (e.g., *Corynebacterium*, *Mycobacterium*, *Nocardia*), *Cryptococcus neoformans*, Aspergillosis, Bacillaceae (e.g., Anthrax, *Clostridium*), Bacteroidaceae, Blastomycosis, *Bordetella*, *Borrelia* (e.g., *Borrelia burgdorferi*, Brucellosis, Candidiasis, *Campylobacter*, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, *E. coli* (e.g., Enterotoxigenic *E. coli* and Enterohemorrhagic *E. coli*), Enterobacteriaceae (*Klebsiella*,  
10 *Salmonella* (e.g., *Salmonella typhi*, and *Salmonella paratyphi*), *Serratia*, *Yersinia*), *Erysipelothrix*, *Helicobacter*, Legionellosis, Leptospirosis, *Listeria*, Mycoplasmatales, *Mycobacterium leprae*, *Vibrio cholerae*, Neisseriaceae (e.g., *Acinetobacter*, Gonorrhea, Meningococcal), *Meisseria meningitidis*, Pasteurellacea Infections (e.g., *Actinobacillus*, *Heamophilus* (e.g., *Heamophilus influenza* type B), *Pasteurella*), *Pseudomonas*,  
15 Rickettsiaceae, Chlamydiaceae, Syphilis, *Shigella* spp., Staphylococcal, Meningiococcal, Pneumococcal and Streptococcal (e.g., *Streptococcus pneumoniae* and Group B *Streptococcus*). These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS  
20 related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis (e.g., meningitis types A and B), Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic  
25 Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. Polynucleotides or polypeptides, agonists or antagonists of the invention, can be used to treat or detect any of these symptoms or diseases. In specific embodiments, Ppolynucleotides, polypeptides,

agonists or antagonists of the invention are used to treat: tetanus, Diphtheria, botulism, and/or meningitis type B.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention include, but not limited to, the following families or class: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas and Sporozoans (e.g., *Plasmodium virax*, *Plasmodium falciparum*, *Plasmodium malariae* and *Plasmodium ovale*). These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), malaria, pregnancy complications, and toxoplasmosis. polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used to treat or detect any of these symptoms or diseases. In specific embodiments, polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat malaria.

Preferably, treatment using a polypeptide or polynucleotide and/or agonist or antagonist of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

## 25 **Regeneration**

A polynucleotide or polypeptide and/or agonist or antagonist of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues



could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

5           Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vasculature (including vascular and lymphatics), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

10           Moreover, a polynucleotide or polypeptide and/or agonist or antagonist of the present invention may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide and/or agonist or antagonist of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be  
15           treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

            Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide and/or agonist or antagonist of the present invention to  
20           proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized  
25           neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide and/or agonist or antagonist of the present invention.

**Chemotaxis**

A polynucleotide or polypeptide and/or agonist or antagonist of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes  
5 cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide and/or agonist or antagonist of the present  
10 invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic  
15 molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide and/or agonist or antagonist of the present invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, a polynucleotide or polypeptide and/or agonist  
20 or antagonist of the present invention could be used as an inhibitor of chemotaxis.

**Binding Activity**

A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of  
25 the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the

5 polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane.

10 Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide,

15 wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product

20 mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can

25 measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

Additionally, the receptor to which a polypeptide of the invention binds can be identified by numerous methods known to those of skill in the art, for example, ligand

panning and FACS sorting (Coligan, et al., Current Protocols in Immun., 1(2), Chapter 5, (1991)). For example, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the polypeptides, for example, NIH3T3 cells which are known to contain multiple receptors for the FGF family proteins, and SC-3 cells, and a  
5 cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the polypeptides. Transfected cells which are grown on glass slides are exposed to the polypeptide of the present invention, after they have been labelled. The polypeptides can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase.

10 Following fixation and incubation, the slides are subjected to auto-radiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an iterative sub-pooling and re-screening process, eventually yielding a single clones that encodes the putative receptor.

As an alternative approach for receptor identification, the labeled polypeptides can  
15 be photoaffinity linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE analysis and exposed to X-ray film. The labeled complex containing the receptors of the polypeptides can be excised, resolved into peptide fragments, and subjected to protein microsequencing. The amino acid sequence obtained from microsequencing would be used to design a set of degenerate  
20 oligonucleotide probes to screen a cDNA library to identify the genes encoding the putative receptors.

Moreover, the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling") may be employed to modulate the activities of polypeptides of the invention thereby effectively generating  
25 agonists and antagonists of polypeptides of the invention. See generally, U.S. Patent Nos. 5,605,793, 5,811,238, 5,830,721, 5,834,252, and 5,837,458, and Patten, P. A., et al., Curr. Opinion Biotechnol. 8:724-33 (1997); Harayama, S. Trends Biotechnol. 16(2):76-82 (1998); Hansson, L. O., et al., J. Mol. Biol. 287:265-76 (1999); and Lorenzo, M. M. and

Blasco, R. *Biotechniques* 24(2):308-13 (1998) (each of these patents and publications are hereby incorporated by reference). In one embodiment, alteration of polynucleotides and corresponding polypeptides of the invention may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments into a desired polynucleotide sequence of the invention molecule by homologous, or site-specific, recombination. In another embodiment, polynucleotides and corresponding polypeptides of the invention may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of the polypeptides of the invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules. In preferred embodiments, the heterologous molecules are family members. In further preferred embodiments, the heterologous molecule is a growth factor such as, for example, platelet-derived growth factor (PDGF), insulin-like growth factor (IGF-I), transforming growth factor (TGF)-alpha, epidermal growth factor (EGF), fibroblast growth factor (FGF), TGF-beta, bone morphogenetic protein (BMP)-2, BMP-4, BMP-5, BMP-6, BMP-7, activins A and B, decapentaplegic(dpp), 60A, OP-2, dorsalin, growth differentiation factors (GDFs), nodal, MIS, inhibin-alpha, TGF-beta1, TGF-beta2, TGF-beta3, TGF-beta5, and glial-derived neurotrophic factor (GDNF).

Other preferred fragments are biologically active fragments of the polypeptides of the invention. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Additionally, this invention provides a method of screening compounds to identify those which modulate the action of the polypeptide of the present invention. An example of such an assay comprises combining a mammalian fibroblast cell, a the polypeptide of the present invention, the compound to be screened and 3[H] thymidine under cell culture conditions where the fibroblast cell would normally proliferate. A control assay may be

performed in the absence of the compound to be screened and compared to the amount of fibroblast proliferation in the presence of the compound to determine if the compound stimulates proliferation by determining the uptake of 3[H] thymidine in each case. The amount of fibroblast cell proliferation is measured by liquid scintillation chromatography which measures the incorporation of 3[H] thymidine. Both agonist and antagonist compounds may be identified by this procedure.

In another method, a mammalian cell or membrane preparation expressing a receptor for a polypeptide of the present invention is incubated with a labeled polypeptide of the present invention in the presence of the compound. The ability of the compound to enhance or block this interaction could then be measured. Alternatively, the response of a known second messenger system following interaction of a compound to be screened and the receptor is measured and the ability of the compound to bind to the receptor and elicit a second messenger response is measured to determine if the compound is a potential agonist or antagonist. Such second messenger systems include but are not limited to, cAMP guanylate cyclase, ion channels or phosphoinositide hydrolysis.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptides of the invention from suitably manipulated cells or tissues. Therefore, the invention includes a method of identifying compounds which bind to the polypeptides of the invention comprising the steps of: (a) incubating a candidate binding compound with the polypeptide; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with the polypeptide, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

Also, one could identify molecules bind a polypeptide of the invention

experimentally by using the beta-pleated sheet regions contained in the polypeptide sequence of the protein. Accordingly, specific embodiments of the invention are directed to polynucleotides encoding polypeptides which comprise, or alternatively consist of, the amino acid sequence of each beta pleated sheet regions in a disclosed polypeptide sequence. Additional embodiments of the invention are directed to polynucleotides encoding polypeptides which comprise, or alternatively consist of, any combination or all of contained in the polypeptide sequences of the invention. Additional preferred embodiments of the invention are directed to polypeptides which comprise, or alternatively consist of, the amino acid sequence of each of the beta pleated sheet regions in one of the polypeptide sequences of the invention. Additional embodiments of the invention are directed to polypeptides which comprise, or alternatively consist of, any combination or all of the beta pleated sheet regions in one of the polypeptide sequences of the invention.

### **Targeted Delivery**

In another embodiment, the invention provides a method of delivering compositions to targeted cells expressing a receptor for a polypeptide of the invention, or cells expressing a cell bound form of a polypeptide of the invention.

As discussed herein, polypeptides or antibodies of the invention may be associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs via hydrophobic, hydrophilic, ionic and/or covalent interactions.

In one embodiment, the invention provides a method for the specific delivery of compositions of the invention to cells by administering polypeptides of the invention (including antibodies) that are associated with heterologous polypeptides or nucleic acids. In one example, the invention provides a method for delivering a therapeutic protein into the targeted cell. In another example, the invention provides a method for delivering a single stranded nucleic acid (e.g., antisense or ribozymes) or double stranded nucleic acid (e.g., DNA that can integrate into the cell's genome or replicate episomally and that can be transcribed) into the targeted cell.

In another embodiment, the invention provides a method for the specific destruction of cells (e.g., the destruction of tumor cells) by administering polypeptides of the invention (e.g., polypeptides of the invention or antibodies of the invention) in association with toxins or cytotoxic prodrugs.

5 By "toxin" is meant compounds that bind and activate endogenous cytotoxic effector systems, radioisotopes, holotoxins, modified toxins, catalytic subunits of toxins, or any molecules or enzymes not normally present in or on the surface of a cell that under defined conditions cause the cell's death. Toxins that may be used according to the methods of the invention include, but are not limited to, radioisotopes known in the art,  
10 compounds such as, for example, antibodies (or complement fixing containing portions thereof) that bind an inherent or induced endogenous cytotoxic effector system, thymidine kinase, endonuclease, RNase, alpha toxin, ricin, abrin, *Pseudomonas* exotoxin A, diphtheria toxin, saporin, momordin, gelonin, pokeweed antiviral protein, alpha-sarcin and cholera toxin. By "cytotoxic prodrug" is meant a non-toxic compound that is converted by  
15 an enzyme, normally present in the cell, into a cytotoxic compound. Cytotoxic prodrugs that may be used according to the methods of the invention include, but are not limited to, glutamyl derivatives of benzoic acid mustard alkylating agent, phosphate derivatives of etoposide or mitomycin C, cytosine arabinoside, daunorubisin, and phenoxyacetamide derivatives of doxorubicin.

20

#### Drug Screening

Further contemplated is the use of the polypeptides of the present invention, or the polynucleotides encoding these polypeptides, to screen for molecules which modify the activities of the polypeptides of the present invention. Such a method would include  
25 contacting the polypeptide of the present invention with a selected compound(s) suspected of having antagonist or agonist activity, and assaying the activity of these polypeptides following binding.

This invention is particularly useful for screening therapeutic compounds by using



the polypeptides of the present invention, or binding fragments thereof, in any of a variety of drug screening techniques. The polypeptide or fragment employed in such a test may be affixed to a solid support, expressed on a cell surface, free in solution, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells  
5 which are stably transformed with recombinant nucleic acids expressing the polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. One may measure, for example, the formulation of complexes between the agent being tested and a polypeptide of the present invention.

Thus, the present invention provides methods of screening for drugs or any other  
10 agents which affect activities mediated by the polypeptides of the present invention. These methods comprise contacting such an agent with a polypeptide of the present invention or a fragment thereof and assaying for the presence of a complex between the agent and the polypeptide or a fragment thereof, by methods well known in the art. In such a competitive binding assay, the agents to screen are typically labeled. Following incubation, free agent  
15 is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of a particular agent to bind to the polypeptides of the present invention.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to the polypeptides of the present invention,  
20 and is described in great detail in European Patent Application 84/03564, published on September 13, 1984, which is incorporated herein by reference herein. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with polypeptides of the present invention and washed. Bound polypeptides are then detected by  
25 methods well known in the art. Purified polypeptides are coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies may be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding polypeptides of the present invention specifically compete with a test compound for binding to the polypeptides or fragments thereof. In this manner, the antibodies are used to detect the presence of any peptide which  
5 shares one or more antigenic epitopes with a polypeptide of the invention.

#### **Antisense And Ribozyme (Antagonists)**

In specific embodiments, antagonists according to the present invention are nucleic acids corresponding to the sequences contained in SEQ ID NO:X, or the complementary  
10 strand thereof, and/or to nucleotide sequences contained a deposited clone. In one embodiment, antisense sequence is generated internally by the organism, in another embodiment, the antisense sequence is separately administered (see, for example, O'Connor, Neurochem., 56:560 (1991). Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Antisense technology can be used  
15 to control gene expression through antisense DNA or RNA, or through triple-helix formation. Antisense techniques are discussed for example, in Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Triple helix formation is discussed in, for instance, Lee et al., Nucleic Acids Research, 6:3073 (1979); Cooney et al., Science, 241:456 (1988); and  
20 Dervan et al., Science, 251:1300 (1991). The methods are based on binding of a polynucleotide to a complementary DNA or RNA.

For example, the use of c-myc and c-myb antisense RNA constructs to inhibit the growth of the non-lymphocytic leukemia cell line HL-60 and other cell lines was previously described. (Wickstrom et al. (1988); Anfossi et al. (1989)). These experiments  
25 were performed in vitro by incubating cells with the oligoribonucleotide. A similar procedure for in vivo use is described in WO 91/15580. Briefly, a pair of oligonucleotides for a given antisense RNA is produced as follows: A sequence complimentary to the first 15 bases of the open reading frame is flanked by an EcoRI site on the 5' end and a HindIII

site on the 3' end. Next, the pair of oligonucleotides is heated at 90°C for one minute and then annealed in 2X ligation buffer (20mM TRIS HCl pH 7.5, 10mM MgCl<sub>2</sub>, 10mM dithiothreitol (DTT) and 0.2 mM ATP) and then ligated to the EcoR1/Hind III site of the retroviral vector PMV7 (WO 91/15580).

5 For example, the 5' coding portion of a polynucleotide that encodes the mature polypeptide of the present invention may be used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription thereby preventing transcription and the production of the receptor. The antisense RNA  
10 oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into receptor polypeptide.

In one embodiment, the antisense nucleic acid of the invention is produced intracellularly by transcription from an exogenous sequence. For example, a vector or a portion thereof, is transcribed, producing an antisense nucleic acid (RNA) of the invention.  
15 Such a vector would contain a sequence encoding the antisense nucleic acid of the invention. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in vertebrate  
20 cells. Expression of the sequence encoding a polypeptide of the invention, or fragments thereof, can be by any promoter known in the art to act in vertebrate, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include, but are not limited to, the SV40 early promoter region (Bernoist and Chambon, Nature, 29:304-310 (1981), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus  
25 (Yamamoto et al., Cell, 22:787-797 (1980), the herpes thymidine promoter (Wagner et al., Proc. Natl. Acad. Sci. U.S.A., 78:1441-1445 (1981), the regulatory sequences of the metallothionein gene (Brinster et al., Nature, 296:39-42 (1982)), etc.

The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a gene of interest. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," referred to herein, means a sequence having sufficient

5 complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double stranded antisense nucleic acids of the invention, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the larger the hybridizing nucleic acid, the more base mismatches with a

10 RNA sequence of the invention it may contain and still form a stable duplex (or triplex as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' end of the message, *e.g.*, the 5' untranslated sequence up to and including the AUG initiation codon, should work most

15 efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have been shown to be effective at inhibiting translation of mRNAs as well. See generally, Wagner, R., *Nature*, 372:333-335 (1994). Thus, oligonucleotides complementary to either the 5' - or 3' - non- translated, non-coding regions of a polynucleotide sequence of the invention could be used in an antisense

20 approach to inhibit translation of endogenous mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are less efficient inhibitors of translation but could be used in accordance with the invention. Whether designed to hybridize to the 5' -, 3' - or coding region of mRNA, antisense

25 nucleic acids should be at least six nucleotides in length, and are preferably oligonucleotides ranging from 6 to about 50 nucleotides in length. In specific aspects the oligonucleotide is at least 10 nucleotides, at least 17 nucleotides, at least 25 nucleotides or at least 50 nucleotides.

The polynucleotides of the invention can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide  
5 may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556 (1989); Lemaitre et al., Proc. Natl. Acad. Sci., 84:648-652 (1987); PCT Publication NO: WO88/09810, published December 15, 1988) or the blood-brain barrier (see, e.g., PCT Publication NO: WO89/10134, published April 25,  
10 1988), hybridization-triggered cleavage agents. (See, e.g., Krol et al., BioTechniques, 6:958-976 (1988)) or intercalating agents. (See, e.g., Zon, Pharm. Res., 5:539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

15 The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including, but not limited to, 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine,  
20 N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine,  
25 pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the antisense oligonucleotide comprises at least one  
5 modified phosphate backbone selected from the group including, but not limited to, a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet another embodiment, the antisense oligonucleotide is an a-anomeric  
10 oligonucleotide. An a-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual b-units, the strands run parallel to each other (Gautier et al., Nucl. Acids Res., 15:6625-6641 (1987)). The oligonucleotide is a 2-O-methylribonucleotide (Inoue et al., Nucl. Acids Res., 15:6131-6148 (1987)), or a chimeric RNA-DNA analogue (Inoue et al., FEBS Lett. 215:327-330 (1987)).

15 Polynucleotides of the invention may be synthesized by standard methods known in the art, e.g. by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (Nucl. Acids Res., 16:3209 (1988)), methylphosphonate oligonucleotides can be prepared by use of controlled  
20 pore glass polymer supports (Sarin et al., Proc. Natl. Acad. Sci. U.S.A., 85:7448-7451 (1988)), etc.

While antisense nucleotides complementary to the coding region sequence of the invention could be used, those complementary to the transcribed untranslated region are most preferred.

25 Potential antagonists according to the invention also include catalytic RNA, or a ribozyme (See, e.g., PCT International Publication WO 90/11364, published October 4, 1990; Sarver et al, Science, 247:1222-1225 (1990)). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy mRNAs corresponding to the

polynucleotides of the invention, the use of hammerhead ribozymes is preferred.

Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and

5 production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, Nature, 334:585-591 (1988). There are numerous potential hammerhead ribozyme cleavage sites within each nucleotide sequence disclosed in the sequence listing. Preferably, the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the mRNA corresponding to the polynucleotides of the  
10 invention; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

As in the antisense approach, the ribozymes of the invention can be composed of modified oligonucleotides (e.g. for improved stability, targeting, etc.) and should be delivered to cells which express the polynucleotides of the invention in vivo. DNA  
15 constructs encoding the ribozyme may be introduced into the cell in the same manner as described above for the introduction of antisense encoding DNA. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive promoter, such as, for example, pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy endogenous  
20 messages and inhibit translation. Since ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Antagonist/agonist compounds may be employed to inhibit the cell growth and proliferation effects of the polypeptides of the present invention on neoplastic cells and tissues, i.e. stimulation of angiogenesis of tumors, and, therefore, retard or prevent  
25 abnormal cellular growth and proliferation, for example, in tumor formation or growth.

The antagonist/agonist may also be employed to prevent hyper-vascular diseases, and prevent the proliferation of epithelial lens cells after extracapsular cataract surgery.

Prevention of the mitogenic activity of the polypeptides of the present invention may also be desirous in cases such as restenosis after balloon angioplasty.

The antagonist/agonist may also be employed to prevent the growth of scar tissue during wound healing.

- 5       The antagonist/agonist may also be employed to treat the diseases described herein. Thus, the invention provides a method of treating disorders or diseases, including but not limited to the disorders or diseases listed throughout this application, associated with overexpression of a polynucleotide of the present invention by administering to a patient
- 10   (a) an antisense molecule directed to the polynucleotide of the present invention, and/or  
(b) a ribozyme directed to the polynucleotide of the present invention

#### **Other Activities**

- The polypeptide of the present invention, as a result of the ability to stimulate vascular endothelial cell growth, may be employed in treatment for stimulating re-vascularization of ischemic tissues due to various disease conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions. These polypeptide may also be
- 15   employed to stimulate angiogenesis and limb regeneration, as discussed above.

- The polypeptide may also be employed for treating wounds due to injuries, burns, post-operative tissue repair, and ulcers since they are mitogenic to various cells of different origins, such as fibroblast cells and skeletal muscle cells, and therefore, facilitate the repair
- 20   or replacement of damaged or diseased tissue.

- The polypeptide of the present invention may also be employed stimulate neuronal growth and to treat and prevent neuronal damage which occurs in certain neuronal disorders or neuro-degenerative conditions such as Alzheimer's disease, Parkinson's disease, and AIDS-related complex. The polypeptide of the invention may have the ability
- 25   to stimulate chondrocyte growth, therefore, they may be employed to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts.

The polypeptide of the present invention may be also be employed to prevent skin aging due to sunburn by stimulating keratinocyte growth.



The polypeptide of the invention may also be employed for preventing hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth. Along the same lines, the polypeptides of the present invention may be employed to stimulate growth and differentiation of hematopoietic cells and bone marrow cells when  
5 used in combination with other cytokines.

The polypeptide of the invention may also be employed to maintain organs before transplantation or for supporting cell culture of primary tissues.

The polypeptide of the present invention may also be employed for inducing tissue of mesodermal origin to differentiate in early embryos.

10 The polypeptide or polynucleotides and/or agonist or antagonists of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

The polypeptide or polynucleotides and/or agonist or antagonists of the present invention may also be used to modulate mammalian characteristics, such as body height,  
15 weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, polypeptides or polynucleotides and/or agonist or antagonists of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

Polypeptide or polynucleotides and/or agonist or antagonists of the present  
20 invention may be used to change a mammal's mental state or physical state by influencing biorhythms, cardiac rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

25 Polypeptide or polynucleotides and/or agonist or antagonists of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

**Other Preferred Embodiments**

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a  
5 sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table XIII.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the  
10 Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table XIII.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the  
15 Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table XIII.

Similarly preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the  
20 First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table XIII.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous  
25 nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table XIII.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which comprises a human cDNA clone identified by a cDNA Clone Identifier in Table XIII, which DNA molecule is contained in the material deposited with the American Type Culture Collection and given the ATCC Deposit Number shown in Table XIII for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table XIII, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table XIII.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

5 A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

10 A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table XIII; and a nucleotide sequence encoded by a human cDNA clone identified by a  
15 cDNA Clone Identifier in Table XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table XIII; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

20 Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from  
25 a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid

molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table XIII; and a nucleotide sequence encoded by a human cDNA clone  
5 identified by a cDNA Clone Identifier in Table XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table XIII.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel  
10 is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table XIII, which method comprises a step of detecting in a biological sample  
15 obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table XIII; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table XIII and  
20 contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table XIII.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95%  
25 identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a

panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table XIII; and a nucleotide sequence encoded by a human  
5 cDNA clone identified by a cDNA Clone Identifier in Table XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table XIII. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino  
10 acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table XIII.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set  
15 forth for SEQ ID NO:Y in Table XIII.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at  
20 least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at  
25 least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table XIII.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in  
5 Table XIII.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table XIII and contained in the deposit with the  
10 ATCC Deposit Number shown for said cDNA clone in Table XIII.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table XIII and contained in the deposit with the  
15 ATCC Deposit Number shown for said cDNA clone in Table XIII.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in  
20 Table XIII.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table XIII; and a  
25 complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table XIII.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table XIII; and a  
5 complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table XIII; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of  
10 said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in  
15 said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table XIII; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone  
20 Identifier in Table XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table XIII.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

25 Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group



consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table XIII; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in  
5 Table XIII.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at  
10 least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table XIII, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a  
15 panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table XIII; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table  
20 XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table XIII.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide  
25 sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as

defined in Table XIII; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table XIII.

5        Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: an amino acid  
10        sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table XIII; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table XIII.

Further preferred is a method of making a recombinant vector comprising inserting  
15        any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

Also preferred is a method of making an isolated polypeptide comprising culturing  
20        this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the  
25        residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table XIII and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table XIII; and an amino acid sequence of a secreted portion of a protein encoded by a human cDNA clone identified by

a cDNA Clone Identifier in Table XIII and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table XIII. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased  
5 level of a secreted protein activity, which method comprises administering to such an individual a pharmaceutical composition comprising an amount of an isolated polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

The above-recited applications have uses in a wide variety of hosts. Such hosts  
10 include, but are not limited to, human, murine, rabbit, goat, guinea pig, camel, horse, mouse, rat, hamster, pig, micro-pig, chicken, goat, cow, sheep, dog, cat, non-human primate, and human. In specific embodiments, the host is a mouse, rabbit, goat, guinea pig, chicken, rat, hamster, pig, sheep, dog or cat. In preferred embodiments, the host is a mammal. In most preferred embodiments, the host is a human.

15

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

20

### **Examples**

#### **Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample**

Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table XIII identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from  
25 which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table XIII as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
	Uni-Zap XR	pBluescript (pBS)
5	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSPORT 2.0	pCMVSPORT 2.0
	pCMVSPORT 3.0	pCMVSPORT 3.0
10	pCR <sup>®</sup> 2.1	pCR <sup>®</sup> 2.1
	Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Altting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Altting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from	
15	Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the	
20	polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.	
25	Vectors pSport1, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an	
30	ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR <sup>®</sup> 2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res.	

16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table XIII, as well as the corresponding plasmid vector sequences designated above.

5       The deposited material in the sample assigned the ATCC Deposit Number cited in Table XIII for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone identified in Table XIII. Typically, each ATCC deposit sample cited in Table XIII comprises a mixture  
10 of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table XIII. First, a plasmid is directly isolated by  
15 screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with <sup>32</sup>P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A  
20 Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a  
25 density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edit., (1989), Cold Spring

Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table XIII) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 ul of reaction mixture with 0.5 ug of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl<sub>2</sub>, 0.01% (w/v) gelatin, 20 uM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94 degree C for 1 min; annealing at 55 degree C for 1 min; elongation at 72 degree C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids Res. 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A<sup>+</sup> RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and  
5 the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA  
10 synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

15

#### **Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide**

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X., according to the method described in Example 1. (See also, Sambrook.)

20

#### **Example 3: Tissue Distribution of Polypeptide**

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by, among others, Sambrook et al. For example, a cDNA probe produced by the method described in  
25 Example 1 is labeled with P<sup>32</sup> using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to

manufacturer's protocol number PT1200-1. The purified labeled probe is then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are mounted and exposed to film at -70 degree C overnight, and the films developed according to standard procedures.

10 **Example 4: Chromosomal Mapping of the Polynucleotides**

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95 degree C; 1 minute, 56 degree C; 1 minute, 70 degree C. This cycle is repeated 32 times followed by one 5 minute cycle at 70 degree C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

**Example 5: Bacterial Expression of a Polypeptide**

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme



sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp<sup>r</sup>), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

5           The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan<sup>r</sup>). Transformants are identified by their ability  
10   to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are  
15   grown to an optical density 600 (O.D.<sup>600</sup>) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6  
20   Molar Guanidine HCl by stirring for 3-4 hours at 4 degree C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995)  
25   QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10

volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4 degree C or frozen at -80 degree C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (lacIq). The origin of replication (oriC) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

**Example 6: Purification of a Polypeptide from an Inclusion Body**

5           The following alternative method can be used to purify a polypeptide expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10 degree C.

          Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10 degree C and the cells harvested by continuous centrifugation at  
10   15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

15           The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

20           The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4 degree C overnight to allow further GuHCl extraction.

          Following high speed centrifugation (30,000 xg) to remove insoluble particles, the  
25   GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4 degree C without mixing for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16  $\mu$ m membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems).

- 5 The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

- Fractions containing the polypeptide are then pooled and mixed with 4 volumes of  
10 water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear  
15 gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant  $A_{280}$  monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

- The resultant polypeptide should exhibit greater than 95% purity after the above  
20 refolding and purification steps. No major contaminant bands should be observed from Commassie blue stained 16% SDS-PAGE gel when 5  $\mu$ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

25 **Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System**

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong

polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene  
5 from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as  
10 pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the  
15 AUG initiation codon and the naturally associated leader sequence identified in Table XIII, is amplified using the PCR protocol described in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A  
20 Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

25 The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("Geneclean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five ug of a plasmid containing the polynucleotide is co-transfected with 1.0 ug of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417 (1987). One ug of BaculoGold™ virus DNA and 5 ug of the plasmid are mixed in a sterile well of a microtiter plate containing 50 ul of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 ul Lipofectin plus 90 ul Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27 degrees C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27 degrees C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 ul of Grace's medium and the suspension containing

the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4 degree C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium  
5 supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant  
baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2.  
If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced  
with SF900 II medium minus methionine and cysteine (available from Life Technologies  
Inc., Rockville, MD). After 42 hours, 5 uCi of <sup>35</sup>S-methionine and 5 uCi <sup>35</sup>S-cysteine  
10 (available from Amersham) are added. The cells are further incubated for 16 hours and  
then are harvested by centrifugation. The proteins in the supernatant as well as the  
intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if  
radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified  
15 protein may be used to determine the amino terminal sequence of the produced protein.

#### **Example 8: Expression of a Polypeptide in Mammalian Cells**

The polypeptide of the present invention can be expressed in a mammalian cell. A  
20 typical mammalian expression vector contains a promoter element, which mediates the  
initiation of transcription of mRNA, a protein coding sequence, and signals required for the  
termination of transcription and polyadenylation of the transcript. Additional elements  
include enhancers, Kozak sequences and intervening sequences flanked by donor and  
acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early  
25 and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g.,  
RSV, HTLV, HIV and the early promoter of the cytomegalovirus (CMV). However,  
cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used include, human Hela, 293,  
5 H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of  
10 the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C.,  
15 Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines  
20 contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al.,  
25 Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and



termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known  
5 in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a  
10 heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and  
15 purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection.  
20 Five  $\mu$ g of the expression plasmid pC6 a pC4 is cotransfected with 0.5  $\mu$ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and  
25 seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM,

800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 uM, 2 uM, 5 uM, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 uM. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

#### **Example 9: Protein Fusions**

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing

the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

10 GGGATCCGGAGCCCAAATCTTCTGACAAACTCACACATGCCACCGTGCCCA  
GCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAACCCAA  
GGACACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGTGGTGGACG  
TAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGA  
GGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC  
15 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA  
GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAACCCCCATCGAGAAAACCA  
TCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA  
TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGG  
CTTCTATCCAAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG  
20 AACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC  
TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCT  
CATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC  
TCCCTGTCTCCGGGTAAATGAGTGCGACGGCCGCGACTCTAGAGGAT (SEQ ID  
NO:1)

25

#### **Example 10: Production of an Antibody from a Polypeptide**

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) As one example of such methods, cells expressing a

polypeptide of the present invention is administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce  
5 polyclonal antisera of greater specific activity.

In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., *Nature* 256:495 (1975); Köhler et al., *Eur. J. Immunol.* 6:511 (1976); Köhler et al., *Eur. J. Immunol.* 6:292  
10 (1976); Hammerling et al., in: *Monoclonal Antibodies and T-Cell Hybridomas*, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented  
15 with 10% fetal bovine serum (inactivated at about 56 degrees C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 ug/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present  
20 invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (*Gastroenterology* 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding  
25 the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain

an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-  
5 idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

It will be appreciated that Fab and F(ab')<sub>2</sub> and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such  
10 fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')<sub>2</sub> fragments). Alternatively, secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized"  
15 chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494;  
20 Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

### **Example 11: Production Of Secreted Protein For High-Throughput Screening**

#### **Assays**

25 The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at  $2 \times 10^5$  cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37 degrees C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (116.6 mg/L of CaCl<sub>2</sub> (anhyd); 0.00130 mg/L CuSO<sub>4</sub>·5H<sub>2</sub>O; 0.050 mg/L of Fe(NO<sub>3</sub>)<sub>3</sub>·9H<sub>2</sub>O; 0.417 mg/L of FeSO<sub>4</sub>·7H<sub>2</sub>O; 311.80 mg/L of Kcl; 28.64 mg/L of MgCl<sub>2</sub>; 48.84 mg/L of MgSO<sub>4</sub>; 6995.50 mg/L of NaCl; 2400.0 mg/L of

5 NaHCO<sub>3</sub>; 62.50 mg/L of NaH<sub>2</sub>PO<sub>4</sub>·H<sub>2</sub>O; 71.02 mg/L of Na<sub>2</sub>HPO<sub>4</sub>; .4320 mg/L of ZnSO<sub>4</sub>·7H<sub>2</sub>O; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitric Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid;

10 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml of L-Asparagine-H<sub>2</sub>O; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL-H<sub>2</sub>O; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H<sub>2</sub>O; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine;

15 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalanine; 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tyrosine-2Na-2H<sub>2</sub>O; 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of

20 Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; and 0.680 mg/L of Vitamin B<sub>12</sub>; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine; 0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate;

25 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; and 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal) with 2mm glutamine and 1x penstrep. (BSA (81-

068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B adds  
5 1.5ml appropriate media to each well. Incubate at 37 degrees C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

10 It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a  
15 particular assay.

#### **Example 12: Construction of GAS Reporter Construct**

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway  
20 bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members  
25 of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations



in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family.

- 5 Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

- The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A  
10 cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN- $\alpha$ , IFN- $\gamma$ , and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal  
15 region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

- Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the  
20 GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

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	<u>Ligand</u>	<u>JAKs</u>				<u>STATS GAS(elements) or ISRE</u>
		<u>tyk2</u>	<u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>	
5	<u>IFN family</u>					
	IFN-a/B	+	+	-	-	1,2,3 ISRE
	IFN-g		+	+	-	1 GAS (IRF1>Lys6>IFP)
	IL-10	+	?	?	-	1,3
10	<u>gp130 family</u>					
	IL-6 (Pleiotrophic)	+	+	+	?	1,3 GAS (IRF1>Lys6>IFP)
	IL-11(Pleiotrophic)	?	+	?	?	1,3
	OnM(Pleiotrophic)	?	+	+	?	1,3
	LIF(Pleiotrophic)	?	+	+	?	1,3
	CNTF(Pleiotrophic)	-/+	+	+	?	1,3
15	G-CSF(Pleiotrophic)	?	+	?	?	1,3
	IL-12(Pleiotrophic)	+	-	+	+	1,3
20	<u>g-C family</u>					
	IL-2 (lymphocytes)	-	+	-	+	1,3,5 GAS
	IL-4 (lymph/myeloid)	-	+	-	+	6 GAS (IRF1 = IFP >>Ly6)(IgH)
	IL-7 (lymphocytes)	-	+	-	+	5 GAS
	IL-9 (lymphocytes)	-	+	-	+	5 GAS
	IL-13 (lymphocyte)	-	+	?	?	6 GAS
	IL-15	?	+	?	+	5 GAS
25	<u>gp140 family</u>					
	IL-3 (myeloid)	-	-	+	-	5 GAS (IRF1>IFP>>Ly6)
	IL-5 (myeloid)	-	-	+	-	5 GAS
	GM-CSF (myeloid)	-	-	+	-	5 GAS
30	<u>Growth hormone family</u>					
	GH	?	-	+	-	5
	PRL	?	+/-	+	-	1,3,5
	EPO	?	-	+	-	5
35	<u>Receptor Tyrosine Kinases</u>					
	EGF	?	+	+	-	1,3 GAS (IRF1)
	PDGF	?	+	+	-	1,3
	CSF-1	?	+	+	-	1,3 GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind

5 STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

5':GCGCCTCGAGATTTCCTCCCGAAATCTAGATTTCCTCCCGAAATGATTTCCTCCCGAA  
 10 ATGATTTCCTCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTGTCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested

15 with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

5':CTCGAGATTTCCTCCCGAAATCTAGATTTCCTCCCGAAATGATTTCCTCCCGAAATGA  
 TTTCCCTCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCCTA  
 ACTCCGCCCCATCCCGCCCCCTAACTCCGCCCCAGTTCCGCCCCATTCTCCGCCCCAT  
 20 GGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGCCTCTGAG  
 CTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAA  
GCTT:3' (SEQ ID NO:5)

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline

25 phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase,

alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

### **Example 13: High-Throughput Screening Assay for T-cell Activity.**

The following protocol is used to assess T-cell activity by identifying factors, and determining whether supernate containing a polypeptide of the invention proliferates and/or differentiates T-cells. T-cell activity is assessed using the GAS/SEAP/Neo

construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can  
5 also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and  
10 transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate  
15 sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1%Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies) with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

During the incubation period, count cell concentration, spin down the required  
20 number of cells ( $10^7$  per transfection), and resuspend in OPTI-MEM to a final concentration of  $10^7$  cells/ml. Then add 1ml of  $1 \times 10^7$  cells in OPTI-MEM to T25 flask and incubate at 37 degrees C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum,  
25 1 mg/ml Gentamicin, and 1% Pen-Strep. These cells are treated with supernatants containing polypeptides of the invention and/or induced polypeptides of the invention as produced by the protocol described in Example 11.

On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are  
5 required.

Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

After all the plates have been seeded, 50 ul of the supernatants are transferred  
10 directly from the 96 well plate containing the supernatants into each well using a 12 channel pipette. In addition, a dose of exogenous interferon gamma (0.1; 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples from  
15 each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20 degrees C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4 degrees C and serve as a source of material for repeating the assay on a specific well if desired.

20 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

The above protocol may be used in the generation of both transient, as well as, stable transfected cells, which would be apparent to those of skill in the art.

25

#### **Example 14: High-Throughput Screening Assay Identifying Myeloid Activity**

The following protocol is used to assess myeloid activity by determining whether polypeptides of the invention proliferates and/or differentiates myeloid cells. Myeloid cell

activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

- 5 To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest  $2 \times 10^7$  U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM  $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$ , 1 mM  $\text{MgCl}_2$ , and 675 uM  $\text{CaCl}_2$ . Incubate at 37 degrees C for 45 min.

- 15 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37 degrees C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

- 20 These cells are tested by harvesting  $1 \times 10^8$  cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of  $5 \times 10^5$  cells/ml. Plate 200 ul cells per well in the 96-well plate (or  $1 \times 10^5$  cells/well).

Add 50 ul of the supernatant prepared by the protocol described in Example 11.

- 25 Incubate at 37 degrees C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

**Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.**

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)

5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.



PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every  
5 three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every  
10 one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

15 The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as  $5 \times 10^5$  cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to  $1 \times 10^5$  cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a  
20 positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

25 **Example 16: High-Throughput Screening Assay for T-cell Activity**

NF-KB (Nuclear Factor KB) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by

expression of certain viral gene products. As a transcription factor, NF-KB regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- KB appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

5 In non-stimulated conditions, NF- KB is retained in the cytoplasm with I-KB (Inhibitor KB). However, upon stimulation, I- KB is phosphorylated and degraded, causing NF- KB to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- KB include IL-2, IL-6, GM-CSF, ICAM-1 and class 1 MHC.

10 Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF-KB promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF-KB would be useful in treating diseases. For example, inhibitors of NF-KB could be used to treat those diseases related to the acute or chronic activation of NF-KB, such as rheumatoid arthritis.

15 To construct a vector containing the NF-KB promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF-KB binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:

5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGACTTT  
20 CCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTGTCAAAGCCTAGGC:3' (SEQ ID NO:4)

25 PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene) Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

5' :CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGACTTTCCATC  
 TGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCCG  
 CCCCTAACTCCGCCCAGTTCCGCCCATTTCTCCGCCCCATGGCTGACTAATTTTT  
 TTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTA  
 5 GTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTT:3' (SEQ ID  
 NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2-promoter plasmid (Clontech) with this NF-KB/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF-KB/SV40/SEAP cassette is removed from the above NF-KB/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the NF-KB/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF-KB/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

#### **Example 17: Assay for SEAP Activity**

As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 ul of 2.5x dilution buffer into Optiplates containing 35 ul of a supernatant. Seal the plates with a plastic

sealer and incubate at 65 degree C for 30 min. Separate the Optiplates to avoid uneven heating.

- Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 ml Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 ul Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.
- 10 Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

**Reaction Buffer Formulation:**

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6
23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25

495

40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

**Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability**

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-4 (Molecular Probes, Inc.; catalog no. F-14202), used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO<sub>2</sub> incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-4 is made in 10% pluronic acid DMSO. To load the cells with fluo-4, 50 ul of 12 ug/ml fluo-4 is added to each well. The plate is incubated at 37 degrees C in a CO<sub>2</sub> incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to  $2-5 \times 10^6$  cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-4 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37 degrees C water bath for 30-60 min. The cells are washed twice with  
5 HBSS, resuspended to  $1 \times 10^6$  cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-4. The supernatant is added to the well, and a change in fluorescence is detected.

10 To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event which has resulted in an increase in the intracellular  $\text{Ca}^{++}$  concentration.

15

#### **Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity**

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase (RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF,  
20 EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

Activation of RPTK by ligands involves ligand-mediated receptor dimerization,  
25 resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members of which mediate signal

transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or calf serum, rinsed with PBS and stored at 4 degree C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na<sub>3</sub>VO<sub>4</sub>, 2 mM Na<sub>4</sub>P<sub>2</sub>O<sub>7</sub> and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4 degrees

C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after  
5 detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4 degrees C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

Generally, the tyrosine kinase activity of a supernatant is evaluated by determining  
10 its ability to phosphorylate a tyrosine residue on a specific substrate (a biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

15 The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg<sub>2+</sub> (5mM ATP/50mM MgCl<sub>2</sub>), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl<sub>2</sub>, 5 mM MnCl<sub>2</sub>, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the components gently  
20 and preincubate the reaction mix at 30 degrees C for 2 min. Initiate the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction  
25 mixture to a microtiter plate (MTP) module and incubating at 37 degrees C for 20 min. This allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-



phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37 degrees C for one hour. Wash the well as above.

Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of tyrosine kinase activity.

**Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity**

As a potential alternative and/or compliment to the assay of protein tyrosine kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase, Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4 degrees C until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in

Example 11 for 5-20 minutes. The cells are then solubilized and extracts filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of  
5 A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA  
10 instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

**Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide**

15 RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95 degrees C for 30 seconds; 60-  
20 120 seconds at 52-58 degrees C; and 60-120 seconds at 70 degrees C, using buffer solutions described in Sidransky et al., Science 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR products  
25 analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton et al., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States

Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to

5 Example 2 are nick-translated with digoxigenin deoxy-uridine 5'-triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium  
10 iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are  
15 performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated disease.

20 **Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample**

A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is  
25 understood that one skilled in the art can modify the following assay to fit their particular needs.

For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific

antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10. The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

### **Example 23: Formulation**

The invention also provides methods of treatment and/or prevention of diseases or disorders (such as, for example, any one or more of the diseases or disorders disclosed herein) by administration to a subject of an effective amount of a Therapeutic. By therapeutic is meant a polynucleotides or polypeptides of the invention (including fragments and variants), agonists or antagonists thereof, and/or antibodies thereto, in combination with a pharmaceutically acceptable carrier type (e.g., a sterile carrier).

The Therapeutic will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the Therapeutic alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to

practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of the Therapeutic administered parenterally per dose will be in the range of about 1ug/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the Therapeutic is typically administered at a dose rate of about 1 ug/kg/hour to about 50 ug/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Therapeutics can be administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention are also suitably administered by sustained-release systems. Suitable examples of sustained-release Therapeutics are administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention are also suitably administered by sustained-release systems. Suitable examples of sustained-release Therapeutics include suitable polymeric materials (such as, for example, semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules), suitable hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, and sparingly soluble derivatives (such as, for example, a sparingly soluble salt).

Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman et al., *Biopolymers* 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (Langer et al., Id.) or poly-D- (-)-3-hydroxybutyric acid (EP 133,988).

Sustained-release Therapeutics also include liposomally entrapped Therapeutics of the invention (*see* generally, Langer, *Science* 249:1527-1533 (1990); Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 317 -327 and 353-365 (1989)). Liposomes containing the Therapeutic are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. (USA) 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci.(USA) 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal Therapeutic.

In yet an additional embodiment, the Therapeutics of the invention are delivered by way of a pump (*see* Langer, *supra*; Sefton, CRC Crit. Ref. Biomed. Eng. 14:201 (1987); Buchwald et al., *Surgery* 88:507 (1980); Saudek et al., *N. Engl. J. Med.* 321:574 (1989)).

Other controlled release systems are discussed in the review by Langer (*Science* 249:1527-1533 (1990)).

For parenteral administration, in one embodiment, the Therapeutic is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to the Therapeutic.

Generally, the formulations are prepared by contacting the Therapeutic uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The Therapeutic is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be

understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any pharmaceutical used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron  
5 membranes). Therapeutics generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Therapeutics ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for  
10 reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous Therapeutic solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized Therapeutic using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more  
15 containers filled with one or more of the ingredients of the Therapeutics of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the Therapeutics may be employed in conjunction with other  
20 therapeutic compounds.

The Therapeutics of the invention may be administered alone or in combination with adjuvants. Adjuvants that may be administered with the Therapeutics of the invention include, but are not limited to, alum, alum plus deoxycholate (ImmunoAg), MTP-PE (Biocine Corp.), QS21 (Genentech, Inc.), BCG, and MPL. In a specific embodiment,  
25 Therapeutics of the invention are administered in combination with alum. In another specific embodiment, Therapeutics of the invention are administered in combination with QS-21. Further adjuvants that may be administered with the Therapeutics of the invention include, but are not limited to, Monophosphoryl lipid immunomodulator, AdjuVax 100a,



QS-21, QS-18, CRL1005, Aluminum salts, MF-59, and Virosomal adjuvant technology. Vaccines that may be administered with the Therapeutics of the invention include, but are not limited to, vaccines directed toward protection against MMR (measles, mumps, rubella), polio, varicella, tetanus/diphtheria, hepatitis A, hepatitis B, haemophilus influenzae B, whooping cough, pneumonia, influenza, Lyme's Disease, rotavirus, cholera, yellow fever, Japanese encephalitis, poliomyelitis, rabies, typhoid fever, and pertussis. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

The Therapeutics of the invention may be administered alone or in combination with other therapeutic agents. Therapeutic agents that may be administered in combination with the Therapeutics of the invention, include but not limited to, other members of the TNF family, chemotherapeutic agents, antibiotics, steroidal and non-steroidal anti-inflammatories, conventional immunotherapeutic agents, cytokines and/or growth factors. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

In one embodiment, the Therapeutics of the invention are administered in combination with members of the TNF family. TNF, TNF-related or TNF-like molecules that may be administered with the Therapeutics of the invention include, but are not limited to, soluble

forms of TNF-alpha, lymphotoxin-alpha (LT-alpha, also known as TNF-beta), LT-beta (found in complex heterotrimer LT-alpha2-beta), OPGL, FasL, CD27L, CD30L, CD40L, 4-1BBL, DcR3, OX40L, TNF-gamma (International Publication No. WO 96/14328), AIM-I (International Publication No. WO 97/33899), endokine-alpha (International Publication No. WO 98/07880), TR6 (International Publication No. WO 98/30694), OPG, and neutrokin-alpha (International Publication No. WO 98/18921, OX40, and nerve growth factor (NGF), and soluble forms of Fas, CD30, CD27, CD40 and 4-1BB, TR2 (International Publication No. WO 96/34095), DR3 (International Publication No. WO 97/33904), DR4 (International Publication No. WO 98/32856), TR5 (International Publication No. WO 98/30693), TR6 (International Publication No. WO 98/30694), TR7 (International Publication No. WO 98/41629), TRANK, TR9 (International Publication No. WO 98/56892), TR10 (International Publication No. WO 98/54202), 312C2 (International Publication No. WO 98/06842), and TR12, and soluble forms CD154, CD70, and CD153.

In certain embodiments, Therapeutics of the invention are administered in combination with antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors. Nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, RETROVIR™ (zidovudine/AZT), VIDEX™ (didanosine/ddI), HIVID™ (zalcitabine/ddC), ZERIT™ (stavudine/d4T), EPIVIR™ (lamivudine/3TC), and COMBIVIR™ (zidovudine/lamivudine). Non-nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, VIRAMUNE™ (nevirapine), RESCRIPTOR™ (delavirdine), and SUSTIVA™ (efavirenz). Protease inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, CRIXIVAN™ (indinavir), NORVIR™ (ritonavir), INVIRASE™ (saquinavir), and VIRACEPT™ (nelfinavir). In a specific embodiment, antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors,

and/or protease inhibitors may be used in any combination with Therapeutics of the invention to treat AIDS and/or to prevent or treat HIV infection.

In other embodiments, Therapeutics of the invention may be administered in combination with anti-opportunistic infection agents. Anti-opportunistic agents that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, TRIMETHOPRIM-SULFAMETHOXAZOLE™, DAPSONE™, PENTAMIDINE™, ATOVAQUONE™, ISONIAZID™, RIFAMPIN™, PYRAZINAMIDE™, ETHAMBUTOL™, RIFABUTIN™, CLARITHROMYCIN™, AZITHROMYCIN™, GANCICLOVIR™, FOSCARNET™, CIDOFOVIR™, FLUCONAZOLE™, ITRACONAZOLE™, KETOCONAZOLE™, ACYCLOVIR™, FAMCICOLVIR™, PYRIMETHAMINE™, LEUCOVORIN™, NEUPOGEN™ (filgrastim/G-CSF), and LEUKINE™ (sargramostim/GM-CSF). In a specific embodiment, Therapeutics of the invention are used in any combination with TRIMETHOPRIM-SULFAMETHOXAZOLE™, DAPSONE™, PENTAMIDINE™, and/or ATOVAQUONE™ to prophylactically treat or prevent an opportunistic *Pneumocystis carinii* pneumonia infection. In another specific embodiment, Therapeutics of the invention are used in any combination with ISONIAZID™, RIFAMPIN™, PYRAZINAMIDE™, and/or ETHAMBUTOL™ to prophylactically treat or prevent an opportunistic *Mycobacterium avium* complex infection. In another specific embodiment, Therapeutics of the invention are used in any combination with RIFABUTIN™, CLARITHROMYCIN™, and/or AZITHROMYCIN™ to prophylactically treat or prevent an opportunistic *Mycobacterium tuberculosis* infection. In another specific embodiment, Therapeutics of the invention are used in any combination with GANCICLOVIR™, FOSCARNET™, and/or CIDOFOVIR™ to prophylactically treat or prevent an opportunistic cytomegalovirus infection. In another specific embodiment, Therapeutics of the invention are used in any combination with FLUCONAZOLE™, ITRACONAZOLE™, and/or KETOCONAZOLE™ to prophylactically treat or prevent an opportunistic fungal infection. In another specific embodiment, Therapeutics of the

invention are used in any combination with ACYCLOVIR™ and/or FAMCICOLVIR™ to prophylactically treat or prevent an opportunistic herpes simplex virus type I and/or type II infection. In another specific embodiment, Therapeutics of the invention are used in any combination with PYRIMETHAMINE™ and/or LEUCOVORIN™ to prophylactically  
5 treat or prevent an opportunistic *Toxoplasma gondii* infection. In another specific embodiment, Therapeutics of the invention are used in any combination with LEUCOVORIN™ and/or NEUPOGEN™ to prophylactically treat or prevent an opportunistic bacterial infection.

In a further embodiment, the Therapeutics of the invention are administered in  
10 combination with an antiviral agent. Antiviral agents that may be administered with the Therapeutics of the invention include, but are not limited to, acyclovir, ribavirin, amantadine, and remantidine.

In a further embodiment, the Therapeutics of the invention are administered in combination with an antibiotic agent. Antibiotic agents that may be administered with the  
15 Therapeutics of the invention include, but are not limited to, amoxicillin, beta-lactamases, aminoglycosides, beta-lactam (glycopeptide), beta-lactamases, Clindamycin, chloramphenicol, cephalosporins, ciprofloxacin, ciprofloxacin, erythromycin, fluoroquinolones, macrolides, metronidazole, penicillins, quinolones, rifampin, streptomycin, sulfonamide, tetracyclines, trimethoprim, trimethoprim-sulfamthoxazole,  
20 and vancomycin.

Conventional nonspecific immunosuppressive agents, that may be administered in combination with the Therapeutics of the invention include, but are not limited to, steroids, cyclosporine, cyclosporine analogs, cyclophosphamide methylprednisone, prednisone, azathioprine, FK-506, 15-deoxyspergualin, and other immunosuppressive  
25 agents that act by suppressing the function of responding T cells.

In specific embodiments, Therapeutics of the invention are administered in combination with immunosuppressants. Immunosuppressants preparations that may be administered with the Therapeutics of the invention include, but are not limited to,

ORTHOCLONE™ (OKT3), SANDIMMUNE™/NEORAL™/SANGDYA™ (cyclosporin),  
PROGRAF™ (tacrolimus), CELLCEPT™ (mycophenolate), Azathioprine,  
glucocorticosteroids, and RAPAMUNE™ (sirolimus). In a specific embodiment,  
immunosuppressants may be used to prevent rejection of organ or bone marrow  
5 transplantation.

In an additional embodiment, Therapeutics of the invention are administered alone  
or in combination with one or more intravenous immune globulin preparations.  
Intravenous immune globulin preparations that may be administered with the Therapeutics  
of the invention include, but not limited to, GAMMAR™, IVEEGAM™,  
10 SANDOGLOBULIN™, GAMMAGARD S/D™, and GAMIMUNE™. In a specific  
embodiment, Therapeutics of the invention are administered in combination with  
intravenous immune globulin preparations in transplantation therapy (e.g., bone marrow  
transplant).

In an additional embodiment, the Therapeutics of the invention are administered  
15 alone or in combination with an anti-inflammatory agent. Anti-inflammatory agents that  
may be administered with the Therapeutics of the invention include, but are not limited to,  
glucocorticoids and the nonsteroidal anti-inflammatories, aminoarylcarboxylic acid  
derivatives, arylacetic acid derivatives, arylbutyric acid derivatives, arylcarboxylic acids,  
arylpropionic acid derivatives, pyrazoles, pyrazolones, salicylic acid derivatives,  
20 thiazinecarboxamides, e-acetamidocaproic acid, S-adenosylmethionine, 3-amino-4-  
hydroxybutyric acid, amixetrine, bendazac, benzydamine, bucolome, difenpiramide,  
ditazol, emorfazone, guaiazulene, nabumetone, nimesulide, orgotein, oxaceprol,  
paranyline, perisoxal, pifoxime, proquazone, proxazole, and tenidap.

In another embodiment, compositions of the invention are administered in  
25 combination with a chemotherapeutic agent. Chemotherapeutic agents that may be  
administered with the Therapeutics of the invention include, but are not limited to,  
antibiotic derivatives (e.g., doxorubicin, bleomycin, daunorubicin, and dactinomycin);  
antiestrogens (e.g., tamoxifen); antimetabolites (e.g., fluorouracil, 5-FU, methotrexate,

floxuridine, interferon alpha-2b, glutamic acid, plicamycin, mercaptopurine, and 6-thioguanine); cytotoxic agents (e.g., carmustine, BCNU, lomustine, CCNU, cytosine arabinoside, cyclophosphamide, estramustine, hydroxyurea, procarbazine, mitomycin, busulfan, cis-platin, and vincristine sulfate); hormones (e.g., medroxyprogesterone, estramustine phosphate sodium, ethinyl estradiol, estradiol, megestrol acetate, methyltestosterone, diethylstilbestrol diphosphate, chlorotrianisene, and testolactone); nitrogen mustard derivatives (e.g., mephallen, chorambucil, mechlorethamine (nitrogen mustard) and thiotepa); steroids and combinations (e.g., bethamethasone sodium phosphate); and others (e.g., dicarbazine, asparaginase, mitotane, vincristine sulfate, vinblastine sulfate, and etoposide).

In a specific embodiment, Therapeutics of the invention are administered in combination with CHOP (cyclophosphamide, doxorubicin, vincristine, and prednisone) or any combination of the components of CHOP. In another embodiment, Therapeutics of the invention are administered in combination with Rituximab. In a further embodiment, Therapeutics of the invention are administered with Rituxmab and CHOP, or Rituxmab and any combination of the components of CHOP.

In an additional embodiment, the Therapeutics of the invention are administered in combination with cytokines. Cytokines that may be administered with the Therapeutics of the invention include, but are not limited to, IL2, IL3, IL4, IL5, IL6, IL7, IL10, IL12, IL13, IL15, anti-CD40, CD40L, IFN-gamma and TNF-alpha. In another embodiment, Therapeutics of the invention may be administered with any interleukin, including, but not limited to, IL-1alpha, IL-1beta, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IL-19, IL-20, and IL-21.

In an additional embodiment, the Therapeutics of the invention are administered in combination with angiogenic proteins. Angiogenic proteins that may be administered with the Therapeutics of the invention include, but are not limited to, Glioma Derived Growth Factor (GDGF), as disclosed in European Patent Number EP-399816; Platelet Derived Growth Factor-A (PDGF-A), as disclosed in European Patent Number EP-682110; Platelet

Derived Growth Factor-B (PDGF-B), as disclosed in European Patent Number EP-282317; Placental Growth Factor (PIGF), as disclosed in International Publication Number WO 92/06194; Placental Growth Factor-2 (PIGF-2), as disclosed in Hauser et al., Growth Factors, 4:259-268 (1993); Vascular Endothelial Growth Factor (VEGF), as disclosed in International Publication Number WO 90/13649; Vascular Endothelial Growth Factor-A (VEGF-A), as disclosed in European Patent Number EP-506477; Vascular Endothelial Growth Factor-2 (VEGF-2), as disclosed in International Publication Number WO 96/39515; Vascular Endothelial Growth Factor B (VEGF-3); Vascular Endothelial Growth Factor B-186 (VEGF-B186), as disclosed in International Publication Number WO 96/26736; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International Publication Number WO 98/02543; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International Publication Number WO 98/07832; and Vascular Endothelial Growth Factor-E (VEGF-E), as disclosed in German Patent Number DE19639601. The above mentioned references are incorporated herein by reference herein.

In an additional embodiment, the Therapeutics of the invention are administered in combination with hematopoietic growth factors. Hematopoietic growth factors that may be administered with the Therapeutics of the invention include, but are not limited to, LEUKINE™ (SARGRAMOSTIM™) and NEUPOGEN™ (FILGRASTIM™).

In an additional embodiment, the Therapeutics of the invention are administered in combination with Fibroblast Growth Factors. Fibroblast Growth Factors that may be administered with the Therapeutics of the invention include, but are not limited to, FGF-1, FGF-2, FGF-3, FGF-4, FGF-5, FGF-6, FGF-7, FGF-8, FGF-9, FGF-10, FGF-11, FGF-12, FGF-13, FGF-14, and FGF-15.

In additional embodiments, the Therapeutics of the invention are administered in combination with other therapeutic or prophylactic regimens, such as, for example, radiation therapy.

**Example 24: Method of Treating Decreased Levels of the Polypeptide**

The present invention relates to a method for treating an individual in need of an increased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an agonist of the invention (including polypeptides of the invention). Moreover, it will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a Therapeutic comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

#### **Example 25: Method of Treating Increased Levels of the Polypeptide**

The present invention also relates to a method of treating an individual in need of a decreased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an antagonist of the invention (including polypeptides and antibodies of the invention).

In one example, antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer. For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.



**Example 26: Method of Treatment Using Gene Therapy-Ex Vivo**

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into  
5 small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added.  
10 The flasks are then incubated at 37 degree C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long  
15 terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in  
20 Example 1 using primers and having appropriate restriction sites and initiation/stop codons, if necessary. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions  
25 appropriate for ligation of the two fragments. The ligation mixture is then used to transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now  
5 produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached  
10 producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo  
15 or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

20 **Example 27: Gene Therapy Using Endogenous Genes Corresponding To Polynucleotides of the Invention**

Another method of gene therapy according to the present invention involves operably associating the endogenous polynucleotide sequence of the invention with a promoter via homologous recombination as described, for example, in U.S. Patent NO:  
25 5,641,670, issued June 24, 1997; International Publication NO: WO 96/29411, published September 26, 1996; International Publication NO: WO 94/12650, published August 4, 1994; Koller et al., *Proc. Natl. Acad. Sci. USA*, 86:8932-8935 (1989); and Zijlstra et al., *Nature*, 342:435-438 (1989). This method involves the activation of a gene which is

present in the target cells, but which is not expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made which contain a promoter and targeting sequences, which are homologous to the 5' non-coding sequence of endogenous polynucleotide sequence, flanking the promoter. The targeting sequence will be sufficiently near the 5' end of the polynucleotide sequence so the promoter will be operably linked to the endogenous sequence upon homologous recombination. The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence contains the same restriction site as the 3' end of the amplified promoter.

The amplified promoter and the amplified targeting sequences are digested with the appropriate restriction enzymes and subsequently treated with calf intestinal phosphatase. The digested promoter and digested targeting sequences are added together in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The construct is size fractionated on an agarose gel then purified by phenol extraction and ethanol precipitation.

In this Example, the polynucleotide constructs are administered as naked polynucleotides via electroporation. However, the polynucleotide constructs may also be administered with transfection-facilitating agents, such as liposomes, viral sequences, viral particles, precipitating agents, etc. Such methods of delivery are known in the art.

Once the cells are transfected, homologous recombination will take place which results in the promoter being operably linked to the endogenous polynucleotide sequence. This results in the expression of polynucleotide corresponding to the polynucleotide in the cell. Expression may be detected by immunological staining, or any other method known in the art.

Fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in DMEM + 10% fetal calf serum. Exponentially growing or early stationary phase fibroblasts are trypsinized and rinsed from the plastic surface with nutrient medium. An aliquot of the cell suspension is removed for counting, and the remaining cells are  
5 subjected to centrifugation. The supernatant is aspirated and the pellet is resuspended in 5 ml of electroporation buffer (20 mM HEPES pH 7.3, 137 mM NaCl, 5 mM KCl, 0.7 mM Na<sub>2</sub> HPO<sub>4</sub>, 6 mM dextrose). The cells are recentrifuged, the supernatant aspirated, and the cells resuspended in electroporation buffer containing 1 mg/ml acetylated bovine serum albumin. The final cell suspension contains approximately 3X10<sup>6</sup> cells/ml. Electroporation  
10 should be performed immediately following resuspension.

Plasmid DNA is prepared according to standard techniques. For example, to construct a plasmid for targeting to the locus corresponding to the polynucleotide of the invention, plasmid pUC18 (MBI Fermentas, Amherst, NY) is digested with HindIII. The CMV promoter is amplified by PCR with an XbaI site on the 5' end and a BamHI site on  
15 the 3' end. Two non-coding sequences are amplified via PCR: one non-coding sequence (fragment 1) is amplified with a HindIII site at the 5' end and an Xba site at the 3' end; the other non-coding sequence (fragment 2) is amplified with a BamHI site at the 5' end and a HindIII site at the 3' end. The CMV promoter and the fragments (1 and 2) are digested with the appropriate enzymes (CMV promoter - XbaI and BamHI; fragment 1 - XbaI; fragment  
20 2 - BamHI) and ligated together. The resulting ligation product is digested with HindIII, and ligated with the HindIII-digested pUC18 plasmid.

Plasmid DNA is added to a sterile cuvette with a 0.4 cm electrode gap (Bio-Rad). The final DNA concentration is generally at least 120 µg/ml. 0.5 ml of the cell suspension (containing approximately 1.5X10<sup>6</sup> cells) is then added to the cuvette, and the cell  
25 suspension and DNA solutions are gently mixed. Electroporation is performed with a Gene-Pulser apparatus (Bio-Rad). Capacitance and voltage are set at 960 µF and 250-300 V, respectively. As voltage increases, cell survival decreases, but the percentage of surviving cells that stably incorporate the introduced DNA into their genome increases

dramatically. Given these parameters, a pulse time of approximately 14-20 mSec should be observed.

Electroporated cells are maintained at room temperature for approximately 5 min, and the contents of the cuvette are then gently removed with a sterile transfer pipette. The  
5 cells are added directly to 10 ml of prewarmed nutrient media (DMEM with 15% calf serum) in a 10 cm dish and incubated at 37 degree C. The following day, the media is aspirated and replaced with 10 ml of fresh media and incubated for a further 16-24 hours.

The engineered fibroblasts are then injected into the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads. The fibroblasts now  
10 produce the protein product. The fibroblasts can then be introduced into a patient as described above.

#### **Example 28: Method of Treatment Using Gene Therapy - In Vivo**

Another aspect of the present invention is using *in vivo* gene therapy methods to  
15 treat disorders, diseases and conditions. The gene therapy method relates to the introduction of naked nucleic acid (DNA, RNA, and antisense DNA or RNA) sequences into an animal to increase or decrease the expression of the polypeptide. The polynucleotide of the present invention may be operatively linked to a promoter or any other genetic elements necessary for the expression of the polypeptide by the target tissue.  
20 Such gene therapy and delivery techniques and methods are known in the art, see, for example, WO90/11092, WO98/11779; U.S. Patent NO. 5693622, 5705151, 5580859; Tabata et al., Cardiovasc. Res. 35(3):470-479 (1997); Chao et al., Pharmacol. Res. 35(6):517-522 (1997); Wolff, Neuromuscul. Disord. 7(5):314-318 (1997); Schwartz et al., Gene Ther. 3(5):405-411 (1996); Tsurumi et al., Circulation 94(12):3281-3290 (1996)  
25 (incorporated herein by reference).

The polynucleotide constructs may be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, intestine and the like). The polynucleotide

constructs can be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

The term "naked" polynucleotide, DNA or RNA, refers to sequences that are free from any delivery vehicle that acts to assist, promote, or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotides of the present invention may also be delivered in liposome formulations (such as those taught in Felgner P.L. et al. (1995) Ann. NY Acad. Sci. 772:126-139 and Abdallah B. et al. (1995) Biol. Cell 85(1):1-7) which can be prepared by methods well known to those skilled in the art.

The polynucleotide vector constructs used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Any strong promoter known to those skilled in the art can be used for driving the expression of DNA. Unlike other gene therapies techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

The polynucleotide construct can be delivered to the interstitial space of tissues within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are

differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. *In vivo* muscle cells are particularly competent in their ability to take up and express polynucleotides.

- 5 For the naked polynucleotide injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 g/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection.
- 10 The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration. The preferred route of administration is by the parenteral route of injection into the interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or
- 15 bronchial tissues, throat or mucous membranes of the nose. In addition, naked polynucleotide constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

The dose response effects of injected polynucleotide in muscle *in vivo* is determined as follows. Suitable template DNA for production of mRNA coding for

20 polypeptide of the present invention is prepared in accordance with a standard recombinant DNA methodology. The template DNA, which may be either circular or linear, is either used as naked DNA or complexed with liposomes. The quadriceps muscles of mice are then injected with various amounts of the template DNA.

Five to six week old female and male Balb/C mice are anesthetized by

25 intraperitoneal injection with 0.3 ml of 2.5% Avertin. A 1.5 cm incision is made on the anterior thigh, and the quadriceps muscle is directly visualized. The template DNA is injected in 0.1 ml of carrier in a 1 cc syringe through a 27 gauge needle over one minute, approximately 0.5 cm from the distal insertion site of the muscle into the knee and about

0.2 cm deep. A suture is placed over the injection site for future localization, and the skin is closed with stainless steel clips.

After an appropriate incubation time (e.g., 7 days) muscle extracts are prepared by excising the entire quadriceps. Every fifth 15  $\mu$ m cross-section of the individual quadriceps muscles is histochemically stained for protein expression. A time course for protein expression may be done in a similar fashion except that quadriceps from different mice are harvested at different times. Persistence of DNA in muscle following injection may be determined by Southern blot analysis after preparing total cellular DNA and HIRT supernatants from injected and control mice. The results of the above experimentation in mice can be used to extrapolate proper dosages and other treatment parameters in humans and other animals using naked DNA.

#### **Example 29: Transgenic Animals.**

The polypeptides of the invention can also be expressed in transgenic animals. Animals of any species, including, but not limited to, mice, rats, rabbits, hamsters, guinea pigs, pigs, micro-pigs, goats, sheep, cows and non-human primates, e.g., baboons, monkeys, and chimpanzees may be used to generate transgenic animals. In a specific embodiment, techniques described herein or otherwise known in the art, are used to express polypeptides of the invention in humans, as part of a gene therapy protocol.

Any technique known in the art may be used to introduce the transgene (i.e., polynucleotides of the invention) into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to, pronuclear microinjection (Paterson et al., Appl. Microbiol. Biotechnol. 40:691-698 (1994); Carver et al., Biotechnology (NY) 11:1263-1270 (1993); Wright et al., Biotechnology (NY) 9:830-834 (1991); and Hoppe et al., U.S. Pat. No. 4,873,191 (1989)); retrovirus mediated gene transfer into germ lines (Van der Putten et al., Proc. Natl. Acad. Sci., USA 82:6148-6152 (1985)), blastocysts or embryos; gene targeting in embryonic stem cells (Thompson et al., Cell 56:313-321 (1989)); electroporation of cells or embryos (Lo, 1983, Mol Cell. Biol.



3:1803-1814 (1983)); introduction of the polynucleotides of the invention using a gene gun (see, e.g., Ulmer et al., Science 259:1745 (1993); introducing nucleic acid constructs into embryonic pluripotent stem cells and transferring the stem cells back into the blastocyst; and sperm-mediated gene transfer (Lavitrano et al., Cell 57:717-723 (1989); etc. For a  
5 review of such techniques, see Gordon, "Transgenic Animals," Intl. Rev. Cytol. 115:171-229 (1989), which is incorporated by reference herein in its entirety.

Any technique known in the art may be used to produce transgenic clones containing polynucleotides of the invention, for example, nuclear transfer into enucleated oocytes of nuclei from cultured embryonic, fetal, or adult cells induced to quiescence  
10 (Campbell et al., Nature 380:64-66 (1996); Wilmut et al., Nature 385:810-813 (1997)).

The present invention provides for transgenic animals that carry the transgene in all their cells, as well as animals which carry the transgene in some, but not all their cells, *i.e.*, mosaic animals or chimeric. The transgene may be integrated as a single transgene or as multiple copies such as in concatamers, *e.g.*, head-to-head tandems or head-to-tail  
15 tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching of Lasko et al. (Lasko et al., Proc. Natl. Acad. Sci. USA 89:6232-6236 (1992)). The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. When it is desired that the polynucleotide  
20 transgene be integrated into the chromosomal site of the endogenous gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous gene are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleotide sequence of the endogenous gene. The transgene  
25 may also be selectively introduced into a particular cell type, thus inactivating the endogenous gene in only that cell type, by following, for example, the teaching of Gu et al. (Gu et al., Science 265:103-106 (1994)). The regulatory sequences required for such a

cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art.

Once transgenic animals have been generated, the expression of the recombinant gene may be assayed utilizing standard techniques. Initial screening may be accomplished  
5 by Southern blot analysis or PCR techniques to analyze animal tissues to verify that integration of the transgene has taken place. The level of mRNA expression of the transgene in the tissues of the transgenic animals may also be assessed using techniques which include, but are not limited to, Northern blot analysis of tissue samples obtained from the animal, *in situ* hybridization analysis, and reverse transcriptase-PCR (rt-PCR).  
10 Samples of transgenic gene-expressing tissue may also be evaluated immunocytochemically or immunohistochemically using antibodies specific for the transgene product.

Once the founder animals are produced, they may be bred, inbred, outbred, or crossbred to produce colonies of the particular animal. Examples of such breeding  
15 strategies include, but are not limited to: outbreeding of founder animals with more than one integration site in order to establish separate lines; inbreeding of separate lines in order to produce compound transgenics that express the transgene at higher levels because of the effects of additive expression of each transgene; crossing of heterozygous transgenic animals to produce animals homozygous for a given integration site in order to both  
20 augment expression and eliminate the need for screening of animals by DNA analysis; crossing of separate homozygous lines to produce compound heterozygous or homozygous lines; and breeding to place the transgene on a distinct background that is appropriate for an experimental model of interest.

Transgenic animals of the invention have uses which include, but are not limited to,  
25 animal model systems useful in elaborating the biological function of polypeptides of the present invention, studying conditions and/or disorders associated with aberrant expression, and in screening for compounds effective in ameliorating such conditions and/or disorders.

**Example 30: Knock-Out Animals.**

Endogenous gene expression can also be reduced by inactivating or "knocking out" the gene and/or its promoter using targeted homologous recombination. (*E.g.*, see  
5 Smithies et al., Nature 317:230-234 (1985); Thomas & Capecchi, Cell 51:503-512 (1987);  
Thompson et al., Cell 5:313-321 (1989); each of which is incorporated by reference herein  
in its entirety). For example, a mutant, non-functional polynucleotide of the invention (or  
a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous  
polynucleotide sequence (either the coding regions or regulatory regions of the gene) can  
10 be used, with or without a selectable marker and/or a negative selectable marker, to  
transfect cells that express polypeptides of the invention *in vivo*. In another embodiment,  
techniques known in the art are used to generate knockouts in cells that contain, but do not  
express the gene of interest. Insertion of the DNA construct, via targeted homologous  
recombination, results in inactivation of the targeted gene. Such approaches are  
15 particularly suited in research and agricultural fields where modifications to embryonic  
stem cells can be used to generate animal offspring with an inactive targeted gene (*e.g.*, see  
Thomas & Capecchi 1987 and Thompson 1989, *supra*). However this approach can be  
routinely adapted for use in humans provided the recombinant DNA constructs are directly  
administered or targeted to the required site *in vivo* using appropriate viral vectors that will  
20 be apparent to those of skill in the art.

In further embodiments of the invention, cells that are genetically engineered to  
express the polypeptides of the invention, or alternatively, that are genetically engineered  
not to express the polypeptides of the invention (*e.g.*, knockouts) are administered to a  
patient *in vivo*. Such cells may be obtained from the patient (*i.e.*, animal, including  
25 human) or an MHC compatible donor and can include, but are not limited to fibroblasts,  
bone marrow cells, blood cells (*e.g.*, lymphocytes), adipocytes, muscle cells, endothelial  
cells etc. The cells are genetically engineered *in vitro* using recombinant DNA techniques  
to introduce the coding sequence of polypeptides of the invention into the cells, or

alternatively, to disrupt the coding sequence and/or endogenous regulatory sequence associated with the polypeptides of the invention, e.g., by transduction (using viral vectors, and preferably vectors that integrate the transgene into the cell genome) or transfection procedures, including, but not limited to, the use of plasmids, cosmids, YACs, naked  
5 DNA, electroporation, liposomes, etc. The coding sequence of the polypeptides of the invention can be placed under the control of a strong constitutive or inducible promoter or promoter/enhancer to achieve expression, and preferably secretion, of the polypeptides of the invention. The engineered cells which express and preferably secrete the polypeptides of the invention can be introduced into the patient systemically, e.g., in the circulation, or  
10 intraperitoneally.

Alternatively, the cells can be incorporated into a matrix and implanted in the body, e.g., genetically engineered fibroblasts can be implanted as part of a skin graft; genetically engineered endothelial cells can be implanted as part of a lymphatic or vascular graft. (See, for example, Anderson et al. U.S. Patent No. 5,399,349; and Mulligan & Wilson,  
15 U.S. Patent No. 5,460,959 each of which is incorporated by reference herein in its entirety).

When the cells to be administered are non-autologous or non-MHC compatible cells, they can be administered using well known techniques which prevent the development of a host immune response against the introduced cells. For example, the  
20 cells may be introduced in an encapsulated form which, while allowing for an exchange of components with the immediate extracellular environment, does not allow the introduced cells to be recognized by the host immune system.

Transgenic and "knock-out" animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of  
25 polypeptides of the present invention, studying conditions and/or disorders associated with aberrant expression, and in screening for compounds effective in ameliorating such conditions and/or disorders.

**Example 31. Isolation of antibody fragments directed against polypeptides of the invention from a library of scFvs.**

Naturally occurring V-genes isolated from human PBLs are constructed into a large library of antibody fragments which contain reactivities against a polypeptide  
5 having the amino acid sequence of SEQ ID NO:Y to which the donor may or may not have been exposed (see e.g., U.S. Patent 5,885,793 incorporated herein in its entirety by reference).

**Rescue of the library.**

A library of scFvs is constructed from the RNA of human PBLs as described in  
10 WO92/01047. To rescue phage displaying antibody fragments, approximately  $10^9$  *E. coli* harboring the phagemid are used to inoculate 50 ml of 2x TY containing 1% glucose and 100 micrograms/ml of ampicillin (2xTY-AMP-GLU) and grown to an O.D. of 0.8 with shaking. Five ml of this culture is used to inoculate 50 ml of 2xTY-AMP-GLU, 2 x  $10^8$  TU of delta gene 3 helper (M13 delta gene III, see WO92/01047) are  
15 added and the culture incubated at 37°C for 45 minutes without shaking and then at 37°C for 45 minutes with shaking. The culture is centrifuged at 4000 r.p.m. for 10 min. and the pellet resuspended in 2 liters of 2x TY containing 100 micrograms/ml ampicillin and 50 micrograms/ml kanamycin and grown overnight. Phage are prepared as described in WO92/01047.

20 M13 delta gene III is prepared as follows: M13 delta gene III helper phage does not encode gene III protein, hence the phage(mid) displaying antibody fragments have a greater avidity of binding to antigen. Infectious M13 delta gene III particles are made by growing the helper phage in cells harboring a pUC19 derivative supplying the wild type gene III protein during phage morphogenesis. The culture is incubated for 1 hour at  
25 37°C without shaking and then for a further hour at 37°C with shaking. Cells were spun down (IEC-Centra 8, 4000 revs/min for 10 min), resuspended in 300 ml 2x TY broth containing 100 micrograms ampicillin/ml and 25 micrograms kanamycin/ml (2x TY-AMP-KAN) and grown overnight, shaking at 37°C. Phage particles are purified and

concentrated from the culture medium by two PEG-precipitations (Sambrook et al., 1990), resuspended in 2 ml PBS and passed through a 0.45 micrometer filter (Minisart NML; Sartorius) to give a final concentration of approximately  $10^{13}$  transducing units/ml (ampicillin-resistant clones).

5           **Panning the Library.**

Immunotubes (Nunc) are coated overnight in PBS with 4 ml of either 100 micrograms/ml or 10 micrograms/ml of a polypeptide of the present invention. Tubes are blocked with 2% Marvel-PBS for 2 hours at 37°C and then washed 3 times in PBS. Approximately  $10^{13}$  TU of phage is applied to the tube and incubated for 30 minutes at  
10 room temperature tumbling on an over and under turntable and then left to stand for another 1.5 hours. Tubes are washed 10 times with PBS 0.1% Tween-20 and 10 times with PBS. Phage are eluted by adding 1 ml of 100 mM triethylamine and rotating 15 minutes on an under and over turntable after which the solution is immediately neutralized with 0.5 ml of 1.0M Tris-HCl, pH 7.4. Phage are then used to infect 10 ml  
15 of mid-log *E. coli* TG1 by incubating eluted phage with bacteria for 30 minutes at 37°C. The *E. coli* are then plated on TYE plates containing 1% glucose and 100 micrograms/ml ampicillin. The resulting bacterial library is then rescued with delta gene 3 helper phage as described above to prepare phage for a subsequent round of selection. This process is then repeated for a total of 4 rounds of affinity purification  
20 with tube-washing increased to 20 times with PBS, 0.1% Tween-20 and 20 times with PBS for rounds 3 and 4.

**Characterization of Binders.**

Eluted phage from the third and fourth rounds of selection are used to infect *E. coli* HB 2151 and soluble scFv is produced (Marks, et al., 1991) from single colonies for  
25 assay. ELISAs are performed with microtiter plates coated with either 10 picograms/ml of the polypeptide of the present invention in 50 mM bicarbonate pH 9.6. Clones positive in ELISA are further characterized by PCR fingerprinting (see e.g., WO92/01047) and then by sequencing.

**Example 32: Assays Detecting Stimulation or Inhibition of B cell Proliferation and Differentiation**

Generation of functional humoral immune responses requires both soluble and cognate  
5 signaling between B-lineage cells and their microenvironment. Signals may impart a positive  
stimulus that allows a B-lineage cell to continue its programmed development, or a negative  
stimulus that instructs the cell to arrest its current developmental pathway. To date, numerous  
stimulatory and inhibitory signals have been found to influence B cell responsiveness including  
10 IL-2, IL-4, IL-5, IL-6, IL-7, IL10, IL-13, IL-14 and IL-15. Interestingly, these signals are by  
themselves weak effectors but can, in combination with various co-stimulatory proteins, induce  
activation, proliferation, differentiation, homing, tolerance and death among B cell populations.

One of the best studied classes of B-cell co-stimulatory proteins is the TNF-  
superfamily. Within this family CD40, CD27, and CD30 along with their respective ligands  
CD154, CD70, and CD153 have been found to regulate a variety of immune responses. Assays  
15 which allow for the detection and/or observation of the proliferation and differentiation of these  
B-cell populations and their precursors are valuable tools in determining the effects various  
proteins may have on these B-cell populations in terms of proliferation and differentiation.  
Listed below are two assays designed to allow for the detection of the differentiation,  
proliferation, or inhibition of B-cell populations and their precursors.

20 In Vitro Assay- Purified polypeptides of the invention, or truncated forms thereof,  
is assessed for its ability to induce activation, proliferation, differentiation or inhibition  
and/or death in B-cell populations and their precursors. The activity of the polypeptides of  
the invention on purified human tonsillar B cells, measured qualitatively over the dose  
range from 0.1 to 10,000 ng/mL, is assessed in a standard B-lymphocyte co-stimulation  
25 assay in which purified tonsillar B cells are cultured in the presence of either formalin-  
fixed Staphylococcus aureus Cowan I (SAC) or immobilized anti-human IgM antibody as  
the priming agent. Second signals such as IL-2 and IL-15 synergize with SAC and IgM  
crosslinking to elicit B cell proliferation as measured by tritiated-thymidine incorporation.

Novel synergizing agents can be readily identified using this assay. The assay involves isolating human tonsillar B cells by magnetic bead (MACS) depletion of CD3-positive cells. The resulting cell population is greater than 95% B cells as assessed by expression of CD45R(B220).

5 Various dilutions of each sample are placed into individual wells of a 96-well plate to which are added  $10^5$  B-cells suspended in culture medium (RPMI 1640 containing 10% FBS,  $5 \times 10^{-5}$ M 2ME, 100U/ml penicillin, 10ug/ml streptomycin, and  $10^{-5}$  dilution of SAC) in a total volume of 150ul. Proliferation or inhibition is quantitated by a 20h pulse (1uCi/well) with 3H-thymidine (6.7 Ci/mM) beginning 72h post factor addition. The  
10 positive and negative controls are IL2 and medium respectively.

In Vivo Assay- BALB/c mice are injected (i.p.) twice per day with buffer only, or 2 mg/Kg of a polypeptide of the invention, or truncated forms thereof. Mice receive this treatment for 4 consecutive days, at which time they are sacrificed and various tissues and serum collected for analyses. Comparison of H&E sections from normal spleens and  
15 spleens treated with polypeptides of the invention identify the results of the activity of the polypeptides on spleen cells, such as the diffusion of peri-arterial lymphatic sheaths, and/or significant increases in the nucleated cellularity of the red pulp regions, which may indicate the activation of the differentiation and proliferation of B-cell populations. Immunohistochemical studies using a B cell marker, anti-CD45R(B220), are used to  
20 determine whether any physiological changes to splenic cells, such as splenic disorganization, are due to increased B-cell representation within loosely defined B-cell zones that infiltrate established T-cell regions.

Flow cytometric analyses of the spleens from mice treated with polypeptide is used to indicate whether the polypeptide specifically increases the proportion of ThB+,  
25 CD45R(B220)dull B cells over that which is observed in control mice.

Likewise, a predicted consequence of increased mature B-cell representation in vivo is a relative increase in serum Ig titers. Accordingly, serum IgM and IgA levels are compared between buffer and polypeptide-treated mice.



The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

5

**Example 33: T Cell Proliferation Assay**

A CD3-induced proliferation assay is performed on PBMCs and is measured by the uptake of  $^3\text{H}$ -thymidine. The assay is performed as follows. Ninety-six well plates are coated with 100  $\mu\text{l}$ /well of mAb to CD3 (HIT3a, Pharmingen) or isotype-matched control mAb (B33.1) overnight at 4 degrees C (1  $\mu\text{g}/\text{ml}$  in .05M bicarbonate buffer, pH 9.5), then  
10 washed three times with PBS. PBMC are isolated by F/H gradient centrifugation from human peripheral blood and added to quadruplicate wells (5 x 10<sup>4</sup>/well) of mAb coated plates in RPMI containing 10% FCS and P/S in the presence of varying concentrations of polypeptides of the invention (total volume 200  $\mu\text{l}$ ). Relevant protein buffer and medium  
15 alone are controls. After 48 hr. culture at 37 degrees C, plates are spun for 2 min. at 1000 rpm and 100  $\mu\text{l}$  of supernatant is removed and stored -20 degrees C for measurement of IL-2 (or other cytokines) if effect on proliferation is observed. Wells are supplemented with 100  $\mu\text{l}$  of medium containing 0.5 uCi of  $^3\text{H}$ -thymidine and cultured at 37 degrees C for 18-24 hr. Wells are harvested and incorporation of  $^3\text{H}$ -thymidine used as a measure of  
20 proliferation. Anti-CD3 alone is the positive control for proliferation. IL-2 (100 U/ml) is also used as a control which enhances proliferation. Control antibody which does not induce proliferation of T cells is used as the negative controls for the effects of polypeptides of the invention.

The studies described in this example tested activity of polypeptides of the  
25 invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

**Example 34: Effect of Polypeptides of the Invention on the Expression of MHC Class II, Costimulatory and Adhesion Molecules and Cell Differentiation of Monocytes and Monocyte-Derived Human Dendritic Cells**

Dendritic cells are generated by the expansion of proliferating precursors found in the peripheral blood: adherent PBMC or elutriated monocytic fractions are cultured for 7-10 days with GM-CSF (50 ng/ml) and IL-4 (20 ng/ml). These dendritic cells have the characteristic phenotype of immature cells (expression of CD1, CD80, CD86, CD40 and MHC class II antigens). Treatment with activating factors, such as TNF- $\alpha$ , causes a rapid change in surface phenotype (increased expression of MHC class I and II, costimulatory and adhesion molecules, downregulation of FC $\gamma$ RII, upregulation of CD83). These changes correlate with increased antigen-presenting capacity and with functional maturation of the dendritic cells.

FACS analysis of surface antigens is performed as follows. Cells are treated 1-3 days with increasing concentrations of polypeptides of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal antibodies for 30 minutes at 4 degrees C. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

Effect on the production of cytokines. Cytokines generated by dendritic cells, in particular IL-12, are important in the initiation of T-cell dependent immune responses. IL-12 strongly influences the development of Th1 helper T-cell immune response, and induces cytotoxic T and NK cell function. An ELISA is used to measure the IL-12 release as follows. Dendritic cells ( $10^6$ /ml) are treated with increasing concentrations of polypeptides of the invention for 24 hours. LPS (100 ng/ml) is added to the cell culture as positive control. Supernatants from the cell cultures are then collected and analyzed for IL-12 content using commercial ELISA kit (e.g., R & D Systems (Minneapolis, MN)). The standard protocols provided with the kits are used.

Effect on the expression of MHC Class II, costimulatory and adhesion molecules. Three major families of cell surface antigens can be identified on monocytes: adhesion molecules, molecules involved in antigen presentation, and Fc receptor. Modulation of the expression of MHC class II antigens and other costimulatory molecules, such as B7 and ICAM-1, may result in changes in the antigen presenting capacity of monocytes and ability to induce T cell activation. Increase expression of Fc receptors may correlate with improved monocyte cytotoxic activity, cytokine release and phagocytosis.

FACS analysis is used to examine the surface antigens as follows. Monocytes are treated 1-5 days with increasing concentrations of polypeptides of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal antibodies for 30 minutes at 4 degreesC. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

Monocyte activation and/or increased survival. Assays for molecules that activate (or alternatively, inactivate) monocytes and/or increase monocyte survival (or alternatively, decrease monocyte survival) are known in the art and may routinely be applied to determine whether a molecule of the invention functions as an inhibitor or activator of monocytes. Polypeptides, agonists, or antagonists of the invention can be screened using the three assays described below. For each of these assays, Peripheral blood mononuclear cells (PBMC) are purified from single donor leukopacks (American Red Cross, Baltimore, MD) by centrifugation through a Histopaque gradient (Sigma). Monocytes are isolated from PBMC by counterflow centrifugal elutriation.

Monocyte Survival Assay. Human peripheral blood monocytes progressively lose viability when cultured in absence of serum or other stimuli. Their death results from internally regulated process (apoptosis). Addition to the culture of activating factors, such

as TNF-alpha dramatically improves cell survival and prevents DNA fragmentation. Propidium iodide (PI) staining is used to measure apoptosis as follows. Monocytes are cultured for 48 hours in polypropylene tubes in serum-free medium (positive control), in the presence of 100 ng/ml TNF-alpha (negative control), and in the presence of varying concentrations of the compound to be tested. Cells are suspended at a concentration of  $2 \times 10^6$ /ml in PBS containing PI at a final concentration of 5  $\mu$ g/ml, and then incubated at room temperature for 5 minutes before FACScan analysis. PI uptake has been demonstrated to correlate with DNA fragmentation in this experimental paradigm.

10        Effect on cytokine release. An important function of monocytes/macrophages is their regulatory activity on other cellular populations of the immune system through the release of cytokines after stimulation. An ELISA to measure cytokine release is performed as follows. Human monocytes are incubated at a density of  $5 \times 10^5$  cells/ml with increasing concentrations of the a polypeptide of the invention and under the same conditions, but in  
15        the absence of the polypeptide. For IL-12 production, the cells are primed overnight with IFN (100 U/ml) in presence of a polypeptide of the invention. LPS (10 ng/ml) is then added. Conditioned media are collected after 24h and kept frozen until use. Measurement of TNF-alpha, IL-10, MCP-1 and IL-8 is then performed using a commercially available ELISA kit (e.g, R & D Systems (Minneapolis, MN)) and applying the standard protocols  
20        provided with the kit.

Oxidative burst. Purified monocytes are plated in 96-w plate at  $2-1 \times 10^5$  cell/well. Increasing concentrations of polypeptides of the invention are added to the wells in a total volume of 0.2 ml culture medium (RPMI 1640 + 10% FCS, glutamine and antibiotics).  
25        After 3 days incubation, the plates are centrifuged and the medium is removed from the wells. To the macrophage monolayers, 0.2 ml per well of phenol red solution (140 mM NaCl, 10 mM potassium phosphate buffer pH 7.0, 5.5 mM dextrose, 0.56 mM phenol red and 19 U/ml of HRPO) is added, together with the stimulant (200 nM PMA). The plates

are incubated at 37°C for 2 hours and the reaction is stopped by adding 20  $\mu$ l 1N NaOH per well. The absorbance is read at 610 nm. To calculate the amount of H<sub>2</sub>O<sub>2</sub> produced by the macrophages, a standard curve of a H<sub>2</sub>O<sub>2</sub> solution of known molarity is performed for each experiment.

5           The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polypeptides, polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

10    **Example 35: Biological Effects of Polypeptides of the Invention**

Astrocyte and Neuronal Assays:

          Recombinant polypeptides of the invention, expressed in *Escherichia coli* and purified as described above, can be tested for activity in promoting the survival, neurite outgrowth, or phenotypic differentiation of cortical neuronal cells and for inducing the  
15   proliferation of glial fibrillary acidic protein immunopositive cells, astrocytes. The selection of cortical cells for the bioassay is based on the prevalent expression of FGF-1 and FGF-2 in cortical structures and on the previously reported enhancement of cortical neuronal survival resulting from FGF-2 treatment. A thymidine incorporation assay, for example, can be used to elucidate a polypeptide of the invention's activity on these cells.

20           Moreover, previous reports describing the biological effects of FGF-2 (basic FGF) on cortical or hippocampal neurons *in vitro* have demonstrated increases in both neuron survival and neurite outgrowth (Walicke et al., "Fibroblast growth factor promotes survival of dissociated hippocampal neurons and enhances neurite extension." *Proc. Natl. Acad. Sci. USA* 83:3012-3016. (1986), assay herein incorporated by reference in its entirety).  
25   However, reports from experiments done on PC-12 cells suggest that these two responses are not necessarily synonymous and may depend on not only which FGF is being tested but also on which receptor(s) are expressed on the target cells. Using the primary cortical

neuronal culture paradigm, the ability of a polypeptide of the invention to induce neurite outgrowth can be compared to the response achieved with FGF-2 using, for example, a thymidine incorporation assay.

5        Fibroblast and endothelial cell assays

Human lung fibroblasts are obtained from Clonetics (San Diego, CA) and maintained in growth media from Clonetics. Dermal microvascular endothelial cells are obtained from Cell Applications (San Diego, CA). For proliferation assays, the human lung fibroblasts and dermal microvascular endothelial cells can be cultured at 5,000  
10 cells/well in a 96-well plate for one day in growth medium. The cells are then incubated for one day in 0.1% BSA basal medium. After replacing the medium with fresh 0.1% BSA medium, the cells are incubated with the test proteins for 3 days. Alamar Blue (Alamar Biosciences, Sacramento, CA) is added to each well to a final concentration of 10%. The cells are incubated for 4 hr. Cell viability is measured by reading in a CytoFluor  
15 fluorescence reader. For the PGE<sub>2</sub> assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or polypeptides of the invention with or without IL-1 $\alpha$  for 24 hours. The supernatants are collected and assayed for PGE<sub>2</sub> by EIA kit (Cayman, Ann Arbor, MI). For the IL-6 assays, the human lung fibroblasts are cultured  
20 at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or with or without polypeptides of the invention IL-1 $\alpha$  for 24 hours. The supernatants are collected and assayed for IL-6 by ELISA kit (Endogen, Cambridge, MA).

Human lung fibroblasts are cultured with FGF-2 or polypeptides of the invention  
25 for 3 days in basal medium before the addition of Alamar Blue to assess effects on growth of the fibroblasts. FGF-2 should show a stimulation at 10 - 2500 ng/ml which can be used to compare stimulation with polypeptides of the invention.



containing hormonal supplements (N1). The cultures are fixed with paraformaldehyde after 8 days in vitro and are processed for tyrosine hydroxylase, a specific marker for dopaminergic neurons, immunohistochemical staining. Dissociated cell cultures are prepared from embryonic rats. The culture medium is changed every third day and the factors are also added at that time.

Since the dopaminergic neurons are isolated from animals at gestation day 14, a developmental time which is past the stage when the dopaminergic precursor cells are proliferating, an increase in the number of tyrosine hydroxylase immunopositive neurons would represent an increase in the number of dopaminergic neurons surviving *in vitro*. Therefore, if a polypeptide of the invention acts to prolong the survival of dopaminergic neurons, it would suggest that the polypeptide may be involved in Parkinson's Disease.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

**Example 36: The Effect of Polypeptides of the Invention on the Growth of Vascular Endothelial Cells**

On day 1, human umbilical vein endothelial cells (HUVEC) are seeded at  $2.5 \times 10^4$  cells/35 mm dish density in M199 medium containing 4% fetal bovine serum (FBS), 16 units/ml heparin, and 50 units/ml endothelial cell growth supplements (ECGS, Biotechnology, Inc.). On day 2, the medium is replaced with M199 containing 10% FBS, 8 units/ml heparin. A polypeptide having the amino acid sequence of SEQ ID NO:Y, and positive controls, such as VEGF and basic FGF (bFGF) are added, at varying concentrations. On days 4 and 6, the medium is replaced. On day 8, cell number is determined with a Coulter Counter.

An increase in the number of HUVEC cells indicates that the polypeptide of the invention may proliferate vascular endothelial cells.



The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

5

**Example 37: Stimulatory Effect of Polypeptides of the Invention on the Proliferation of Vascular Endothelial Cells**

For evaluation of mitogenic activity of growth factors, the colorimetric MTS (3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulphophenyl)2H-tetrazolium) assay with the electron coupling reagent PMS (phenazine methosulfate) was performed (CellTiter 96 AQ, Promega). Cells are seeded in a 96-well plate (5,000 cells/well) in 0.1 mL serum-supplemented medium and are allowed to attach overnight. After serum-starvation for 12 hours in 0.5% FBS, conditions (bFGF, VEGF<sub>165</sub> or a polypeptide of the invention in 0.5% FBS) with or without Heparin (8 U/ml) are added to wells for 48 hours. 20 mg of MTS/PMS mixture (1:0.05) are added per well and allowed to incubate for 1 hour at 37°C before measuring the absorbance at 490 nm in an ELISA plate reader. Background absorbance from control wells (some media, no cells) is subtracted, and seven wells are performed in parallel for each condition. See, Leak *et al. In Vitro Cell. Dev. Biol.* 30A:512-518 (1994).

20 The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

25 **Example 38: Inhibition of PDGF-induced Vascular Smooth Muscle Cell Proliferation Stimulatory Effect**

HAoSMC proliferation can be measured, for example, by BrdUrd incorporation. Briefly, subconfluent, quiescent cells grown on the 4-chamber slides are transfected with

CRP or FITC-labeled AT2-3LP. Then, the cells are pulsed with 10% calf serum and 6 mg/ml BrdUrd. After 24 h, immunocytochemistry is performed by using BrdUrd Staining Kit (Zymed Laboratories). In brief, the cells are incubated with the biotinylated mouse anti-BrdUrd antibody at 4 degrees C for 2 h after being exposed to denaturing solution and  
5 then incubated with the streptavidin-peroxidase and diaminobenzidine. After counterstaining with hematoxylin, the cells are mounted for microscopic examination, and the BrdUrd-positive cells are counted. The BrdUrd index is calculated as a percent of the BrdUrd-positive cells to the total cell number. In addition, the simultaneous detection of the BrdUrd staining (nucleus) and the FITC uptake (cytoplasm) is performed for individual  
10 cells by the concomitant use of bright field illumination and dark field-UV fluorescent illumination. See, Hayashida et al., J. Biol. Chem. 6:271(36):21985-21992 (1996).

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the  
15 invention.

#### **Example 39: Stimulation of Endothelial Migration**

This example will be used to explore the possibility that a polypeptide of the invention may stimulate lymphatic endothelial cell migration.

20 Endothelial cell migration assays are performed using a 48 well microchemotaxis chamber (Neuroprobe Inc., Cabin John, MD; Falk, W., et al., J. Immunological Methods 1980;33:239-247). Polyvinylpyrrolidone-free polycarbonate filters with a pore size of 8 um (Nucleopore Corp. Cambridge, MA) are coated with 0.1% gelatin for at least 6 hours at room temperature and dried under sterile air. Test substances are diluted to appropriate  
25 concentrations in M199 supplemented with 0.25% bovine serum albumin (BSA), and 25 ul of the final dilution is placed in the lower chamber of the modified Boyden apparatus. Subconfluent, early passage (2-6) HUVEC or BMEC cultures are washed and trypsinized for the minimum time required to achieve cell detachment. After placing the filter between

lower and upper chamber,  $2.5 \times 10^5$  cells suspended in 50 ul M199 containing 1% FBS are seeded in the upper compartment. The apparatus is then incubated for 5 hours at 37°C in a humidified chamber with 5% CO<sub>2</sub> to allow cell migration. After the incubation period, the filter is removed and the upper side of the filter with the non-migrated cells is scraped with  
5 a rubber policeman. The filters are fixed with methanol and stained with a Giemsa solution (Diff-Quick, Baxter, McGraw Park, IL). Migration is quantified by counting cells of three random high-power fields (40x) in each well, and all groups are performed in quadruplicate.

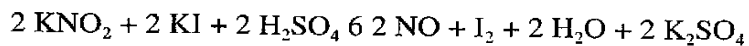
The studies described in this example tested activity of a polypeptide of the  
10 invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

#### **Example 40: Stimulation of Nitric Oxide Production by Endothelial Cells**

15 Nitric oxide released by the vascular endothelium is believed to be a mediator of vascular endothelium relaxation. Thus, activity of a polypeptide of the invention can be assayed by determining nitric oxide production by endothelial cells in response to the polypeptide.

Nitric oxide is measured in 96-well plates of confluent microvascular endothelial  
20 cells after 24 hours starvation and a subsequent 4 hr exposure to various levels of a positive control (such as VEGF-1) and the polypeptide of the invention. Nitric oxide in the medium is determined by use of the Griess reagent to measure total nitrite after reduction of nitric oxide-derived nitrate by nitrate reductase. The effect of the polypeptide of the invention on nitric oxide release is examined on HUVEC.

25 Briefly, NO release from cultured HUVEC monolayer is measured with a NO-specific polarographic electrode connected to a NO meter (Iso-NO, World Precision Instruments Inc.) (1049). Calibration of the NO elements is performed according to the following equation:



The standard calibration curve is obtained by adding graded concentrations of  $\text{KNO}_2$  (0, 5, 10, 25, 50, 100, 250, and 500 nmol/L) into the calibration solution containing KI and  $\text{H}_2\text{SO}_4$ . The specificity of the Iso-NO electrode to NO is previously determined by measurement of NO from authentic NO gas (1050). The culture medium is removed and HUVECs are washed twice with Dulbecco's phosphate buffered saline. The cells are then bathed in 5 ml of filtered Krebs-Henseleit solution in 6-well plates, and the cell plates are kept on a slide warmer (Lab Line Instruments Inc.) To maintain the temperature at 37°C. The NO sensor probe is inserted vertically into the wells, keeping the tip of the electrode 2 mm under the surface of the solution, before addition of the different conditions. S-nitroso acetyl penicillamin (SNAP) is used as a positive control. The amount of released NO is expressed as picomoles per  $1 \times 10^6$  endothelial cells. All values reported are means of four to six measurements in each group (number of cell culture wells). See, Leak *et al. Biochem. and Biophys. Res. Comm.* 217:96-105 (1995).

The studies described in this example tested activity of polypeptides of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

#### **Example 41: Effect of Polypeptides of the Invention on Cord Formation in Angiogenesis**

Another step in angiogenesis is cord formation, marked by differentiation of endothelial cells. This bioassay measures the ability of microvascular endothelial cells to form capillary-like structures (hollow structures) when cultured *in vitro*.

CADMEC (microvascular endothelial cells) are purchased from Cell Applications, Inc. as proliferating (passage 2) cells and are cultured in Cell Applications' CADMEC Growth Medium and used at passage 5. For the *in vitro* angiogenesis assay, the wells of a 48-well cell culture plate are coated with Cell Applications' Attachment Factor Medium

(200 ml/well) for 30 min. at 37°C. CADMEC are seeded onto the coated wells at 7,500 cells/well and cultured overnight in Growth Medium. The Growth Medium is then replaced with 300 mg Cell Applications' Chord Formation Medium containing control buffer or a polypeptide of the invention (0.1 to 100 ng/ml) and the cells are cultured for an  
5 additional 48 hr. The numbers and lengths of the capillary-like chords are quantitated through use of the Boeckeler VIA-170 video image analyzer. All assays are done in triplicate.

Commercial (R&D) VEGF (50 ng/ml) is used as a positive control. b-esteradiol (1 ng/ml) is used as a negative control. The appropriate buffer (without protein) is also  
10 utilized as a control.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.  
15

#### **Example 42: Angiogenic Effect on Chick Chorioallantoic Membrane**

Chick chorioallantoic membrane (CAM) is a well-established system to examine angiogenesis. Blood vessel formation on CAM is easily visible and quantifiable. The ability of polypeptides of the invention to stimulate angiogenesis in CAM can be  
20 examined.

Fertilized eggs of the White Leghorn chick (*Gallus gallus*) and the Japanese quail (*Coturnix coturnix*) are incubated at 37.8°C and 80% humidity. Differentiated CAM of 16-day-old chick and 13-day-old quail embryos is studied with the following methods.

On Day 4 of development, a window is made into the egg shell of chick eggs. The  
25 embryos are checked for normal development and the eggs sealed with cellotape. They are further incubated until Day 13. Thermanox coverslips (Nunc, Naperville, IL) are cut into disks of about 5 mm in diameter. Sterile and salt-free growth factors are dissolved in distilled water and about 3.3 mg/ 5 ml are pipetted on the disks. After air-drying, the

inverted disks are applied on CAM. After 3 days, the specimens are fixed in 3% glutaraldehyde and 2% formaldehyde and rinsed in 0.12 M sodium cacodylate buffer. They are photographed with a stereo microscope [Wild M8] and embedded for semi- and ultrathin sectioning as described above. Controls are performed with carrier disks alone.

5       The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

10    **Example 43: Angiogenesis Assay Using a Matrigel Implant in Mouse**

*In vivo* angiogenesis assay of a polypeptide of the invention measures the ability of an existing capillary network to form new vessels in an implanted capsule of murine extracellular matrix material (Matrigel). The protein is mixed with the liquid Matrigel at 4 degree C and the mixture is then injected subcutaneously in mice where it solidifies. After  
15   7 days, the solid "plug" of Matrigel is removed and examined for the presence of new blood vessels. Matrigel is purchased from Becton Dickinson Labware/Collaborative Biomedical Products.

When thawed at 4 degree C the Matrigel material is a liquid. The Matrigel is mixed with a polypeptide of the invention at 150 ng/ml at 4 degrees C and drawn into cold  
20   3 ml syringes. Female C57Bl/6 mice approximately 8 weeks old are injected with the mixture of Matrigel and experimental protein at 2 sites at the midventral aspect of the abdomen (0.5 ml/site). After 7 days, the mice are sacrificed by cervical dislocation, the Matrigel plugs are removed and cleaned (i.e., all clinging membranes and fibrous tissue is removed). Replicate whole plugs are fixed in neutral buffered 10% formaldehyde,  
25   embedded in paraffin and used to produce sections for histological examination after staining with Masson's Trichrome. Cross sections from 3 different regions of each plug are processed. Selected sections are stained for the presence of vWF. The positive control

for this assay is bovine basic FGF (150 ng/ml). Matrigel alone is used to determine basal levels of angiogenesis.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

#### **Example 44: Rescue of Ischemia in Rabbit Lower Limb Model**

To study the in vivo effects of polynucleotides and polypeptides of the invention on ischemia, a rabbit hindlimb ischemia model is created by surgical removal of one femoral arteries as described previously (Takeshita *et al.*, *Am J. Pathol* 147:1649-1660 (1995)). The excision of the femoral artery results in retrograde propagation of thrombus and occlusion of the external iliac artery. Consequently, blood flow to the ischemic limb is dependent upon collateral vessels originating from the internal iliac artery (Takeshita *et al.* *Am J. Pathol* 147:1649-1660 (1995)). An interval of 10 days is allowed for post-operative recovery of rabbits and development of endogenous collateral vessels. At 10 day post-operatively (day 0), after performing a baseline angiogram, the internal iliac artery of the ischemic limb is transfected with 500 mg naked expression plasmid containing a polynucleotide of the invention by arterial gene transfer technology using a hydrogel-coated balloon catheter as described (Riessen *et al.* *Hum Gene Ther.* 4:749-758 (1993); Leclerc *et al.* *J. Clin. Invest.* 90: 936-944 (1992)). When a polypeptide of the invention is used in the treatment, a single bolus of 500 mg polypeptide of the invention or control is delivered into the internal iliac artery of the ischemic limb over a period of 1 min. through an infusion catheter. On day 30, various parameters are measured in these rabbits: (a) BP ratio - The blood pressure ratio of systolic pressure of the ischemic limb to that of normal limb; (b) Blood Flow and Flow Reserve - Resting FL: the blood flow during undilated condition and Max FL: the blood flow during fully dilated condition (also an indirect measure of the blood vessel amount) and Flow Reserve is reflected by the ratio of max FL:

resting FL; (c) Angiographic Score - This is measured by the angiogram of collateral vessels. A score is determined by the percentage of circles in an overlaying grid that with crossing opacified arteries divided by the total number in the rabbit thigh; (d) Capillary density - The number of collateral capillaries determined in light microscopic sections  
5 taken from hindlimbs.

The studies described in this example tested activity of polynucleotides and polypeptides of the invention. However, one skilled in the art could easily modify the exemplified studies to test the agonists, and/or antagonists of the invention.

10 **Example 45: Effect of Polypeptides of the Invention on Vasodilation**

Since dilation of vascular endothelium is important in reducing blood pressure, the ability of polypeptides of the invention to affect the blood pressure in spontaneously hypertensive rats (SHR) is examined. Increasing doses (0, 10, 30, 100, 300, and 900 mg/kg) of the polypeptides of the invention are administered to 13-14 week old  
15 spontaneously hypertensive rats (SHR). Data are expressed as the mean +/- SEM. Statistical analysis are performed with a paired t-test and statistical significance is defined as  $p < 0.05$  vs. the response to buffer alone.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to  
20 test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

**Example 46: Rat Ischemic Skin Flap Model**

The evaluation parameters include skin blood flow, skin temperature, and factor  
25 VIII immunohistochemistry or endothelial alkaline phosphatase reaction. Expression of polypeptides of the invention, during the skin ischemia, is studied using in situ hybridization.

The study in this model is divided into three parts as follows:



- a) Ischemic skin
- b) Ischemic skin wounds
- c) Normal wounds

The experimental protocol includes:

- 5       a) Raising a 3x4 cm, single pedicle full-thickness random skin flap (myocutaneous flap over the lower back of the animal).
- b) An excisional wounding (4-6 mm in diameter) in the ischemic skin (skin-flap).
- c) Topical treatment with a polypeptide of the invention of the excisional wounds (day 0, 1, 2, 3, 4 post-wounding) at the following various dosage ranges: 1mg to 100 mg.
- 10       d) Harvesting the wound tissues at day 3, 5, 7, 10, 14 and 21 post-wounding for histological, immunohistochemical, and in situ studies.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the  
15   invention.

#### **Example 47: Peripheral Arterial Disease Model**

Angiogenic therapy using a polypeptide of the invention is a novel therapeutic strategy to obtain restoration of blood flow around the ischemia in case of peripheral  
20   arterial diseases. The experimental protocol includes:

- a) One side of the femoral artery is ligated to create ischemic muscle of the hindlimb, the other side of hindlimb serves as a control.
- b) a polypeptide of the invention, in a dosage range of 20 mg - 500 mg, is delivered intravenously and/or intramuscularly 3 times (perhaps more) per week for 2-3 weeks.
- 25       c) The ischemic muscle tissue is collected after ligation of the femoral artery at 1, 2, and 3 weeks for the analysis of expression of a polypeptide of the invention and histology. Biopsy is also performed on the other side of normal muscle of the contralateral hindlimb.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

5

**Example 48: Ischemic Myocardial Disease Model**

A polypeptide of the invention is evaluated as a potent mitogen capable of stimulating the development of collateral vessels, and restructuring new vessels after coronary artery occlusion. Alteration of expression of the polypeptide is investigated in situ. The experimental protocol includes:

10

a) The heart is exposed through a left-side thoracotomy in the rat. Immediately, the left coronary artery is occluded with a thin suture (6-0) and the thorax is closed.

b) a polypeptide of the invention, in a dosage range of 20 mg - 500 mg, is delivered intravenously and/or intramuscularly 3 times (perhaps more) per week for 2-4 weeks.

15

c) Thirty days after the surgery, the heart is removed and cross-sectioned for morphometric and in situ analyzes.

20

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

**Example 49: Rat Corneal Wound Healing Model**

This animal model shows the effect of a polypeptide of the invention on neovascularization. The experimental protocol includes:

25

a) Making a 1-1.5 mm long incision from the center of cornea into the stromal layer.

b) Inserting a spatula below the lip of the incision facing the outer corner of the eye.

c) Making a pocket (its base is 1-1.5 mm from the edge of the eye).

d) Positioning a pellet, containing 50ng- 5ug of a polypeptide of the invention,  
5 within the pocket.

e) Treatment with a polypeptide of the invention can also be applied topically to the corneal wounds in a dosage range of 20mg - 500mg (daily treatment for five days).

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to  
10 test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

#### **Example 50: Diabetic Mouse and Glucocorticoid-Impaired Wound Healing Models**

##### ***A. Diabetic db+/db+ Mouse Model.***

15 To demonstrate that a polypeptide of the invention accelerates the healing process, the genetically diabetic mouse model of wound healing is used. The full thickness wound healing model in the db+/db+ mouse is a well characterized, clinically relevant and reproducible model of impaired wound healing. Healing of the diabetic wound is dependent on formation of granulation tissue and re-epithelialization rather than  
20 contraction (Gartner, M.H. *et al.*, *J. Surg. Res.* 52:389 (1992); Greenhalgh, D.G. *et al.*, *Am. J. Pathol.* 136:1235 (1990)).

The diabetic animals have many of the characteristic features observed in Type II diabetes mellitus. Homozygous (db+/db+) mice are obese in comparison to their normal heterozygous (db+/+m) littermates. Mutant diabetic (db+/db+) mice have a single  
25 autosomal recessive mutation on chromosome 4 (db+) (Coleman *et al.* *Proc. Natl. Acad. Sci. USA* 77:283-293 (1982)). Animals show polyphagia, polydipsia and polyuria. Mutant diabetic mice (db+/db+) have elevated blood glucose, increased or normal insulin levels, and suppressed cell-mediated immunity (Mandel *et al.*, *J. Immunol.* 120:1375 (1978);

Debray-Sachs, M. *et al.*, *Clin. Exp. Immunol.* 51(1):1-7 (1983); Leiter *et al.*, *Am. J. of Pathol.* 114:46-55 (1985)). Peripheral neuropathy, myocardial complications, and microvascular lesions, basement membrane thickening and glomerular filtration abnormalities have been described in these animals (Norido, F. *et al.*, *Exp. Neurol.* 83(2):221-232 (1984); Robertson *et al.*, *Diabetes* 29(1):60-67 (1980); Giacomelli *et al.*, *Lab Invest.* 40(4):460-473 (1979); Coleman, D.L., *Diabetes* 31 (Suppl):1-6 (1982)). These homozygous diabetic mice develop hyperglycemia that is resistant to insulin analogous to human type II diabetes (Mandel *et al.*, *J. Immunol.* 120:1375-1377 (1978)).

The characteristics observed in these animals suggests that healing in this model may be similar to the healing observed in human diabetes (Greenhalgh, *et al.*, *Am. J. of Pathol.* 136:1235-1246 (1990)).

Genetically diabetic female C57BL/KsJ (db+/db+) mice and their non-diabetic (db+/+m) heterozygous littermates are used in this study (Jackson Laboratories). The animals are purchased at 6 weeks of age and are 8 weeks old at the beginning of the study. Animals are individually housed and received food and water ad libitum. All manipulations are performed using aseptic techniques. The experiments are conducted according to the rules and guidelines of Human Genome Sciences, Inc. Institutional Animal Care and Use Committee and the Guidelines for the Care and Use of Laboratory Animals.

Wounding protocol is performed according to previously reported methods (Tsuboi, R. and Rifkin, D.B., *J. Exp. Med.* 172:245-251 (1990)). Briefly, on the day of wounding, animals are anesthetized with an intraperitoneal injection of Avertin (0.01 mg/mL), 2,2,2-tribromoethanol and 2-methyl-2-butanol dissolved in deionized water. The dorsal region of the animal is shaved and the skin washed with 70% ethanol solution and iodine. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is then created using a Keyes tissue punch. Immediately following wounding, the surrounding skin is gently stretched to eliminate wound expansion. The wounds are left open for the duration of the experiment. Application of the treatment is

given topically for 5 consecutive days commencing on the day of wounding. Prior to treatment, wounds are gently cleansed with sterile saline and gauze sponges.

Wounds are visually examined and photographed at a fixed distance at the day of surgery and at two day intervals thereafter. Wound closure is determined by daily measurement on days 1-5 and on day 8. Wounds are measured horizontally and vertically using a calibrated Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and the wound is covered by a continuous epithelium.

A polypeptide of the invention is administered using at a range different doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups received 50mL of vehicle solution.

Animals are euthanized on day 8 with an intraperitoneal injection of sodium pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for histology and immunohistochemistry. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes between biopsy sponges for further processing.

Three groups of 10 animals each (5 diabetic and 5 non-diabetic controls) are evaluated: 1) Vehicle placebo control, 2) untreated group, and 3) treated group.

Wound closure is analyzed by measuring the area in the vertical and horizontal axis and obtaining the total square area of the wound. Contraction is then estimated by establishing the differences between the initial wound area (day 0) and that of post treatment (day 8). The wound area on day 1 is 64mm<sup>2</sup>, the corresponding size of the dermal punch. Calculations are made using the following formula:

$$[\text{Open area on day 8}] - [\text{Open area on day 1}] / [\text{Open area on day 1}]$$

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned perpendicular to the wound surface (5mm) and cut using a Reichert-Jung microtome. Routine hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected wounds. Histologic examination of the wounds are used to assess whether the

healing process and the morphologic appearance of the repaired skin is altered by treatment with a polypeptide of the invention. This assessment included verification of the presence of cell accumulation, inflammatory cells, capillaries, fibroblasts, re-epithelialization and epidermal maturity (Greenhalgh, D.G. *et al.*, *Am. J. Pathol.* 136:1235 (1990)). A calibrated lens micrometer is used by a blinded observer.

Tissue sections are also stained immunohistochemically with a polyclonal rabbit anti-human keratin antibody using ABC Elite detection system. Human skin is used as a positive tissue control while non-immune IgG is used as a negative control. Keratinocyte growth is determined by evaluating the extent of reepithelialization of the wound using a calibrated lens micrometer.

Proliferating cell nuclear antigen/cyclin (PCNA) in skin specimens is demonstrated by using anti-PCNA antibody (1:50) with an ABC Elite detection system. Human colon cancer can serve as a positive tissue control and human brain tissue can be used as a negative tissue control. Each specimen includes a section with omission of the primary antibody and substitution with non-immune mouse IgG. Ranking of these sections is based on the extent of proliferation on a scale of 0-8, the lower side of the scale reflecting slight proliferation to the higher side reflecting intense proliferation.

Experimental data are analyzed using an unpaired t test. A p value of < 0.05 is considered significant.

### ***B. Steroid Impaired Rat Model***

The inhibition of wound healing by steroids has been well documented in various *in vitro* and *in vivo* systems (Wahl, Glucocorticoids and Wound healing. In: Anti-Inflammatory Steroid Action: Basic and Clinical Aspects. 280-302 (1989); Wahlet *et al.*, *J. Immunol.* 115: 476-481 (1975); Werb *et al.*, *J. Exp. Med.* 147:1684-1694 (1978)). Glucocorticoids retard wound healing by inhibiting angiogenesis, decreasing vascular permeability (Ebert *et al.*, *An. Intern. Med.* 37:701-705 (1952)), fibroblast proliferation, and collagen synthesis (Beck *et al.*, *Growth Factors.* 5: 295-304 (1991); Haynes *et al.*, *J.*

*Clin. Invest.* 61: 703-797 (1978)) and producing a transient reduction of circulating monocytes (Haynes et al., *J. Clin. Invest.* 61: 703-797 (1978); Wahl, "Glucocorticoids and wound healing", *In: Antiinflammatory Steroid Action: Basic and Clinical Aspects*, Academic Press, New York, pp. 280-302 (1989)). The systemic administration of steroids  
5 to impaired wound healing is a well establish phenomenon in rats (Beck *et al.*, *Growth Factors.* 5: 295-304 (1991); Haynes *et al.*, *J. Clin. Invest.* 61: 703-797 (1978); Wahl, "Glucocorticoids and wound healing", *In: Antiinflammatory Steroid Action: Basic and Clinical Aspects*, Academic Press, New York, pp. 280-302 (1989); Pierce *et al.*, *Proc. Natl. Acad. Sci. USA* 86: 2229-2233 (1989)).

10 To demonstrate that a polypeptide of the invention can accelerate the healing process, the effects of multiple topical applications of the polypeptide on full thickness excisional skin wounds in rats in which healing has been impaired by the systemic administration of methylprednisolone is assessed.

Young adult male Sprague Dawley rats weighing 250-300 g (Charles River  
15 Laboratories) are used in this example. The animals are purchased at 8 weeks of age and are 9 weeks old at the beginning of the study. The healing response of rats is impaired by the systemic administration of methylprednisolone (17mg/kg/rat intramuscularly) at the time of wounding. Animals are individually housed and received food and water *ad libitum*. All manipulations are performed using aseptic techniques. This study is  
20 conducted according to the rules and guidelines of Human Genome Sciences, Inc. Institutional Animal Care and Use Committee and the Guidelines for the Care and Use of Laboratory Animals.

The wounding protocol is followed according to section A, above. On the day of wounding, animals are anesthetized with an intramuscular injection of ketamine (50  
25 mg/kg) and xylazine (5 mg/kg). The dorsal region of the animal is shaved and the skin washed with 70% ethanol and iodine solutions. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is created using a Keyes tissue punch. The wounds are left open for the duration of the experiment. Applications of the

testing materials are given topically once a day for 7 consecutive days commencing on the day of wounding and subsequent to methylprednisolone administration. Prior to treatment, wounds are gently cleansed with sterile saline and gauze sponges.

Wounds are visually examined and photographed at a fixed distance at the day of wounding and at the end of treatment. Wound closure is determined by daily measurement on days 1-5 and on day 8. Wounds are measured horizontally and vertically using a calibrated Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and the wound is covered by a continuous epithelium.

The polypeptide of the invention is administered using at a range different doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups received 50mL of vehicle solution.

Animals are euthanized on day 8 with an intraperitoneal injection of sodium pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for histology. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes between biopsy sponges for further processing.

Four groups of 10 animals each (5 with methylprednisolone and 5 without glucocorticoid) are evaluated: 1) Untreated group 2) Vehicle placebo control 3) treated groups.

Wound closure is analyzed by measuring the area in the vertical and horizontal axis and obtaining the total area of the wound. Closure is then estimated by establishing the differences between the initial wound area (day 0) and that of post treatment (day 8). The wound area on day 1 is 64mm<sup>2</sup>, the corresponding size of the dermal punch. Calculations are made using the following formula:

$$[\text{Open area on day 8}] - [\text{Open area on day 1}] / [\text{Open area on day 1}]$$

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned perpendicular to the wound surface (5mm) and cut using an Olympus



microtome. Routine hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected wounds. Histologic examination of the wounds allows assessment of whether the healing process and the morphologic appearance of the repaired skin is improved by treatment with a polypeptide of the invention. A calibrated lens micrometer is used by a  
5 blinded observer to determine the distance of the wound gap.

Experimental data are analyzed using an unpaired t test. A p value of  $< 0.05$  is considered significant.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to  
10 test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

#### **Example 51: Lymphadema Animal Model**

or The purpose of this experimental approach is to create an appropriate and  
15 consistent lymphedema model for testing the therapeutic effects of a polypeptide of the invention in lymphangiogenesis and re-establishment of the lymphatic circulatory system in the rat hind limb. Effectiveness is measured by swelling volume of the affected limb, quantification of the amount of lymphatic vasculature, total blood plasma protein, and histopathology. Acute lymphedema is observed for 7-10 days. Perhaps more importantly,  
20 the chronic progress of the edema is followed for up to 3-4 weeks.

Prior to beginning surgery, blood sample is drawn for protein concentration analysis. Male rats weighing approximately ~350g are dosed with Pentobarbital. Subsequently, the right legs are shaved from knee to hip. The shaved area is swabbed with gauze soaked in 70% EtOH. Blood is drawn for serum total protein testing.  
25 Circumference and volumetric measurements are made prior to injecting dye into paws after marking 2 measurement levels (0.5 cm above heel, at mid-pt of dorsal paw). The intradermal dorsum of both right and left paws are injected with 0.05 ml of 1% Evan's

Blue. Circumference and volumetric measurements are then made following injection of dye into paws.

Using the knee joint as a landmark, a mid-leg inguinal incision is made circumferentially allowing the femoral vessels to be located. Forceps and hemostats are  
5 used to dissect and separate the skin flaps. After locating the femoral vessels, the lymphatic vessel that runs along side and underneath the vessel(s) is located. The main lymphatic vessels in this area are then electrically coagulated suture ligated.

Using a microscope, muscles in back of the leg (near the semitendinosus and adductors) are bluntly dissected. The popliteal lymph node is then located. The 2  
10 proximal and 2 distal lymphatic vessels and distal blood supply of the popliteal node are then and ligated by suturing. The popliteal lymph node, and any accompanying adipose tissue, is then removed by cutting connective tissues.

Care is taken to control any mild bleeding resulting from this procedure. After lymphatics are occluded, the skin flaps are sealed by using liquid skin (Vetbond) (AJ  
15 Buck). The separated skin edges are sealed to the underlying muscle tissue while leaving a gap of ~0.5 cm around the leg. Skin also may be anchored by suturing to underlying muscle when necessary.

To avoid infection, animals are housed individually with mesh (no bedding). Recovering animals are checked daily through the optimal edematous peak, which  
20 typically occurred by day 5-7. The plateau edematous peak are then observed. To evaluate the intensity of the lymphedema, the circumference and volumes of 2 designated places on each paw before operation and daily for 7 days are measured. The effect plasma proteins on lymphedema is determined and whether protein analysis is a useful testing perimeter is also investigated. The weights of both control and edematous limbs are  
25 evaluated at 2 places. Analysis is performed in a blind manner.

Circumference Measurements: Under brief gas anesthetic to prevent limb movement, a cloth tape is used to measure limb circumference. Measurements are done at

the ankle bone and dorsal paw by 2 different people then those 2 readings are averaged. Readings are taken from both control and edematous limbs.

Volumetric Measurements: On the day of surgery, animals are anesthetized with Pentobarbital and are tested prior to surgery. For daily volumetrics animals are under brief  
5 halothane anesthetic (rapid immobilization and quick recovery), both legs are shaved and equally marked using waterproof marker on legs. Legs are first dipped in water, then dipped into instrument to each marked level then measured by Buxco edema software(Chen/Victor). Data is recorded by one person, while the other is dipping the limb to marked area.

10 Blood-plasma protein measurements: Blood is drawn, spun, and serum separated prior to surgery and then at conclusion for total protein and Ca<sup>2+</sup> comparison.

Limb Weight Comparison: After drawing blood, the animal is prepared for tissue collection. The limbs are amputated using a quillitine, then both experimental and control legs are cut at the ligature and weighed. A second weighing is done as the tibio-cacaneal  
15 joint is disarticulated and the foot is weighed.

Histological Preparations: The transverse muscle located behind the knee (popliteal) area is dissected and arranged in a metal mold, filled with freezeGel, dipped into cold methylbutane, placed into labeled sample bags at - 80EC until sectioning. Upon sectioning, the muscle is observed under fluorescent microscopy for lymphatics..

20 The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

25 **Example 52: Suppression of TNF alpha-induced adhesion molecule expression by a Polypeptide of the Invention**

The recruitment of lymphocytes to areas of inflammation and angiogenesis involves specific receptor-ligand interactions between cell surface adhesion molecules

(CAMs) on lymphocytes and the vascular endothelium. The adhesion process, in both normal and pathological settings, follows a multi-step cascade that involves intercellular adhesion molecule-1 (ICAM-1), vascular cell adhesion molecule-1 (VCAM-1), and endothelial leukocyte adhesion molecule-1 (E-selectin) expression on endothelial cells (EC). The expression of these molecules and others on the vascular endothelium determines the efficiency with which leukocytes may adhere to the local vasculature and extravasate into the local tissue during the development of an inflammatory response. The local concentration of cytokines and growth factor participate in the modulation of the expression of these CAMs.

Tumor necrosis factor alpha (TNF- $\alpha$ ), a potent proinflammatory cytokine, is a stimulator of all three CAMs on endothelial cells and may be involved in a wide variety of inflammatory responses, often resulting in a pathological outcome.

The potential of a polypeptide of the invention to mediate a suppression of TNF- $\alpha$  induced CAM expression can be examined. A modified ELISA assay which uses ECs as a solid phase absorbent is employed to measure the amount of CAM expression on TNF- $\alpha$  treated ECs when co-stimulated with a member of the FGF family of proteins.

To perform the experiment, human umbilical vein endothelial cell (HUVEC) cultures are obtained from pooled cord harvests and maintained in growth medium (EGM-2; Clonetics, San Diego, CA) supplemented with 10% FCS and 1% penicillin/streptomycin in a 37 degree C humidified incubator containing 5% CO<sub>2</sub>. HUVECs are seeded in 96-well plates at concentrations of  $1 \times 10^4$  cells/well in EGM medium at 37 degree C for 18-24 hrs or until confluent. The monolayers are subsequently washed 3 times with a serum-free solution of RPMI-1640 supplemented with 100 U/ml penicillin and 100 mg/ml streptomycin, and treated with a given cytokine and/or growth factor(s) for 24 h at 37 degree C. Following incubation, the cells are then evaluated for CAM expression.

Human Umbilical Vein Endothelial cells (HUVECs) are grown in a standard 96 well plate to confluence. Growth medium is removed from the cells and replaced with 90  $\mu$ l of 199 Medium (10% FBS). Samples for testing and positive or negative controls are

added to the plate in triplicate (in 10  $\mu$ l volumes). Plates are incubated at 37 degree C for either 5 h (selectin and integrin expression) or 24 h (integrin expression only). Plates are aspirated to remove medium and 100  $\mu$ l of 0.1% paraformaldehyde-PBS(with Ca++ and Mg++) is added to each well. Plates are held at 4°C for 30 min.

5        Fixative is then removed from the wells and wells are washed 1X with PBS(+Ca,Mg)+0.5% BSA and drained. Do not allow the wells to dry. Add 10  $\mu$ l of diluted primary antibody to the test and control wells. Anti-ICAM-1-Biotin, Anti-VCAM-1-Biotin and Anti-E-selectin-Biotin are used at a concentration of 10  $\mu$ g/ml (1:10 dilution of 0.1 mg/ml stock antibody). Cells are incubated at 37°C for 30 min. in a humidified  
10        environment. Wells are washed X3 with PBS(+Ca,Mg)+0.5% BSA.

          Then add 20  $\mu$ l of diluted ExtrAvidin-Alkaline Phosphatase (1:5,000 dilution) to each well and incubated at 37°C for 30 min. Wells are washed X3 with PBS(+Ca,Mg)+0.5% BSA. 1 tablet of p-Nitrophenol Phosphate pNPP is dissolved in 5 ml of glycine buffer (pH 10.4). 100  $\mu$ l of pNPP substrate in glycine buffer is added to each  
15        test well. Standard wells in triplicate are prepared from the working dilution of the ExtrAvidin-Alkaline Phosphatase in glycine buffer: 1:5,000 ( $10^0$ ) >  $10^{-0.5}$  >  $10^{-1}$  >  $10^{-1.5}$ . 5  $\mu$ l of each dilution is added to triplicate wells and the resulting AP content in each well is 5.50 ng, 1.74 ng, 0.55 ng, 0.18 ng. 100  $\mu$ l of pNPP reagent must then be added to each of the standard wells. The plate must be incubated at 37°C for 4h. A volume of 50  $\mu$ l of 3M  
20        NaOH is added to all wells. The results are quantified on a plate reader at 405 nm. The background subtraction option is used on blank wells filled with glycine buffer only. The template is set up to indicate the concentration of AP-conjugate in each standard well [ 5.50 ng; 1.74 ng; 0.55 ng; 0.18 ng]. Results are indicated as amount of bound AP-conjugate in each sample.

25        The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference. Further, the hard copy of the sequence listing submitted herewith and the corresponding computer readable form are both incorporated herein by reference in their entireties.

**Example 53: Cloning, sequence analysis and chromosomal localization of the novel human integrin alpha 11 subunit.**

**Abstract**

The integrins are a large family of cell adhesion molecules consisting of noncovalently associated  $\alpha\beta$  heterodimers. We have cloned and sequenced a novel human integrin  $\alpha$  - subunit cDNA, designated  $\alpha 11$ . The  $\alpha 11$  cDNA encodes a protein with a 22 amino acid signal peptide, a large 1120 residue extracellular domain that contains an I-domain of 207 residues and is linked by a transmembrane domain to a short cytoplasmic domain of 24 amino acids. The deduced  $\alpha 11$  protein shows the typical structural features of integrin  $\alpha$ -subunits and is similar to a distinct group of  $\alpha$ -subunits from collagen-binding integrins. However, it differs from most integrin  $\alpha$ -chains by an incompletely preserved cytoplasmic GFFKR motif. The human *ITGA11* gene was located to bands q22.3-23 on chromosome 15, and its transcripts were found predominantly in bone, cartilage as well as in cardiac and skeletal muscle. Expression of the 5.5 kilobase  $\alpha 11$  mRNA was also detectable in ovary and small intestine.

## Introduction

All vertebrate cells express members of the integrin family of cell adhesion molecules, which mediate cellular adhesion to other cells and extracellular substratum, cell migration and participate in important physiologic processes from signal transduction to cell proliferation and differentiation {Hynes, 92; Springer, 92}. Integrins are structurally homologous heterodimeric type-I membrane glycoproteins formed by the noncovalent association of one of eight  $\beta$ -subunits with one of the 17 different  $\alpha$ -subunits described to date, resulting in at least 22 different  $\alpha\beta$  complexes. Their binding specificities for cellular and extracellular ligands are determined by both subunits and are dynamically regulated in a cell-type-specific mode by the cellular environment as well as by the developmental and activation state of the cell {Diamond and Springer, 94}. In integrin  $\alpha$ -subunits, the aminoterminal region of the large extracellular domain consists of a seven-fold repeated structure which is predicted to fold into a  $\beta$ -propeller domain {Corbi *et al.*, 1987; Springer, 1997}. The three or four C-terminal repeats contain putative divalent cation binding motifs that are thought to be important for ligand binding and subunit association {Diamond and Springer, 94}. The  $\alpha^1$ ,  $\alpha^2$ ,  $\alpha^{10}$ ,  $\alpha^D$ ,  $\alpha^E$ ,  $\alpha^L$ ,  $\alpha^M$  and  $\alpha^X$ -subunits contain an approximately 200 amino acid I-domain inserted between the second and third repeat that is not present in other  $\alpha$ -chains {Larson *et al.*, 1989}. Several isolated I-domains have been shown to independently bind the ligands of the parent integrin heterodimer {Kamata and Takada, 1994; Randi and Hogg, 1994}. The  $\alpha^3$ ,  $\alpha^{5-8}$ ,  $\alpha^{11b}$  and  $\alpha^V$ -subunits are proteolytically processed at a conserved site into disulphide-linked heavy and light chains, while the  $\alpha^4$ -subunit is cleaved at a more aminoterminal site into two fragments that remain noncovalently associated {Hemler *et al.*, 90}. Additional  $\alpha$ -subunit variants are generated by alternative splicing of primary transcripts {Ziober *et al.*, 93; Delwel *et al.*, 95; Leung *et al.*, 98}. The extracellular domains of  $\alpha$ -integrin subunits are connected by a single spanning transmembrane domain to short, diverse cytoplasmic domains whose only conserved feature is a membrane-proximal KXGFF(K/R)R motif {Sastry and Horwitz,

1993}. The cytoplasmic domains have been implicated in the cell-type-specific modulation of integrin affinity states {Williams *et al.*, 1994}.

Here we report the cDNA cloning, sequence analysis, expression and chromosomal  
5 localization of the human  $\alpha$ -integrin subunit.

#### Materials and Methods

##### *Library screening and DNA sequencing.*

A human fetal heart cDNA library in  $\lambda$ gt10 (Clontech Laboratories, Inc., Palo Alto, CA,  
10 USA) was screened with  $^{32}$ P-labelled (*rediprime*, Amersham New Zealand Ltd., Auckland, New Zealand) probes corresponding to the regions 473 to 749 and 2394 to 3189 of the  $\alpha$ 11 cDNA using standard procedures. Inserts were subcloned from  $\lambda$ gt10 into pUC21 and sequenced on both strands according to a successive specific primer strategy on an automated sequencer (Applied Biosystems 373A, The Centre for Gene Technology, School  
15 of Biological Sciences, The University of Auckland).

##### *Northern Blot Analysis and Tissue distribution.*

A 1341bp PCR fragment corresponding to the region 351-1692 of the  $\alpha$  cDNA was  $^{32}$ P-labelled (*rediprime*) and hybridized with human multiple tissue Northern blots (MTN I and  
20 MTN II, Clontech) for 16h at 60°C in ExpressHyb solution (Clontech). Filters were washed twice with 0.1xSSC/1% SDS at 50°C for 30min, and autoradiographed. Human DNA from 63 tissue-specific cDNA libraries (Express-Check<sup>TM</sup>, American Type Culture Collection, Manassas, VA, USA) was amplified using primers KL120 (5'-GCAGGGATGCCACCTGCC) and KL119 (5'-GATGAAGACTGTGGTGTCTGAAGG)  
25 according to the manufacturers instructions. PCR-products were resolved by agarose gel electrophoresis and transferred to Hybond C+ (Amersham). Filters were hybridized by standard procedures {Ausubel *et al.*, 98} with a 502bp  $^{32}$ P-labelled (*rediprime*) probe fragment obtained from the cloned  $^{11}$  cDNA with the same oligonucleotides.



*Chromosomal assignment.*

500ng genomic DNA prepared from a panel of 21 human-rodent somatic cell hybrids or from human, mouse and hamster cells {Kelsell *et al.*, 95} was amplified with  
5 oligonucleotides KL175 (5'-GGTGCCAGACCTACATGGAC) and KL189 (5'-CGTGCAAATTCAATGCCAAATGCC) in a standard PCR reaction of 30 cycles (94°C for 1min, 55°C for 1min, 72°C for 2min). All PCR reactions were resolved in a 2% agarose gel. Southern hybridization was performed as detailed above, except that the probe fragment was obtained from clone HOHBY69 with oligonucleotides KL175 and KL189.  
10 For fluorescent in situ hybridization, metaphase spreads were prepared from phytohemagglutinin-stimulated peripheral blood lymphocytes of a 46,XY male donor using standard cytogenetic procedures. A purified 3.7kB fragment representing the entire coding region of clone HOHBY69 was labelled with biotin-16-dUTP using the High Prime labelling kit (Roche Molecular Biochemicals, Auckland, NZ). Conditions for hybridization  
15 and immunofluorescent detection were essentially as described {Morris *et al.*, 93}, except that  $C_0t-1$  suppression was not required, slides were washed to a stringency of 0.1xSSC/60°C after hybridization, and an additional amplification step was needed because of the small size of the probe. For precise chromosome band localization, DAPI and FITC images were captured using a Photometrics KAF1400 CCD camera and QUIPS  
20 Smartcapture FISH software version 1.3 (Vysis Inc., Downers Grove, IL, USA). QUIPS CGH/Karyotyping software (version 3.0.2) assisted karyotype analysis.

**Results***Cloning of a novel human  $\alpha$ -integrin subunit cDNA:*

25 A protein homology search {Altschul *et al.*, 90} of the human expressed sequence tag (EST) databases of Human Genome Sciences, Inc. {Ni *et al.*, 97} and The Institute for Genomic Research {Kirkness and Kerlavage, 97} identified the clones HRDAF83 and HOEAM34 as candidate novel integrin  $\alpha$ -subunit cDNAs. Clone HRDAF83 was isolated

from a human rhabdomyosarcoma cDNA library and sequenced on both strands. The 1223bp insert contains largely incompletely processed hnRNA and a 277bp region that showed homology to the aminoterminal half of the  $\alpha$ 1-integrin I-domain . The 2517bp insert of clone HOEAM34 was derived from a human osteoblast cDNA library. It is

5 homologous to the C-terminal part of the human  $\alpha$ 1-subunit and contains 1324 nucleotides of 3'-untranslated region . In order to isolate the full-length cDNAs for these integrin  $\alpha$ -subunits, a cDNA library prepared from human fetal heart in  $\lambda$ gt10 was screened with the 277bp fragment from clone HRDAF83 homologous to the  $\alpha$ 1-I-domain. Two clones,  $\lambda$ 831 and  $\lambda$ 832, were isolated and both strands of their inserts sequenced. Clone  $\lambda$ 832 contains

10 the entire 5' half of a novel  $\alpha$ -subunit cDNA, while clone  $\lambda$ 831 covers the same region, but is 358bp and 173bp shorter than  $\lambda$ 831 at its 5'- and 3'-ends, respectively. A screening of the same library with a 795bp fragment from the extreme 5'-terminus of clone HOEAM34 identified clone  $\lambda$ 342, which contained essentially the same region as clone HOEAM34 but has a 317bp shorter 3'-untranslated region . Rescreening the EST databases with the

15 sequences derived from the human fetal heart library led to the identification of clone HOHBY69, which was isolated from a osteoblast cDNA libray. Both strands of the 4681bp insert of clone HOHBY69 were sequenced. The 5'-region of HOHBY69 was identical to the HRDAF83/ $\lambda$ 832/ $\lambda$ 831-group, while the 3'-region of HOHBY69 was largely identical to HOEAM34 and  $\lambda$ 342, thereby demonstrating that the two groups of partial cDNAs

20 represent the 5'- and 3'-portions of the same cDNA . One major difference between the HOHBY69 and HOEAM34/ $\lambda$ 342 is the presence of an additional GTA-triplet at position 3088 in HOHBY69. From the overlapping clones, a total of 4986bp of cDNA was assembled to the composite sequence shown in Figure 2 and has been submitted to GenBank<sup>™</sup> with accession number AF109681. This cDNA encodes a previously

25 unidentified human integrin  $\alpha$ -subunit that was designated  $\alpha$ 11.

*Structure of the human  $\alpha 11$ -subunit.*

The  $\alpha 11$  cDNA contains a 5'-untranslated region of 72 nucleotides and a single open reading frame extending from a predicted translation initiation codon at position +1 to a TGA termination codon at position 3570 . This is followed by 1324 nucleotides of 3'

5 untranslated region which contains an AATTAAA polyadenylation signal {Wahle and Keller, 1996} 12 nucleotides upstream of a poly(A) stretch. The deduced amino acid sequence contains a 22 residue N-terminal region with the characteristics of a cleaved signal peptide {von Heijne, 83; Nielsen *et al.*, 97}, a large extracellular domain of 1120 amino acids followed by a 23 amino acid hydrophobic stretch that resembles a

10 transmembrane domain, and a short 24 residue cytoplasmic domain. The molecular weight of the mature 1167 amino acid  $\alpha 11$ -subunit is predicted to be 131 kDa, but the addition of carbohydrate side chains to any of the 15 potential N-glycosylation sequons [NX(S/T)] within the extracellular domain is likely to increase the molecular weight of the native protein. An I-domain of 207 amino acids is inserted between the second and third repeat .

15 Consistent with the structure of an typical I-domain-containing integrin  $\alpha$ -subunit, it lacks a potential dibasic protease cleavage site in the C-terminal region of the extracellular domain.

The  $\alpha 11$ -subunit is most closely related to the recently discovered  $\alpha 10$ -subunit (Camper *et al.*, 98, Lehnert *et al.*, in preparation) and the  $\alpha 1$ - and  $\alpha 2$ -subunits. Overall, the mature

20  $\alpha 11$ -protein is 45% identical to the  $\alpha 10$  chain, while the homologies to the  $\alpha 1$ - and  $\alpha 2$ -subunits are 41% and 39%, respectively. Even greater homology exists between the I-domains of the  $\alpha 10$ - and  $\alpha 11$ -subunits which are 60% identical to each other. The high degree of homology seen in the extracellular domains of the subunits is in contrast to the low similarity of their cytoplasmic domains. Interestingly, the KXGFF(K/R)R motif that is

25 absolutely conserved in all other  $\alpha$ -subunit cytoplasmic domains is only partially preserved in both subunits. The sequence in  $\alpha 11$  is KLGFFRS, while the  $\alpha 10$ -subunit contains a KLGFFAH motif. A graphical comparison of the similarity between all integrin  $\alpha$ -subunits is shown in Fig. 3. Together with the  $\alpha$ -subunits from the collagen-binding integrins  $\alpha 1\beta 1$ ,

$\alpha 2\beta 1$  and  $\alpha 10\beta 1$ , the  $\alpha 11$ -subunit forms a group distinct from the other I-domain-containing integrin subunits.

*Tissue distribution and expression of the integrin  $\alpha 11$ -subunit.*

5 The tissue distribution of the  $\alpha 11$  mRNA was assessed by screening multiple human tissue Northern blots with a probe corresponding to the region 351-1692 of the  $\alpha 11$  cDNA. A single transcript of approximately 5.5kb was found weakly expressed only in ovary and small intestine . Integrin  $\alpha 11$ -subunit expression was further analyzed by amplification and Southern hybridization of a 502bp fragment corresponding to the region 1988-2490 in  
10 the  $\alpha 11$  cDNA from tissue-specific human cDNA libraries.  $\alpha 11$  cDNA was detected in five different cDNA libraries prepared from fetal heart (day 57-75), in two fetal brain libraries, and in a cDNA library from large intestine (not shown). An analysis of the Human Genome Sciences Database revealed eight different  $\alpha 11$ -related ESTs in human osteoblast libraries, three EST in a human chondrosarcoma cDNA library and two EST in a  
15 human stromal osteoclastoma library.

*Chromosomal localization of the integrin  $\alpha 11$ -subunit.*

Genomic DNA from a collection of 21 human-rodent somatic cell hybrids {Kelsell *et al.*, 95} was amplified by PCR using oligonucleotide primers directed to the region 473 to  
20 749 of the human  $\alpha 11$  cDNA. In Southern hybridization, a signal corresponding to a 1.4kb fragment was detectable only with DNA from a hybrid cell line that contains human chromosome 15. A fragment of the same size was also amplified from human genomic DNA, but not from mouse or hamster DNA (Fig. 5C). Cloning and sequence of the PCR product from chromosome 15 revealed the presence of a 1154bp intron inserted after  
25 cDNA-position 600, thus resulting in a PCR-product of 1431bp. The *ITGA11* gene was also localized by fluorescent in situ hybridization of metaphase chromosomes with the entire coding region from clone HOHBY69. All of 20 metaphase cells analyzed showed

fluorescent signal on both chromosomes 15, specifically across bands q22.3-q23. No additional signals were detected on any other chromosome (Fig. 5A).

#### Discussion:

- 5 We have cloned and sequenced a novel cDNA encoding a protein that shares extensive structural homology with integrin  $\alpha$ -chains. The aminoterminal 22 amino acids of the deduced protein sequence show the characteristic features of a hydrophobic leader peptide, including a signal peptidase recognition motif at positions -3 and -1 {von Heijne 83}. Proteolytic cleavage of the precursor protein at this position would result in an
- 10 aminoterminal sequence for the mature  $\alpha 11$ -chain of FNMD, which is similar to the consensus sequence[(F/Y)N(L/V)D] of all other integrin  $\alpha 11$ -subunits {Tuckwell *et al.*, 94}. The N-terminal half of the large extracellular region of  $\alpha 11$  is composed of seven repeats that each contain FG--GAP--GxxY consensus motifs (FG-GAP repeats). These repeats can be found in all integrin  $\alpha 1$ -subunits and are predicted to fold into a  $\beta$ -propeller
- 15 domain {Springer, 97}. Inserted between the second and third FG-GAP repeats is a 207 amino acid I-domain spanning from glutamine<sup>138</sup> to methionine<sup>344</sup>. It contains a divalent cation coordination motif that has been shown to directly bind  $Mg^{2+}$  ions in the  $\alpha^M$  subunit {Michishita *et al.*, 96}. The noncontiguous amino acid side chains involved in the coordination of magnesium or manganese ions have been identified by mutagenesis
- 20 analysis and from crystal structures of the isolated  $\alpha^2$ ,  $\alpha^L$  and  $\alpha^M$ -subunit I-domains {Emsley *et al.*, 97; Qu and Leahy, 95; Lee *et al.*, 95; }. All residues required for the coordination of the divalent cations in these subunits are preserved in the  $\alpha 11$ -I-domain. These are the asparagines at positions 148 and 249, the serine residues at position 150 and 152, and the threonine at position 218.
- 25 The crystal sctructure of the  $\alpha 2$ -subunit has revealed a small " -helix that is not present in the I-domains of the  $\beta 2$ -associated  $\alpha$ -subunits. Together with the MIDAS sphere, amino acid residues from this C-helix and the adjacent turn region have been proposed to make physical contacts to a collagen triple helix {Emsley *et al.*, 97}. Interestingly, the small C-

helix is structurally conserved in the  $\alpha$ -subunits of the collagen-binding integrins  $\alpha 1\beta 1$ ,  $\alpha 2\beta 1$  and  $\alpha 10\beta 1$ , and is also present in the  $\alpha 11$  I-domain ( $G^{279}YYNR^{283}$ ). In addition, asparagine<sup>154</sup> and histidine<sup>258</sup> of the  $\alpha 2$ -I-domain were predicted to contact the collagen triple helix, and both are preserved in the  $\alpha 1$ ,  $\alpha 10$  and  $\alpha 11$ -I-domains, but not in other integrin  $\alpha 11$ -subunits. The conservation of structural motifs required for collagen binding suggests that collagen may be a ligand for the  $\alpha 11$  integrin. Each of the repeats 5-7 of the  $\alpha 11$ -subunit accomodates the sequence Dx(D/N)xDxxxD. Three or four copies of these putative divalent cation binding sites are conserved in all integrin  $\alpha$ -subunits and their presence is consistent with the divalent cation requirement for the adhesive function of integrins {Larson *et al.*, 89; Fujimura and Phillips, 83; Hynes, 92}. The extracellular domain of the integrin  $\alpha 11$ -subunit contains 20 cysteine residues. Only the intramolecular disulfide bonds in the "I<sup>IIb</sup>" subunit have been biochemically characterized {Calvete *et al.*, 89}, but the location of many cysteines is conserved in integrin  $\alpha$ -subunits. In the  $\alpha 11$ -subunit, the cysteine residues 637 and 646, 652 and 707, 759 and 765, and 859 and 871 are homologous to the residues that form the four carboxyterminal disulfide bonds in the heavy chain of "I<sup>IIb</sup>" {Calvete *et al.*, 89}. Based on the proposed structure of the integrin  $\alpha$ -subunit propeller domain {Springer *et al.*, 97}, additional disulfide bonds within the  $\alpha 11$  subunit can be predicted between cysteine residues 54 and 61, 99 and 117, and between 107 and 137. Two additional cysteine residues are found within a short segment (residues 783 to 798) that is unique to the  $\alpha 11$ -subunit.

The integrin cytoplasmic domains play central roles in integrin affinity modulation and in cellular signal transmission. The membrane-proximal sequence KxGFF(K/R)R is strictly conserved among integrin  $\alpha$ -subunit cytoplasmic domains {Williams *et al.*, 94}. Within this motif, both phenylalanine residues and the last arginine have been implicated in maintaining the default low affinity state of integrins  $\alpha^L\beta_2$  and  $\alpha^{IIb}\beta_3$ , as their substitution or deletion resulted in constitutively activated ligand binding {O'Toole *et al.*, 94, Lu and Spriner 97}. Interestingly, the last arginine residue is replaced by a serine in the  $\alpha 11$  cytoplasmic domain and with a histidine in the  $\alpha 10$  subunit, suggesting that both integrins

might be in a default "high" affinity state. It will be interesting to analyze whether substitution of these residues with a conserved arginine will affect their affinity status.

We have isolated  $\alpha 11$  cDNAs from osteoclast, osteoblast, myosarcoma and fetal heart libraries. Amongst the HGS EST databases, integrin  $\alpha 11$  transcripts were predominantly found in libraries prepared from osteoblast, osteoclast and chondrosarcoma cells. A search for further " $\alpha 11$ "-related sequences in the EST division of the GenBank database revealed two clones (accession numbers Z50157 and Z50167) from primary human myoblasts {Genini *et al.*, 96}, two clones from human trabecular bone cells (AA852614 and AA852615), as well as clones from fibroblast cells (W45078), pancreatic tumor (U53091) and breast tissue (H16112). In contrast, Northern blot analysis detected  $\alpha 11$ -expression only in ovary and small intestine. only fetal heart, fetal brain and large intestine. Of the tissues represented in the tissue-specific cDNA-library panel, only fetal heart, fetal brain and large intestine showed detectable  $\alpha 11$ -expression. However, bone- and muscle-derived tissues were not included in the Northern blot, and cDNA libraries prepared from these tissues were also not represented in the tissue-specific cDNA panel.

The *ITGA11* gene was localized to chromosome 15, bands q22.3-23, by FISH and PCR analysis of human-rodent somatic cell hybrids. This segment is overrepresented in squamous cell carcinomas {Wolff *et al.*, 1998}, but appears to only infrequently affected in other cancers. Genes at this region encode neogenin, a protein expressed ubiquitously expressed in human tissues {Meyerhardt *et al.*, 97}; tropomyosin 1, expressed in cardiac and skeletal muscle tissues {Tiso *et al.*, 97}; and the human homologue of the metalloprotease-disintegrin kuzbanian, which is overexpressed in tumors of sympathoadrenal origin {Yavari *et al.*, 98}. In addition, the region 15q22.3-q23 is linked to Bardet-Biedl syndrome 4, a heterogeneous autosomal disorder characterized by obesity and associated with cardiovascular anomalies {Carmi *et al.*, 95}.

In conclusion, we have cloned and sequenced the cDNA for the novel integrin  $\alpha 11$ -subunit which is closely related to the " $\alpha$ "-subunits of the collagen-binding integrins  $\alpha 1\beta 1$ ,  $\alpha 2\beta 1$  and

$\alpha 10\beta 1$ . The high degree of homology of  $\alpha 11$  to these subunits suggests that it associates with the integrin  $\beta 1$ -subunit, and may function as an additional collagen receptor.

All references referred to above and presented below are hereby incorporated herein by  
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Applicant's or agent's file reference number	575 PF489PCT	International applica unassigned
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RO/US 15 FEB 2000

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>8</u> , line <u>30</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit November 17, 1998	Accession Number 203484
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States) Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer <i>My Marilyn J. Young</i>	Authorized officer

**ATCC Deposit No. 203484****CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

**NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

**AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

**FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

**UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

**ATCC Deposit No. 203484****DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

*What Is Claimed Is:*

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;

(f) a polynucleotide which is a variant of SEQ ID NO:X;

(g) a polynucleotide which is an allelic variant of SEQ ID NO:X;

(h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;

(i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID



NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(g) a variant of SEQ ID NO:Y;

(h) an allelic variant of SEQ ID NO:Y; or

(i) a species homologue of the SEQ ID NO:Y.

12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.

14. A recombinant host cell that expresses the isolated polypeptide of claim 11.

15. A method of making an isolated polypeptide comprising:

(a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and

(b) recovering said polypeptide.

16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

(a) contacting the polypeptide of claim 11 with a binding partner; and

(b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

22. A method of identifying an activity in a biological assay, wherein the method comprises:

(a) expressing SEQ ID NO:X in a cell;

(b) isolating the supernatant;

(c) detecting an activity in a biological assay; and

(d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 20.

FIG. 1A

1 GCGTCCGGGGCCAAAATGCTGAGAACGTCCACTCCTAATCTGTGTGGTGGTCTGCATTGCC 60  
61 GGGCCCCCTGGCTCTCTTCTGGCATTCTCTGCCTCTGCCTCATATTCTTGTTAGGCCAGG 120  
121 TGGCCTTGCTGCAGGGACACCCCAAGTGCCTGGATTACGGGGCCCCCTTTCCAGCCCCCTC 180  
181 TGCACCTTGAGTTTGTCTGACTATGAGTCCTTCGGCTGCTGTGATCAGCACAAGGACC 240  
241 GCCGCATCGCTGCCCCGTACTGGGACATCATGGAATATTTTGATCTGAAGAGACATGAGC 300  
301 TGTGTGGAGATTACATTAAAGACATCCTTTGCCAGGAGTGCCTCGCCCTACGCAGCCCCACT 360  
361 CTACGACGCCGAAAACACCCAGACGCCTCTCCGGAATCTCCCGGGCCTCTGCTCTGATTA 420  
421 CTGCTCTGCCTTCCATTCTAACTGTCACTCAGCCATTTCCCTGCTGACCAATGACCGCGG 480  
481 CCTCCAGGAGTCTCATGGAAGGGACGGTACCCGCTTCTGCCACCTCCTGGACCTTCCTGA 540  
541 CAAGGACTATTGCTTCCCTAATGTCCTGAGGAACGACTATCTCAACCGCCACCTGGGCAT 600  
1 M 1  
601 GGTGGCCCAAGATCCTCAGGGCTGCCTGCAGCTCTGCCTGAGCGAGGTGGCCAACGGGCT 660  
2 V A Q D P Q G C L Q L C L S E V A N G L 21  
661 GAGGAACCCCGTCTCCATGGTCCATGCTGGGGACGGCACCCATCGCTTCTTTGTTGCCGA 720  
22 R N P V S M V H A G D G T H R F F V A E 41  
721 GCAGGTAGGAGTGGTGFGGGTCTACCTCCCTGATGGGAGTGCCTGGAGCAACCCCTTCCT 780  
42 Q V G V V W V Y L P D G S R L E Q P F L 61  
781 GGACCTCAAGAACATCGTGTGACCAACCCCATGGATCGGGGATGAGAGAGGCTTCTTGGG 840  
62 D L K N I V L T T P W I G D E R G F L G 81  
841 GTTGGCTTTTCACCCCAAATCCGCCACAATCGCAAGTTCTATATTATTATTTCGTGCCT 900  
82 L A F H P K F R H N R K F Y I Y Y S C L 101  
901 GGACAAGAAGAAGGTAGAAAAGATCCGAATTAGTGAGATGAAGGTTTCTCGGGCTGATCC 960  
102 D K K K V E K I R I S E M K V S R A D P 121  
961 TAACAAAGCTGACCTGAAATCAGAGAGGGTCATCTTGGAGATTGAAGAACCAGCCTCAAA 1020  
122 N K A D L K S E R V I L E I E E P A S N 141  
1021 CCATAATGGCGGACAACTTCTTTTGGCCTGGATGGCTATATGTACATATTCACTGGGGA 1080  
142 H N G G Q L L F G L D G Y M Y I F T G D 161  
1081 CGGGGGACAGGCTGGAGATCCCTTTGGCCTGTTTGGAAATGCTCAGAACAAAAGTTCCT 1140  
162 G G Q A G D P F G L F G N A Q N K S S L 181

FIG. 1B

1141	GCTGGGAAAAGTTTAAAGGATCGATGTGAACAGGGCAGGCTCACATGGCAAGCGGTACCG	1200
182	L G K V L R I D V N R A G S H G K R Y R	201
1201	AGTCCCCTCGGACAATCCATTTGTTTCTGAGCCAGGGGGCCACCCCGCCATCTATGCCTA	1260
202	V P S D N P F V S E P G A H P A I Y A Y	221
1261	TGGGATCAGGAACATGTGGCGTTGTGCTGTGGACCGAGGGGACCCCATCACGCGCCAGGG	1320
222	G I R N M W R C A V D R G D P I T R Q G	241
1321	CCGAGGCCGGATATTCTGTGGGGACGTGGGCCAGAACAGGTTTGAAGAGGTTGACCTCAT	1380
242	R G R I F C G D V G Q N R F E E V D L I	261
1381	TTTGAAAGGTGGAAGTATGGCTGGAGAGCAAAGGAAGGGTTTGCATGTTATGACAAAAA	1440
262	L K G G N Y G W R A K E G F A C Y D K K	281
1441	ACTTTGTCACAATGCCTCTTTGGATGATGTTCTGCCAATCTATGCTTATGGCCATGCAGT	1500
282	L C H N A S L D D V L P I Y A Y G H A V	301
1501	GGGGAAGTCAGTCAGTGGAGGTTATGTCTATCGTGCTTGTGAATCCCCAAATCTCAATGG	1560
302	G K S V T G G Y V Y R G C E S P N L N G	321
1561	CCTGTATATCTTTGGAGACTTCATGAGTGGTCCACTTATGGCTTTGCAGGAAGATAGAAA	1620
322	L Y I F G D F M S G R L M A L Q E D R K	341
1621	AAACAAGAAATGGAAGAAGCAGGATCTTTGCCTGGGCAGCACCACGTCCTGTGCCTTCCC	1680
342	N K K W K K Q D L C L G S T T S C A F P	361
1681	AGGGCTGATCAGCACCCATAGCAAGTTCATCATCTCCTTTGCTGAAGATGAAGCAGGGGA	1740
362	G L I S T H S K F I I S F A E D E A G E	381
1741	GCTGTATTTCCCTGGCGACCTCTTACCCAAGTGCCTATGCACCACGTTGGATCTATTTACAA	1800
382	L Y F L A T S Y P S A Y A P R G S I Y K	401
1801	GTTTGTGACCCCTCAAGGCGAGCACCCCGAGGCAAGTGCAAATACAAGCCAGTGCCCGT	1860
402	F V D P S R R A P P G K C K Y K P V P V	421
1861	CAGAACCAAGAGTAAGCGGATCCCGTTCAGACCACTCGCCAAGACAGTCTTGGACTTGCT	1920
422	R T K S K R I P F R P L A K T V L D L L	441
1921	AAAGGAACAATCAGAGAAAGCTGCTAGAAAAATCTTCCAGTGCAACCTTAGCTTCTGGCCC	1980
442	K E Q S E K A A R K S S S A T L A S G P	461
1981	AGCCCAGGGTTTGTCTGAGAAAGGCTCCTCCAAGAAGCTGGCTTCTCCTACAAGCAGCAA	2040
462	A Q G L S E K G S S K K L A S P T S S K	481
2041	GAATACATTGCGAGGGCCTGGTACAAAGAAGAAAGCCAGAGTGGGGCCCCACGTCCGCCA	2100
482	N T L R G P G T K K K A R V G P H V R Q	501

## FIG. 1C

2101 GGGCAAGAGGAGGAAGAGCCTGAAAAGCCACAGTGGCAGGATGAGGCCATCAGCAGAGCA 2160  
502 G K R R K S L K S H S G R M R P S A E Q 521

2161 GAAGCGAGCTGGCAGAAGTCTCCCTTGACCTATTGGTCAAGGTGGCCGACAGGGTGACGT 2220  
522 K R A G R S L P \* 530

2221 GAGAGAGGAGAGCCACCTCATCAAATGAAAGTCACTGCTGAATAAAGACCTTAGAAGTCT 2280

2281 GGGAAAGCCAGGGTAGAGGTGGGGCAGGGCGGTTTTCCTCTCCCTGGGAAATCTTGCTGTC 2340

2341 TACTGAATAAATAAATGCACCTTCTCTGTATGCAGTGCTTCTGTGGGAGACCATATCCCA 2400

2401 GATTGCTGGTGCACCTGGGTTATGGTAAGCACTATCCATGAGCCTGCTTGGAATCACACT 2460

2461 GGATGTCTCCGTTTTGTCTTGTAATGCCTACAACCTGAGGTAATAAATCAACATTGCT 2520

2521 CAAACTGGCAAA 2580

2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2609

FIG. 2A

		10	20	30	40								
1	M	-----	-----	-----	-----	HACAB64.aa							
1	M	PKPTPN	SERVS	SVRFPG	CRTGMH	MISVSL							
1	M	LKM-----	LSF-----	KL	LLLA	VALGF-----	FE	gi 1234787					
		50	60	70	80								
2	-----	-----	-----	-----	-----	HACAB64.aa							
41	G	VLLG-----	HP	QCLD	YGPP-----	FK	PLVH	LEF	gi 1234787				
22	D	AKFGER	SEGS	GARRRR	RCLNG	NPPK	RRLK	RRDR	RVMS	QLEL	gb AAD31172.1		
		90	100	110	120								
2	-----	-----	-----	-----	-----	HACAB64.aa							
65	-----	CSE	-YET	FGCC	DQDR	NVIA	EKYW	SIMD	YFDL	N	gi 1234787		
62	L	SGGE	ILCG	GFYPR	VSCCL	QSDS	PGLG---	RLEN	KIFS	SAT	gb AAD31172.1		
		130	140	150	160								
2	-----	-----	-----	-----	-----	HACAB64.aa							
97	N	YHIC	GGYI	KDIL	CQEC	SPYA	AHLY	DAED	PHTP	LR---	VI	gi 1234787	
99	N	NSECS	RLLLEE	IQCA	PCSP	PHSQ	SLFY	TPE-	RDVL	DGDL	AL	gb AAD31172.1	
		170	180	190	200								
2	-----	-----	-----	-----	-----	HACAB64.aa							
134	P	GLCF	NYCSE	FHLK	CQNS	ITLL	TEDK	QIRE	SCDK	GRDL	FC	gi 1234787	
138	P	LLCK	DYCKE	FFYT	CRGH	IPGL	LQTTA-----	DE	FC		gb AAD31172.1		
		210	220	230	240								
2	-----	-----	-----	-----	-----	HACAB64.aa							
174	S	LLNL	PDE	DYCF	PNV-----	LH	NTEL	NNNL	GS	V	gi 1234787		
169	F	YARK	DAGL	CFPD	FPRK	QVRG	PASN	YLGQ	MEDY	EKVG	GI	gb AAD31172.1	
		250	260	270	280								
3	A	-QDP	QGC	LQCL	SEVA	NGLR	NPVSM	VHAG	DGTH	RFFV	AE	HACAB64.aa	
202	V	-E	PEGC	IKLC	LIEV	ANGLR	NPVLM	MLHA	NDGT	HRMF	VAE	gi 1234787	
209	S	RKH	KHN	C--	LQ	VQEV	MSGL	RQPV	SAVH	SGDG	SHRL	EILE	gb AAD31172.1
		290	300	310	320								
42	Q	VGVV	VVYL	PDGS	RLEQ	PFDL	LKNIV	LTPW	IGDER	GFLG	HACAB64.aa		
241	Q	IGF	VVVV	LPDG	SRLYE	EPFL	NLRRT	VLAT	PWLG	DERG	LLG	gi 1234787	
247	K	EGY	VKILT	PEG	ELFK	EYLD	IHKLV	QSGIK	GDERG	LLS	gb AAD31172.1		
		330	340	350	360								
82	L	AFHP	KFER	HNRK	FYIY	YSCL	DKK-----	KVE	KIRI	SEMK	V	HACAB64.aa	
281	M	AFHP	KYQN	NRKF	VYYS	IMDE	Y-----	RNE	KIRI	SEFQ	V	gi 1234787	
287	L	AFHP	NYKK	NGKL	VSYT	TNQER	WAIG	PHDH	ILRV	VEYT	V	gb AAD31172.1	
		370	380	390	400								
117	S	RADP	NKAD	LKSE	RVI	LEIE	EPAS	NHNG	GQLL	FGLD	GYMY	HACAB64.aa	
316	E	EHE	IKKAD	PYSE	RLEI	EEPA	ANHN	GGG	ILFG	KDGY	LY	gi 1234787	
327	S	RKN	PHQV	DVRT	ARV	FLE	VAEL	HRRK	HLGG	QLLF	GPDG	FLLY	gb AAD31172.1
		410	420	430	440								
157	I	FTGD	GGGQ	AGDP	FLFG	NAQN	KSSL	LGKV	LRID	VNRAG	SH	HACAB64.aa	
356	I	FTGD	GGGK	AGDP	FLFG	NAQN	KSSV	LGKV	LRID	VNRAG	SH	gi 1234787	
367	I	TLG	DGM	IT---	LDD	MEEM	DGLS	DFTG	SVLR	LDV	DTDM	CN	gb AAD31172.1

FIG. 2B

197	GKRYRVPSDEPFVSEFGAHPAIYAYGIRNMWRCVAVDRGDP	HAQAB64.aa
396	GKPYGTPESENPTLSEFGAHPAEVHAYGVNMMWRCVAVDRGDP	gi 1234787
404	V-PYSIPRSPHFNSTNQPPPEVFAHGLHDPGRCAVER-HP	gb AAD31172.1
237	ITRGGEGRIFCGDV-GQNRFEEDVL-ILKGGNYGVRAKEG	HAQAB64.aa
436	VTGRGKGEIFCGDV-GQNRFEEDDI-IVIGGGNYGVRAKEG	gi 1234787
442	TDININLTILGSDSNGNHRESSARILQTIKGRDYE-----	gb AAD31172.1
275	FACYDKKLCNNASEDDVLPFIYAYGHAVGKSVTGGYVYRGC	HAQAB64.aa
474	FFCFDLKLCQNSLDDILPIFAIGHQVGKSVTGGYVYRGC	gi 1234787
476	-----SEPSLLEFKF-FSNG-----PLVGGFVYRGC	gb AAD31172.1
315	ESPNDLNGLYIFGDFMSGRMLALQEDRNKKKKQDLCLGS	HAQAB64.aa
514	ESPNDLNGVYIFGDFMNGRLMALQEDGVGTWKKQDLICMGD	gi 1234787
501	QSERLYGSGYVFGD-RNNGNFLTLCQSPVTKQWQEKPLCLGA	gb AAD31172.1
355	TTSCAPPGLISTHSKFIISFAEDEAGELYFLATSYPSAYA	HAQAB64.aa
554	STICAFPRRLINKYSKFIISFGEDEAGELFLFLSTSQASAYS	gi 1234787
540	SSSCR-----GYFSGHILGFGEDELGEVYILSSSKSMTQT	gb AAD31172.1
395	PRGSIYKFVDPSRRAPPCKCKYKVPVVRTKSKRIPFRPLA	HAQAB64.aa
594	PQGSIYKLVDPSSRAAPGCKCKYKVPVVRTSKRLVFFIEKE	gi 1234787
575	HNGKLYKIVDPKREPLMEEECIRV-----	gb AAD31172.1
435	KTVDLLKE--QSEKAARKSSSATLAS-----	HAQAB64.aa
634	KTVDLEIVNESVKPTKAPRRKTPTKFPTKVPPTPTKFPTKV	gi 1234787
597	-----TVQPAQP-----	gb AAD31172.1
460	--GPAQ-----GLSEKG	HAQAB64.aa
674	PPTPTQFPTKVPPIPTKVPSKVPPPTPTQFPTKVPPPTPTKV	gi 1234787
604	-----	gb AAD31172.1
470	SSKKLA-----SPTSEKNTLRGPGTKKKKARVGPQVR	HAQAB64.aa
714	STKVLSTPTIAHTKVSPSTSLRLPSKAPSTQTMVPTKVHPHT	gi 1234787
604	-----LTSDCSRLCRNGYYTPTGKCCCSPGW	gb AAD31172.1
501	QGK-----	HAQAB64.aa
754	PTKLPTKVPPITTKVSNKVLLTSPELPTKVPPPTPTKLPTN	gi 1234787
630	EGDF-----	gb AAD31172.1
504	-----	HAQAB64.aa
794	APPTSILLSPTPIKLPTKISLTLTSVPIKNQLTSAKLLTT	gi 1234787
634	-----	gb AAD31172.1



FIG. 2C

	890	900	910	920	
504	-----				HAQAB64.aa
834	TLP ISTKRATKLPSTSTSVPSNTSCILTHVQPKMLPTETR				gi 1234787
634	-----CRIAKCEPACRHGGVCV-----				gb AAD31172.1
	930	940	950	960	
504	-----ERKSLKSESGRM-----RPSA				HAQAB64.aa
874	VPNKMPKPTRIPTMSMYITKKPPILRKNSSAKKVTDKSRPTK				gi 1234787
651	-----RPNKCLCKKGYLGFPQCEQVDRNVRRVT-----				gb AAD31172.1
	970	980	990	1000	
520	EQKRA-----GRSLP-----				HAQAB64.aa
914	SPKTTTKPPKPPKSKTSVVNQPKKKETKTGVNNKTKNLRPPK				gi 1234787
678	-----RAGILDQ-----IIDMTSYL-----				gb AAD31172.1
	1010	1020	1030	1040	
530	-----				HAQAB64.aa
954	AKEPKKEKKTIVKVKQPVSHYFPPQKPKKQKTIKKMQKEGNE				gi 1234787
693	-----LDLTSYIV				gb AAD31172.1
	-----				
	-----				
530	-----				HAQAB64.aa
994	K S				gi 1234787
700	-----				gb AAD31172.1

Decoration 'Decoration #1': Shade (with solid black) residues that match HAQAB64.aa exactly.

FIG. 3

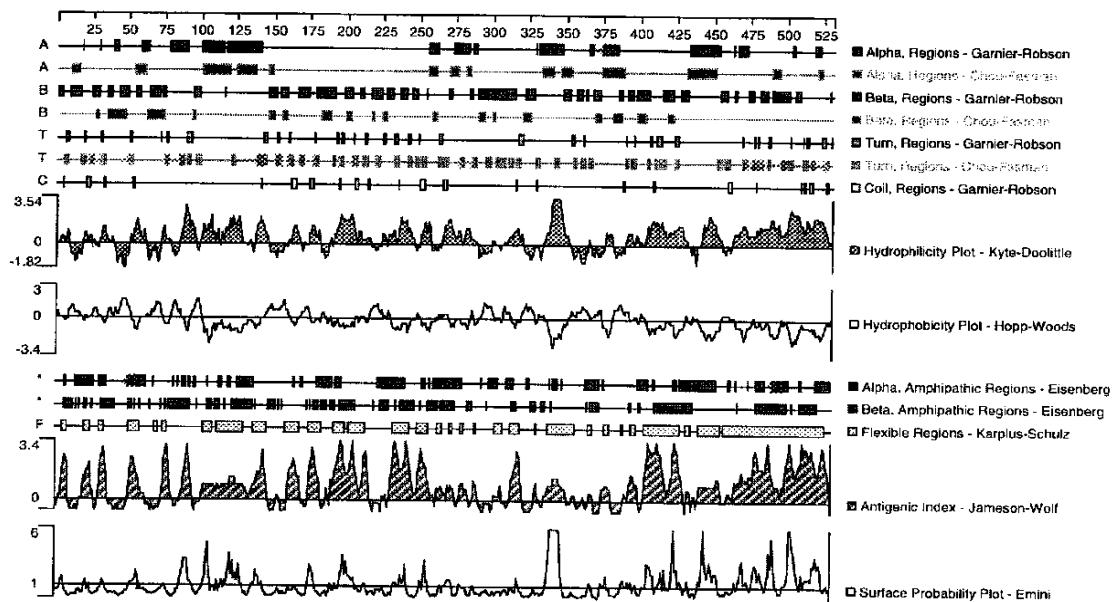


FIG. 4A

1 CACCAGCACCCCGCCAGAGCAGTGCCGCTGCCCAAATCCTCGCAGGCAGCTCATCAACG 60  
61 CAATTGCAACTCCGGCTGGAGCCCCGGACCTGCAAGCCTGGGTGTCCGTGGGTCCGTCTG 120  
121 CCCAGCCATCTGCTGGTGGCACCTCTCCCTCCTGCCGCCTCCCTCGGTGAACCCACCTT 180  
181 GCAGAAGTGACAGCTCGCCCGAGCAGCCCAGGAGCTCAGCATGCGTCCCCAGGCCTCAG 240  
1 M R P P G F R 7  
241 GAACTTCTTGCTGCTGGCGTCCCTCCCTTCTCTTTGCTGGGTGTGACGTGTTCTCCTCAAAG 300  
8 N F L L L A S S L L F A G L S A V P Q S 27  
301 CTTCTCGCCATCTCTGAGGAGCTGGCCGGGCGCCGCTGACAGGCTGTCCCGGGCCGAGTC 360  
28 F S P S L R S W P G A A C R L S R A E S 47  
361 GGAGCGACGCTGCCCGGCACCTGGGCAGCCCCCGGGGGCCGCGCTGTGCCACGGCCGGGG 420  
48 E R R C R A P [REDACTED] 67  
421 CCGCTGCGACTGCGGCGCTCTGCATCTGCCACGTGACTGAGCCGGGCATGTTCTTCGGGCC 480  
68 [REDACTED] 87  
481 CCTGTGTGAGTGCCATGAGTGGGTGTGCGAGACCTACGACGGGAGCACCTGTGCAGGCCA 540  
88 [REDACTED] E C H E W V C [REDACTED] 107  
541 TGGTAAGTGTGACTGTGGCAAGTGCAAGTGTGACCAGGGATGGTATGGGGATGCTTGCCA 600  
108 [REDACTED] 127  
601 GTACCCAACTAACTGTGACTTGACAAAGAAGAAAAGTAACCAAATGTGCAAGAATTACAA 660  
128 [REDACTED] P T N C D L T K K K S N Q [REDACTED] 147  
661 AGACATCATCTGCTCTAATGCAGGTACATGTCACTGTGCCAGGTGTAAGTGTGATAATTC 720  
148 [REDACTED] 167  
721 AGATGGAAGTGGACTTGTGTATGGTAAATTTTGTGAGTGTGACGATAGAGAATGCATAGA 780  
168 [REDACTED] K F C E C D D R E C [REDACTED] 187  
781 CGATGAAACAGAAGAAATATGTGGAGGCCATGGGAAGTGTACTGTGGAAACTGCTACTG 840  
188 [REDACTED] 207  
841 CAAGGCTGGTGGCATGGAGATAAATGTGAATTCCAGTGCATATCACCCCTCGGAAAG 900  
208 [REDACTED] E F O C D I T P W E S 227

FIG. 4B

901 CAAGCGAAGATGCACGCTCTCCAGATGGCAAAATCTGCAGTAACAGAGGGACTTGTGTATG 960  
228 [REDACTED] 247

961 TGGTGAATGTACCTGTACGATGTTGATCCGACTGGGGACTGGGGAGATATTTCATGGGGA 1020  
248 [REDACTED] G D I H G D 267

1021 CACCTGTGAATGTGATGAGAGGGACTGTAGAGCTGTCTATGACCGATATTCTGATGACTT 1080  
268 T C E C D E R D C R A V Y [REDACTED] 287

1081 CTGTTCAAGTCATGGACAGTGTAATTGCGGAAGATCTGACTGCAAACCAGGCTGCTATGG 1140  
288 [REDACTED] 307

1141 GAAGAAGTGTGAGCACCCACAGTCTGTCACGCTGTGAGTGAAGAGAGCATCAGGAAGTG 1200  
308 [REDACTED] S C T L S A E E S I R K [REDACTED] 327

1201 CCAGGGAAGCTCGGATCTGCCTTGCTCTGGGAGGGGTAAATGTGAATGTGGCAAATGCAC 1260  
328 [REDACTED] 347

1261 CTGCTATCCTCCAGGAGATCGCCGGGTGTATGGCAAGACTTGTGAGTGTGATGATCGCCG 1320  
348 [REDACTED] K T C E C D D R R 367

1321 CTGTGAAGACCTCGATGGTGTGGTCTGTGAGGCCACGGCACATGTTCTGTGGTCTGCTG 1380  
368 [REDACTED] 387

1381 TGTGTTGTGAGAGAGCATGGTTTGGAAAGCTCTGCCAACATCCGCGGAAGTGTAAACATGAC 1440  
388 [REDACTED] O H P R K C N M T 407

1441 GGAAGAACAAGCAAGAATCTGTGTAATCAGCAGATGGCATATTGTGCTCGGGGAAGGG 1500  
408 E E Q S K N L C E [REDACTED] 427

1501 TTCTTGTCATTGTGGAAGTGCATTTGTTCTGCTGAAGAGTGGTATATTCTGCGGGAGTT 1560  
428 [REDACTED] 447

1561 CTGTGACTGTGATGACAGAGACTGCGACAAACATGATGGTCTCATTGTTACAGGGAATGG 1620  
448 [REDACTED] D C D D R D [REDACTED] 467

1621 AATATGTAGCTGTGAAACTGTGAATGCTGGGATGGATGGAATGGAAATGCATGTGAAAT 1680  
468 [REDACTED] 487

1681 CTGGCTTGGCTCAGAATATCCTTAACAATTACATGAGAGAGGTCTGCATTCTTATTTTTT 1740  
488 W L G S E Y P \* 495

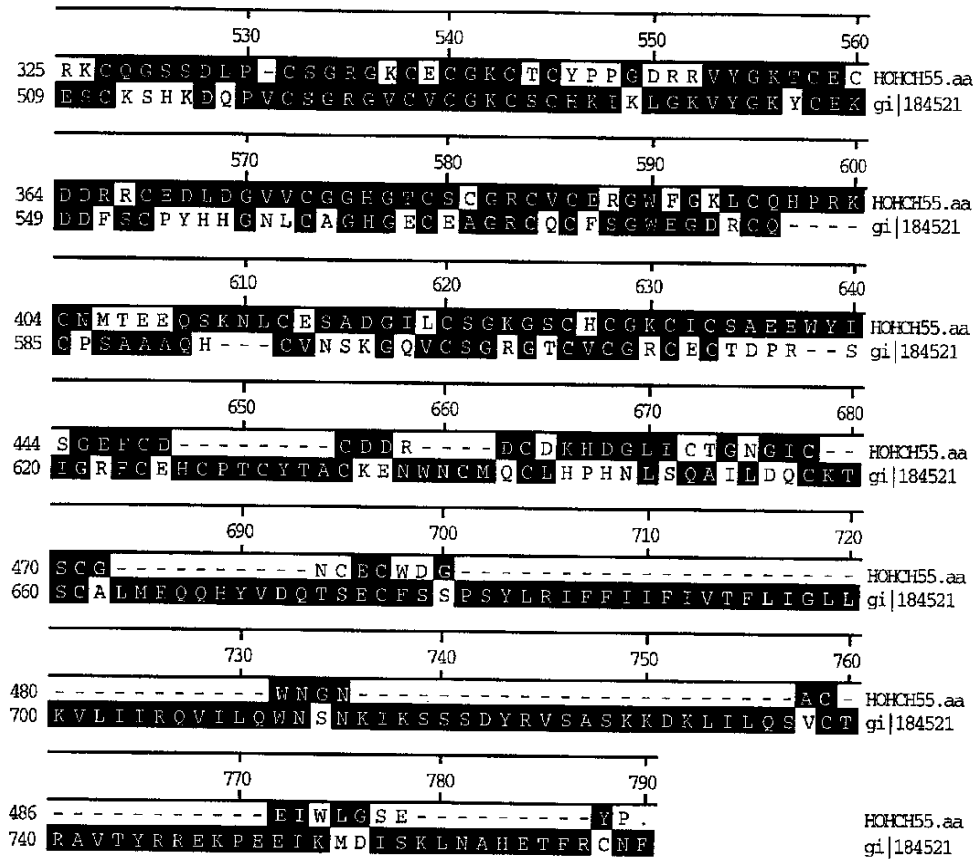
## FIG. 4C

1741 CTGGGCCATTAGAACATATAAATGCGAAGGAAACCATGTATATTCACCACTAGGACAGGT 1800  
1801 TAAAAAGACCATTGTATGTTTTTCTATTTCTGAATTACGAATGAAATCCGAGTACCTATT 1860  
1861 AGAAATGAGTTATGCAAATTTAGATGCAAATAACATTAGAAAAAAAGATTCTTCCATAA 1920  
1921 TTAACATAAGTGGTTCCTAACGAGAGCAATTTTCCACCCAAAAGTCATTTGGCAACATC 1980  
1981 TACAGACAATTTTGATTGTCCACTGGGTCCGGTAGGAAGGTATGCTGCAGACATTTGGT 2040  
2041 GGGTAGAGGCCAGGGATGCTGCTGAGCATCCCGCAGTGTACAGGACAGCCCCAAACAAG 2100  
2101 GAATTATCCAGCCCCAAATGCCAATAGGGCTCAGACTGAGAAACATTGAGTTATATGGCT 2160  
2161 ATTAGAAATCCACATTCTTACACAAGAAAGACCATATTAGAATCTAAGGAAAACATGCAT 2220  
2221 ATTCACATTAATTAATCGATCAGATTTTCCAGAATTCCGTATCAGTCACCATTTTAATA 2280  
2281 TGGGGACAATGAAGACAAGCACACAGGAGGTAGAATATCAGAGTGGGGCTGGATCAAGGG 2340  
2341 CAAAAACTGGTCATTAAGTCATCTGACATTAAATCATTTAGCCACTAAGTTATTTGTGTA 2400  
2401 CTCTCACTTTAAACTCACCAAAGAAGATTCTCTTAAAGAAATTATGAAAAATGTACAATT 2460  
2461 TAACATTTTAAATAAATAGTGACAGAAGTTGTTTAAAAA 2499

FIG. 5A

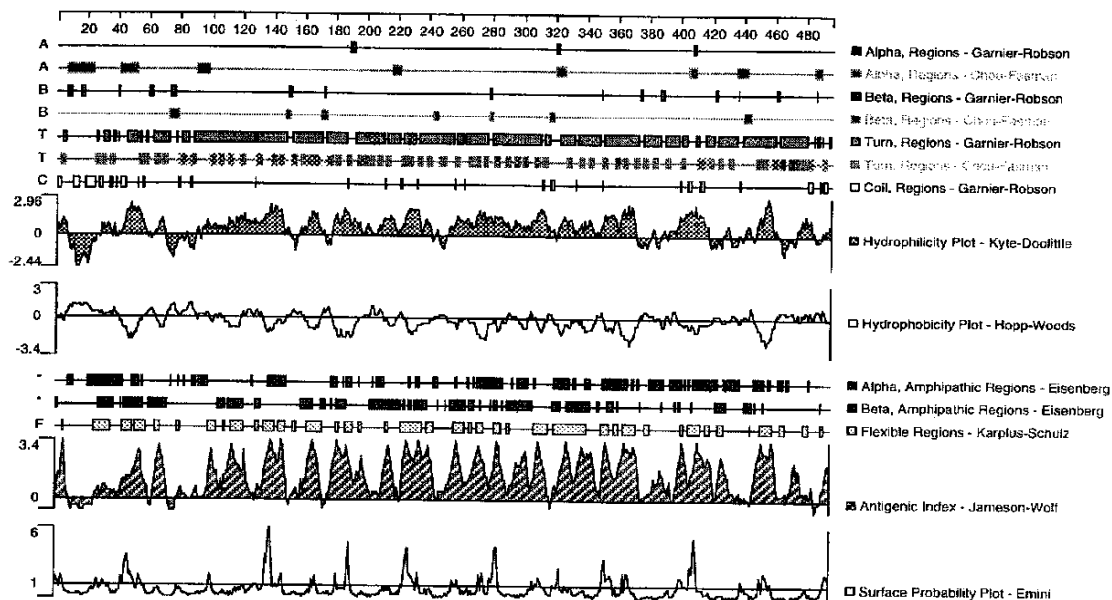
	10	20	30	40	
1	NRPPGFRNFLLASSLLFAGLSAVPOSFSPSLRS-WP-GA	HOHCH55.aa			
1	MCGSALAFFE-----TAATVCHQNDRRGPASFIWAAWVFSL	gi 184521			
	50	60	70	80	
39	ACRMSRAESERRCRAPGQPPGAALCHGRGRCDGVC I---	HOHCH55.aa			
36	VLGLEQGE-DNRC-ASSNAASCARCLALGP-ECGWCVQED	gi 184521			
	90	100	110	120	
76	-----CHVTE-----	HOHCH55.aa			
73	FISGGSRSEKCDIVSNLISKGCSVDSIEYPSVHVIIPTEN	gi 184521			
	130	140	150	160	
81	-----PG-----MFFG	HOHCH55.aa			
113	EINTQVTPGGEVSIQLRPGAEANFMLKVHPLKKYPVDLYY-	gi 184521			
	170	180	190	200	
87	PLICECHEWVCETYDGGSTCAGHC-----	HOHCH55.aa			
152	-LVDVSASMHNNIEKLNISVGNDSLRSKMAFFSRDFRLGFGS	gi 184521			
	210	220	230	240	
109	---KCDQ GKCKCDQG WYGDAC-QYPTNC-----DL	HOHCH55.aa			
191	YVDKTVSPYLSIHPERIHNQCS DYNLD CMPPHGYIHVLSL	gi 184521			
	250	260	270	280	
135	TKK-----KSNQMCKNSQDIICSNAG-----TC--HC	HOHCH55.aa			
231	TENITEFEKAVHRQKISGNIDTPEGGFDA MLQA AVCESHI	gi 184521			
	290	300	310	320	
160	GRCKCD-----NSDGSGLVY GKFCFCDDR	HOHCH55.aa			
271	GW RKEAKRLLLVMTDQTSHLALDSKL AGI VVPNDGNCHLK	gi 184521			
	330	340	350	360	
184	EC-----IDDETEETICGGH GKCY--	HOHCH55.aa			
311	NNVYVKSTTMEHPSLGQLSEKLIDNNTNVIFAVQ GKQFHW	gi 184521			
	370	380	390	400	
202	-----CGNCYCKAGWHGDKCEFQC DITPWESKR	HOHCH55.aa			
351	YKDLLPLLP GTIAGEIESKAANLNNLVVEAY QKLISEVKV	gi 184521			
	410	420	430	440	
230	RCTSPDGKICSNRGTCVCGECT-----CHDV DPTGD-W	HOHCH55.aa			
391	QVENQVQGIYFNI-TAICPDGSRKPGMEGCRNVTSNDEVL	gi 184521			
	450	460	470	480	
262	GDIHGDTCECDERDCRAVD RYSDDFC SG-----HGQCNC	HOHCH55.aa			
430	FNVTVTMKKCDVTGGKNYAIKPIGFNETAKIHHRNCSC	gi 184521			
	490	500	510	520	
297	GRCD-----CKAGWY-GKKCEH--POSCTLSAEE-SI	HOHCH55.aa			
470	-QCEDNRGPAGKCVDETFLDSKCFQCDENKCHFDDEQFS	gi 184521			

FIG. 5B



Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 6



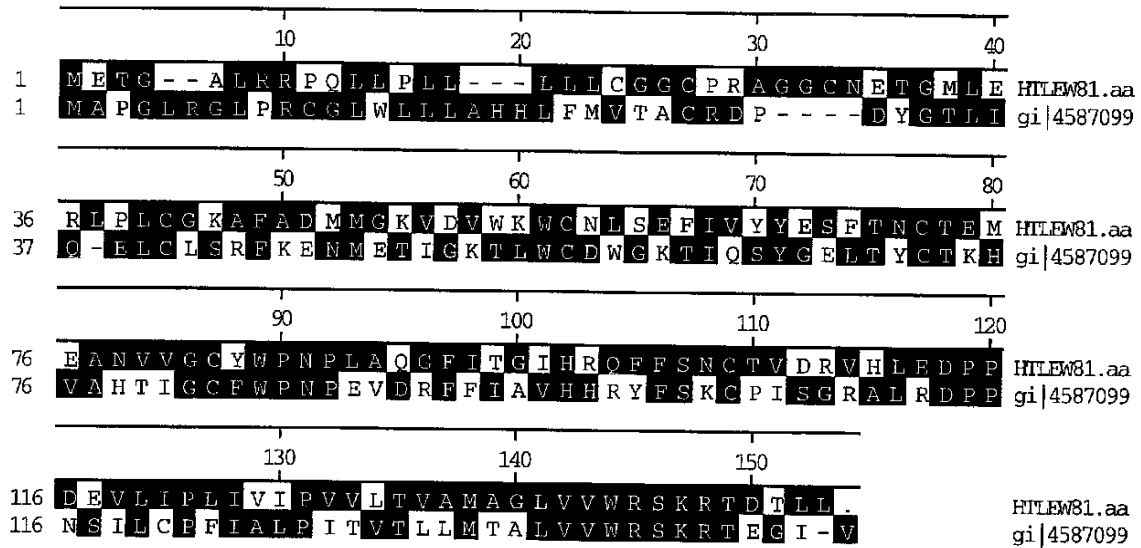




## FIG. 7B

961 CAGGGGCTCTTGGAAGACGTTCCGTGCTGTGACCTCCGAGCCCTCCTGGTGGGAAGACAG 1020  
1021 CTGGAAAGGCTGGGAGGAGAAGGGAGGGGTTGGGGGTTCCAGGAGCCATGCCTGGCCTG 1080  
1081 CAGAGTCCATTCCATCATGATGCTGTGCCCCGCTATGGGCTGTGTCCATGACCAGAGGCTG 1140  
1141 GAGTGGGGGTGTGTTAGAGCCCCCTACCGGGACTTGCTGTGCGGATGGGGCCTGGGCCTC 1200  
1201 CTTCTACAGGGGCTCCTCTGTGGGTGAGGGGCCCTCTGGAATGGCATCCCATGAGCTTG 1260  
1261 TGGCCTCTATCTGCTACCATCTGTGTTTATCTGAGTAAAGTTACCTTACTTCTGGAAAA 1320  
1321 AAAAAAAAAAAAAAAAAA 1339

FIG. 8



Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 9

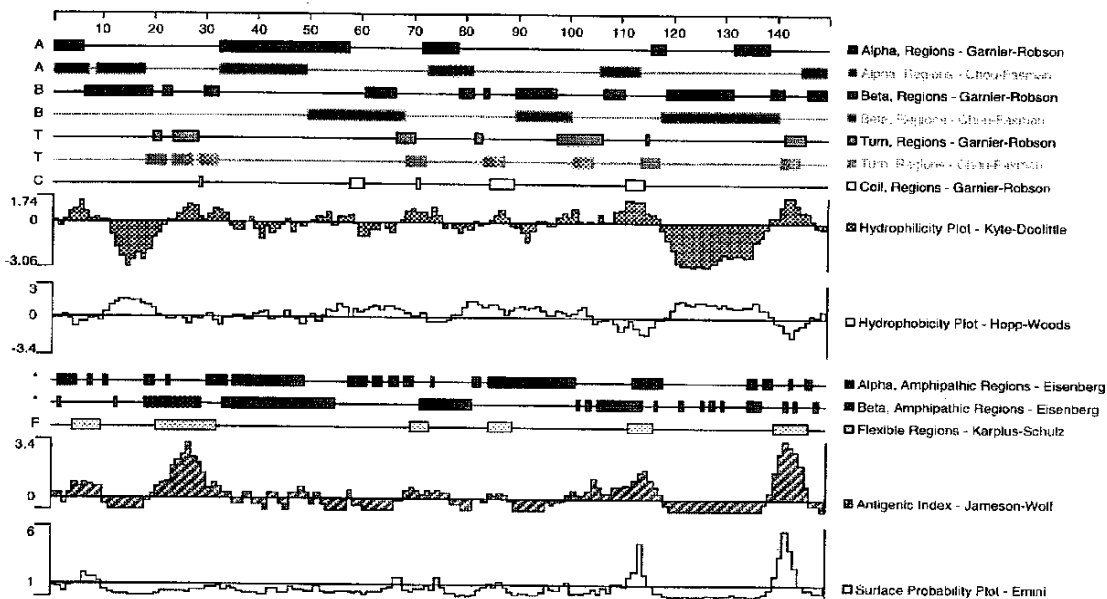


FIG. 10A

1 GGCACGAGGACAGCCTCCACCAGAGTCCCCACCTTTCTGGAAGCTGCAGGGCTCTCCATC 60  
61 CAGGATCCAGAAGCATTGAAGGGGACCAGCCCTGAAGGGATTCTCAGTCCCATCTGACT 120  
121 CCCCATGAGGCTCCTGGCTTTCTGAGTCTGCTGGCCTTGGTGCTGCAGGAGACAGGGAC 180  
1 M R L L A F L S L L A L V L Q E T G T 19  
181 AGCTTCTCTCCCAAGGAAGGAGAGGAAGAGGAGAGAGGAGCAGATGCCAGGGAAGGCGA 240  
20 A S L P R K E R K R R E E Q M P R E G D 39  
241 TTCCTTTGAAGTTCTGCCTCTGCGGAATGATGTCTGAACCCAGACAACCTATGGTGAAGT 300  
40 S F E V L P L R N D V L N P D N Y G E V 59  
301 CATTGACCTGAGCAACTATGAGGAGCTCAGATTATGGGGACCAACTCCCCGAGGTTAA 360  
60 I D L S N Y E E L T D Y G D Q L P E V K 79  
361 GGTGACTAGCCTCGCTCCTGCAACCAGCATCAGTCCCGCCAAGAGCACTACGGCTCCAGG 420  
80 V T S L A P A T S I S P A K S T T A P G 99  
421 GACACCCTCGTCAAACCCACGATGACCAGACCTACTACAGCAGGGCTGCTACTGAGTTC 480  
100 T P S S N P T M T R P T T A G L L L S S 119  
481 CCAGCCCAACCATGGTCTGCCCCACCTGCCTGGTCTGCGTGTGCTCGGTTCTCTGTGTA 540  
120 Q P N H G L P T C L V C V C L G S S V Y 139  
541 TTGCGATGACATTGACCTAGAGGACATTCTCTCTTCTCTCGGAGGACTGCCTACCTGTA 600  
140 C D D I D L E D I P P L P R R T A Y L Y 159  
601 TGCACGCTTCAACCGCATCAGCCGTATCAGGGCCGAAGACTTCAAAGGGCTGACAAAGTT 660  
160 A R F N R I S R I R A E D F K G L T K L 179  
661 GAAGAGGATTGACCTCTCCAACAACCTCATTTCTCCATCGATAATGATGCCTTCCGCCT 720  
180 K R I D L S N N L I S S I D N D A F R L 199  
721 GCTACATGCCCTCCAGGACCTCATCCTCCCAGAGAACCAGTTGGAAGCTCTGCCCCGTGCT 780  
200 L H A L Q D L I L P E N Q L E A L P V L 219  
781 GCCCAGTGGCATTGAGTTCCTGGATGTCCGCCTAAATCGGCTCCAGAGCTCGGGGATACA 840  
220 P S G I E F L D V R L N R L Q S S G I Q 239  
841 GCCTGCAGCCTTCAGGGCAATGGAGAAGCTGCAGTTCCTTTACCTGTGACACAACCTGCT 900  
240 P A A F R A M E K L Q F L Y L S D N L L 259

## FIG. 10B

901 GGATTCTATCCCGGGGCCTTTGCCCGGAGCCTGCGCTCTGTACACCTGCAGAATAACCT 960  
260 D S I P G P L P P S L R S V H L Q N N L 279

961 GATAGAGACCATGCAGAGAGACGTCTTCTGTGACCCCGAGGAGCACAAACACACCCGCAG 1020  
280 I E T M Q R D V F C D P E E H K H T R R 299

1021 GCAGCTGGAAGACATCCGCCTGGATGGCAACCCCATCAACCTCAGCCTCTTCCCCAGCGC 1080  
300 Q L E D I R L D G N P I N L S L F P S A 319

1081 CTACTTCTGCCTGCCTCGGCTCCCCATCGGCCGCTTCACGTAGCTCGGAGCCCTTCCACT 1140  
320 Y F C L P R L P I G R F T \* 333

1141 CCTCCCAGGTCATCTCTTGGACCAGCGGGCATCACATTCTCCAGCAGCCGCCATCTCACA 1200

1201 CGCCTCCCTCCTGTGGCCGCGCCGAGCATGGACAAAGGTCTCCATGCAGGGGAGGAGGC 1260

1261 CTGCTTCTTTCCCCACAGCTCTCACGTCTCCCTTCTCCCTGCGGGTGACAAAGAAGCCCA 1320

1321 AGGACCACCTCCTTCTGCCTCATTTGTAATAAAATTCCCCACACTGAAAAAAAAAAAAAA 1380

1381 AAAAAAAAAA 1389

FIG. 11

		10		20		30		40																																			
1	M	R	L	L	A	F	L	S	L	L	A	L	V	L	Q	E	-	-	-	T	G	T	A	S	L	P	R	K	E	R	K	R	E	E	Q	M	P	R	E		HARAO44.aa		
1	M	G	M	L	A	R	V	A	L	G	L	I	I	I	D	A	V	L	A	A	P	T	T	E	L	F	N	Y	D	S	E	V	Y	D	A	I	L	E	D	T		gi 1620005	
		50		60		70		80																																			
38	G	D	S	F	E	V	L	P	L	R	N	D	V	L	N	P	D	N	Y	G	E	V	I	D	L	S	N	Y	E	E	L	T	D	Y	G	D	Q	L	P	E		HARAO44.aa	
41	G	T	F	Y	N	Y	E	H	I	P	D	N	H	V	E	N	E	K	V	S	E	-	-	R	L	S	G	N	R	E	L	L	T	P	G	P	Q	L	G	D		gi 1620005	
		90		100		110		120																																			
78	V	K	V	T	S	L	A	P	A	T	S	I	S	P	A	K	S	T	T	A	P	G	T	P	S	S	N	P	T	M	T	R	P	T	A	G	L	L	L		HARAO44.aa		
79	N	Q	-	-	-	-	-	-	-	-	-	-	-	D	E	D	K	D	E	E	S	T	P	R	L	I	D	G	S	S	P	Q	E	E	F	F	P	G	L	L	-	gi 1620005	
		130		140		150		160																																			
118	S	S	Q	P	N	H	G	L	P	T	C	L	V	C	V	C	L	G	S	S	V	Y	C	D	D	I	D	L	E	D	I	P	P	L	P	R	R	T	A	Y		HARAO44.aa	
108	G	P	H	T	N	E	D	F	P	T	C	L	L	C	T	C	I	S	T	T	V	Y	C	D	D	H	E	L	D	A	I	P	P	L	P	K	K	T	T	Y		gi 1620005	
		170		180		190		200																																			
158	L	Y	A	R	F	N	R	I	S	R	I	R	A	E	D	F	K	G	L	T	K	L	K	R	I	D	L	S	N	N	L	I	S	S	I	D	N	D	A	F		HARAO44.aa	
148	F	Y	S	R	E	N	R	I	K	K	I	N	K	N	D	F	A	S	L	N	D	L	K	R	I	D	L	T	S	N	L	I	S	E	I	D	E	D	A	F		gi 1620005	
		210		220		230		240																																			
198	R	L	L	H	A	L	Q	D	L	I	L	P	E	N	Q	L	E	A	L	P	V	L	P	S	G	I	E	F	L	D	V	R	L	N	R	L	Q	S	S	G		HARAO44.aa	
188	R	K	L	P	H	L	Q	E	L	V	L	R	D	N	K	I	K	Q	L	P	E	L	P	N	T	L	T	F	I	D	I	S	N	N	R	L	G	R	K	G		gi 1620005	
		250		260		270		280																																			
238	I	Q	P	A	A	F	R	A	M	E	K	L	Q	F	L	Y	L	S	D	N	L	D	S	I	P	G	P	L	P	P	S	L	R	S	V	H	L	Q	N		HARAO44.aa		
228	I	K	Q	E	A	F	K	D	M	Y	D	L	H	H	L	Y	I	T	D	N	S	L	D	H	I	P	I	P	L	P	E	S	L	R	A	L	H	L	Q	N		gi 1620005	
		290		300		310		320																																			
278	N	L	I	E	T	M	Q	R	D	V	F	C	D	P	E	E	H	K	H	T	R	R	Q	L	E	D	I	R	L	D	G	N	P	I	N	L	S	L	F	P		HARAO44.aa	
268	N	D	I	L	E	M	H	E	D	T	F	C	N	V	K	N	L	T	Y	V	R	K	A	E	D	I	R	L	D	G	N	P	I	N	L	S	R	T	P		gi 1620005		
		330																																									
318	S	A	Y	F	C	L	P	R	L	P	I	G	R	F	T	.																											HARAO44.aa
308	Q	A	Y	M	C	L	P	R	L	P	I	G	S	F	-	I																											gi 1620005

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 12

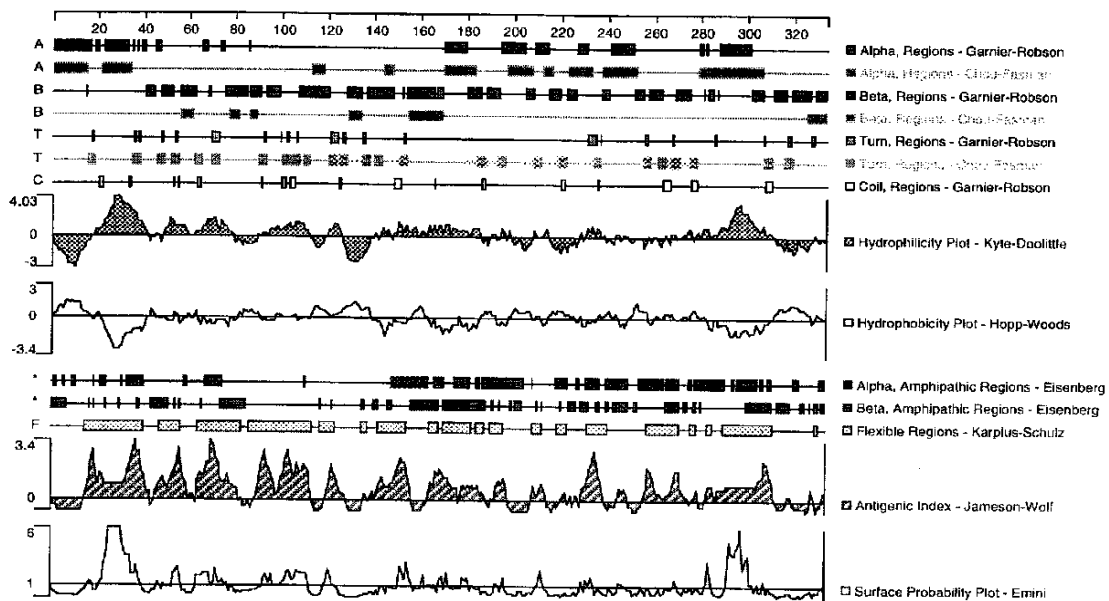




FIG. 13A

1	CCACGCGTCCGAGAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATG	60
1	<u>M</u>	1
61	CTACTGCCACTGCTGCTGTCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTG	120
2	<u>L L P L L L S S L L G G S Q A M D G R F</u>	21
121	TGGATACGAGTGCAGGAGTCAGTGATGGTGCCGAGGCCTGTGACATCTCTGTGCCCTGC	180
22	W I R V Q E S V M V P E A C D I S V P C	41
181	TCTTTCTCCTACCCCGACAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTG	240
42	S F S Y P R Q D W T G S T P A Y G Y W F	61
241	AAAGCAGTGAAGTGCAGACAACCAAGGGTCTCCTGTGGCCACAAACCACAGAGTCGACAG	300
62	K A V T E T T K G A P V A T N H Q S R E	81
301	GTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAGTGC	360
82	V E M S T R G R F Q L T G D P A K G N C	101
361	TCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCCGGGTGGAG	420
102	S L V I R D A Q M Q D E S Q Y F F R V E	121
421	AGAGGAAGCTATGTGAGATATAATTTTCATGAACGATGGGTTCTTTCTAAAAGTAACAGTG	480
122	R G S Y V R Y N F M N D G F F L K V T V	141
481	CTCAGCTTCACGCCCAGACCCAGGACCAACACCGACCTCACCTGCCATGTGGACTTC	540
142	L S F T P R P Q D H N T D L T C H V D F	161
541	TCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCCAGA	600
162	S R K G V S A Q R T V R L R V A Y A P R	181
601	GACCTTGTATCAGCATTTACAGTGACAACACGCCAGCCCTGGAGCCCCAGCCCCAGGGA	660
182	D L V I S I S R D N T P A L E P Q P Q G	201
661	AATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCTCTGCGGCTCCTCTGTGCTGCTGAC	720
202	N V P Y L E A Q K G Q F L R L L C A A D	221
721	AGCCAGCCCCCTGCCACACTGAGCTGGGTCTCTGCAGAACAGAGTCCTCTCCTCGTCCCAT	780
222	S Q P P A T L S W V L Q N R V L S S S H	241
781	CCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGTGAAGGCTGGGGATTACAGGG	840
242	P W G P R P L G L E L P G V K A G D S G	261

FIG. 13B

841	CGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCT	900
262	R Y T C R A E N R L G S Q Q R A L D L S	281
901	GTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACACTCCTG	960
282	V Q Y P P E N L R V M V S Q A N R T V L	301
961	GAAAACCTTGGGAACGGCACGTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCCTGGTCTC	1020
302	E N L G N G T S L P V L E G Q S L C L V	321
1021	TGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGACAGGTTCTG	1080
322	C V T H S S P P A R L S W T Q R G Q V L	341
1081	AGCCCCCTCCCAGCCCTCAGACCCCGGGGCTCCTGGAGCTGCCTCGGGTTCAAGTGGAGCAC	1140
342	S P S Q P S D P G V L E L P R V Q V E H	361
1141	GAAGGAGAGTTCACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGTCTCTCTCAGC	1200
362	E G E F T C H A R H P L G S Q H V S L S	381
1201	CTCTCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCCTCCTGCTCCTGGGAGGCTGAGGGT	1260
382	L S V H Y S P K L L G P S C S W E A E G	401
1261	CTGCACTGCAGCTGCTCCTCCCAGGCCAGCCCGGCCCCCTCTCTGCGCTGGTGGCTTGGG	1320
402	L H C S C S S Q A S P A P S L R W W L G	421
1321	GAGGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCTCAGCC	1380
422	E E L L E G N S S Q D S F E V T P S S A	441
1381	GGGCCCTGGGCCAACAGCTCCCTGAGCCTCCATGGAGGGCTCAGCTCCGGCCTCAGGCTC	1440
442	G P W A N S S L S L H G G L S S G L R L	461
1441	CGCTGTGAGGCCTGGAACGTCCATGGGGCCCAGAGTGGATCCATCCTGCAGCTGCCAGAT	1500
462	R C E A W N V H G A Q S G S I L Q L P D	481
1501	AAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGCATCAGC	1560
482	K K G L I S T A F S N G A F <u>L G I G I T</u>	501
1561	GCTCTTCTTTTCTCTGCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGGACT	1620
502	<u>A L L F L C L A L I I</u> M K I L P K R R T	521
1621	CAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCACGATCCTGGATTACATCAAT	1680
522	Q T E T P R P R F S R H S T I L D Y I N	541

FIG. 13C

1681 GTGGTCCCACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACACCAAACAGT 1740  
542 V V P T A G P L A Q K R N Q K A T P N S 561

1741 CCTCGGACCCCTCTTCCACCAGGTGCTCCCCTCCCAGAAATCAAAGAAGAACCCAGAAAAAG 1800  
562 P R T P L P P G A P S P E S K K N Q K K 581

1801 CAGTATCAGTTGCCCAGTTTCCACAGAACCCAAATCATCCACTCAAGCCCCAGAAATCCCAG 1860  
582 Q Y Q L P S F P E P K S S T Q A P E S Q 601

1861 GAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCT 1920  
602 E S Q E E L H Y A T L N F P G V R P R P 621

1921 GAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAAGTCAAGTTCCAATGAGGG 1980  
622 E A R M P K G T Q A D Y A E V K F Q \* 640

1981 TCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGAGGAAGGTAGAGTAGAAGTTGAAGAT 2040

2041 AACCAGGTGCAAGAGTTTCTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2100

2101 TTCTCTCTCTTTTAAAAAACTCTGGCCACGGCACAGTGGCTCACGCCTGTAATCCAG 2160

2161 CACTTTGGGAAGTTGAAGTTGGGCCAAATCCCCCTGAGTCCCGATTGAAAACAGCCTGGC 2220

2221 CAACTTGTGAAAACCCGTCTCTACTTAAAAATACCCAAATTACCTGGGCATTGTGGCAGG 2280

2281 GGCCTGTTTATCCTT 2295

FIG. 14A

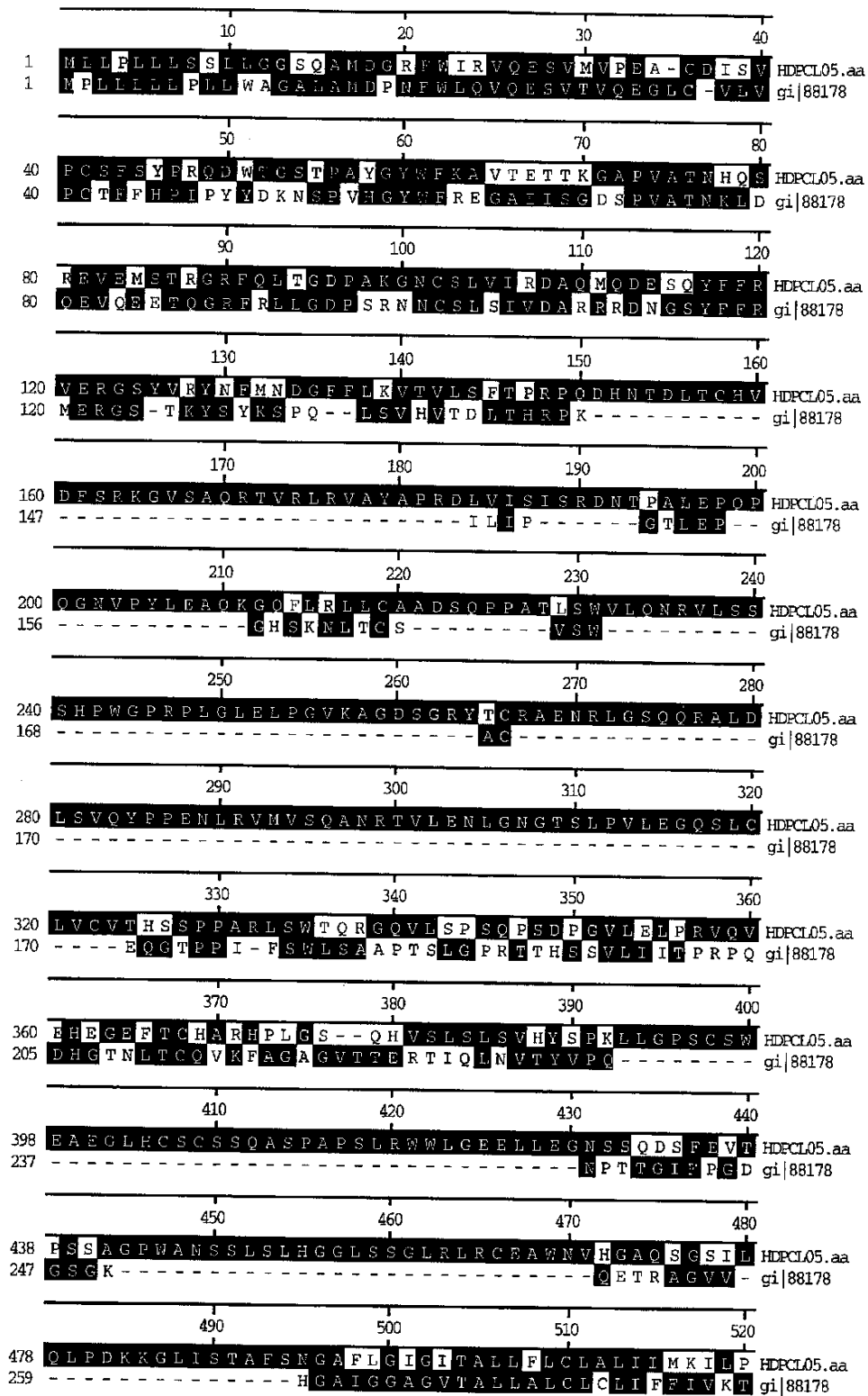
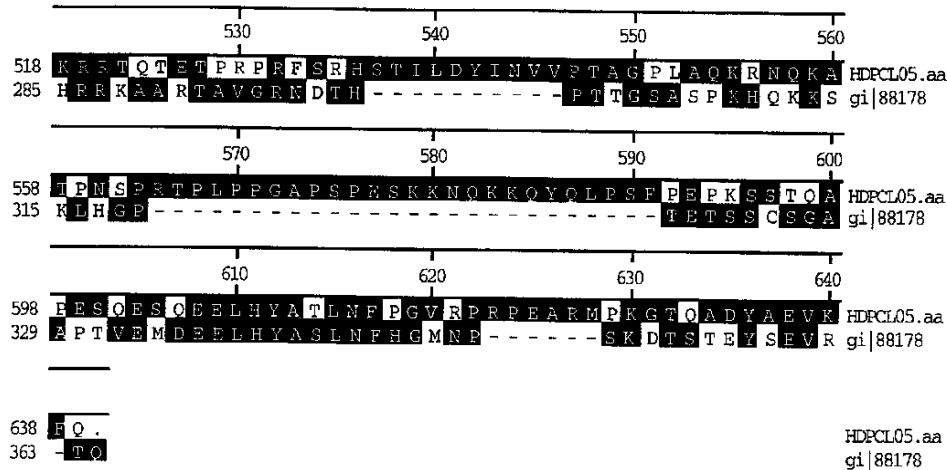


FIG. 14B



Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 15

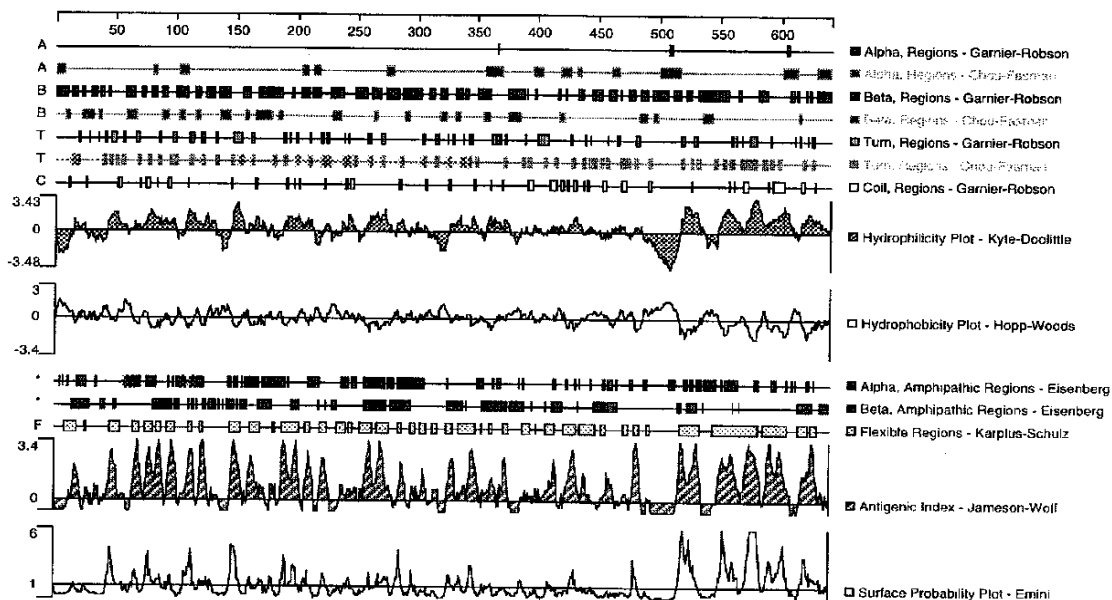


FIG. 16A

1	AGACGTTCCCTCGCGGCCCTGGCACCTCCAACCCAGATATGCTGCTGCTGCTGCTG	60
1	<u>M L L L L L L</u>	7
61	CCCCTGCTCTGGGGGAGGGAGAGGGTGGAAAGGACAGAAGAGTAACCGGAAGGATTACTCG	120
8	<u>P L L W G R E R V E G</u> Q K S N R K D Y S	27
121	CTGACGATGCAGAGTTCCGTGACCGTGCAAGAGGGCATGTGTGCCATGTGCGCTGCTCC	180
28	L T M Q S S V T V Q E G M C V H V R C S	47
181	TTCTCCTACCCAGTGGACAGCCAGACTGACTCTGACCCAGTTCATGGCTACTGGTTCCGG	240
48	F S Y P V D S Q T D S D P V H G Y W F R	67
241	GCAGGGAATGATATAAGCTGGAAGGCTCCAGTGGCCACAAACAACCCAGCTTGGGCAGTG	300
68	A G N D I S W K A P V A T N N P A W A V	87
301	CAGGAGGAAACTCGGGACCGATTCCACCTCCTTGGGGACCCACAGACCAAAAATTGCACC	360
88	Q E E T R D R F H L L G D P Q T K N C T	107
361	CTGAGCATCAGAGATGCCAGAATGAGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAA	420
108	L S I R D A R M S D A G R Y F F R M E K	127
421	GGAAATATAAAATGGAATTATAAATATGACCAGCTCTCTGTGAACGTGACAGCCTTGACC	480
128	G N I K W N Y K Y D Q L S V N V T A L T	147
481	CACAGGCCCAACATCCTTATCCCCGGTACCCTGGAGTCTGGCTGCTTCCAGAATCTGACC	540
148	H R P N I L I P G T L E S G C F Q N L T	167
541	TGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACGCCCCCTATGATCTCCTGGATGGGGACC	600
168	C S V P W A C E Q G T P P M I S W M G T	187
601	TCTGTGTCCCCCTGCACCCCTCCACCACCCGCTCCTCAGTGCTCACCTCATCCACAG	660
188	S V S P L H P S T T R S S V L T L I P Q	207
661	CCCCAGCACACGGCACCAGCCTCACCTGTGAGGTGACCTTGCCCTGGGGCCGGCGTGACC	720
208	P Q H H G T S L T C Q V T L P G A G V T	227
721	ACGAACAGGACCATCCAACCTCAATGTGTCTACCCTCCTCAGAACTTGACTGTGACTGTC	780
228	T N R T I Q L N V S Y P P Q N L T V T V	247
781	TTCCAAGGAGAAGGCACAGCATCCACAGCTCTGGGGAACAGCTCATCTCTTTCAGTCCTA	840
248	F Q G E G T A S T A L G N S S S L S V L	267

FIG. 16B

841 GAGGGCCAGTCTCTGCGCTTGGTCTGTGCTGTGACAGCAATCCCCCTGCCAGGCTGAGC 900  
268 E G Q S L R L V C A V D S N P P A R L S 287

901 TGGACCTGGAGGAGTCTGACCCCTGTACCCCTCACAGCCCTCAAACCCCTCTGGTACTGGAG 960  
288 W T W R S L T L Y P S Q P S N P L V L E 307

961 CTGCAAGTGCACCTGGGGGATGAAGGGGAATTACCTGTGAGCTCAGAACTCTCTGGGT 1020  
308 L Q V H L G D E G E F T C R A Q N S L G 327

1021 TCCCAGCACGTTCCCTGAACCTCTCCCTGCAACAGGAGTACACAGGCAAAATGAGGCCCT 1080  
328 S Q H V S L N L S L Q Q E Y T G K M R P 347

1081 GTATCAGGAGTCTTGCTGGGGGCGGTGCGGGGAGCTGGAGCCACAGCCCTGGTCTTCCTC 1140  
348 V S G V L L G A V G G A G A T A L V F L 367

1141 TCCTTCTGTGTCATCTTCATTGTAGTGAGGTCCTGCAGGAAGAAATCGGCAAGGCCAGCA 1200  
368 S F C V I F I V V R S C R K K S A R P A 387

1201 GCGGACGTGGGAGACATAGGCATGAAGGATGCAAACACCATCAGGGGCTCAGCCTCTCAG 1260  
388 A D V G D I G M K D A N T I R G S A S Q 407

1261 GGTAACCTGACTGAGTCTTGGGCAGATGATAACCCCCGACACCATGGCCTGGCTGCCCCAC 1320  
408 G N L T E S W A D D N P R H H G L A A H 427

1321 TCCTCAGGGGAGGAAAGAGAGATCCAGTATGCACCCCTCAGCTTTCATAAGGGGGAGCCT 1380  
428 S S G E E R E I Q Y A P L S F H K G E P 447

1381 CAGGACCTATCAGGTCAAGAAGCCACCAACAATGAGTACTCAGAGATCAAGATCCCCAAG 1440  
448 Q D L S G Q E A T N N E Y S E I K I P K 467

1441 TAAGAAAATGCAGAGGCTCGGGCTTGTTTGAGGGTTACAGACCCCTCCAGCAAAGGAGTC 1500  
468 \* 468

1501 TGAGGCTGATTCCAGTAGAATTAGCAGCCCTCAATGCTGTGCAACAAGACATCAGAACTT 1560

1561 ATTCCTCTTGCTTAAGTGAATAATGCATGCCTGATGACCAAATCTCCCTTTCCCCATCCA 1620

1621 ATCGGTCCACACTCCCCGCCCTGGCCTCTGGTACCCACCATCTCCTCTGTACTTCTCTA 1680

1681 AGGATGACTACTTTAGATTCCGAATATAGTGAGATTGTACGTGAAAAAAAAAAAAAAAAA 1740

1741 AAAAAAAA 1748

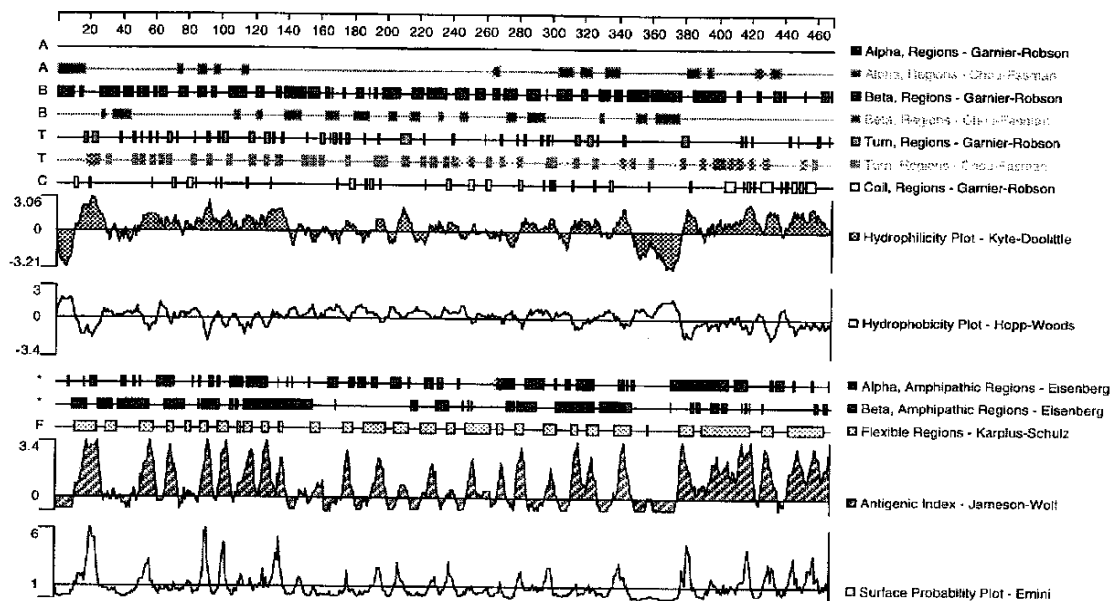


FIG. 17

		10	20	30	40	
1		M L L L L L L P L L W G R E R V E G Q K S N R K D Y S L T M Q S S V T V Q E G M	HDPFW68.aa			
1		M L P L L L - P L L W A - - - - G A L A Q E R R F Q L E G P E S L T V Q E G L	gi 2913995			
		50	60	70	80	
41		C V H V R C S F S Y P V D S Q T D S D P V H G Y W F R A G N D I S W K A P V A T	HDPFW68.aa			
35		C V L V P C R L P T T L P A S Y Y G - - - Y G Y W F L E G A D V - - - - P V A T	gi 2913995			
		90	100	110	120	
81		N N P A W A V Q E E T R D R F H L L G D P Q T K N C T L S I R D A R M S D A G R	HDPFW68.aa			
68		N D P D E E V Q E E T R G R F H L L W D P R R K N C S L S I R D A R R R D N A A	gi 2913995			
		130	140	150	160	
121		Y F F R M E K G N I K W N Y K Y D Q L S V N V T A L T H R P N I L I P G T L E S	HDPFW68.aa			
108		Y F F R L K S K W M K Y G Y T S S K L S V R V M A L T H R P N I S I P G T L E S	gi 2913995			
		170	180	190	200	
161		G C F Q N L T C S V P W A C E Q G T P P M I S W M G T S V S P L H P S T T R S S	HDPFW68.aa			
148		G H P S N L T C S V P W V C E Q G T P P I F S W M S A A P T S L G P R T T Q S S	gi 2913995			
		210	220	230	240	
201		V L T L I P Q P Q H H G T S L T C Q V T L P G A G V T T N R T I Q L N V S Y P P	HDPFW68.aa			
188		V L T I T E R P Q D H S T N L T C Q V T F P G A G V T M E R T I Q L N V S Y A P	gi 2913995			
		250	260	270	280	
241		Q N L T V T V F Q G E G T A S T A L G N S S S L S V L E G Q S L R L V C A V D S	HDPFW68.aa			
228		Q K V A I S I F Q G N S A A F K I L Q N T S S L P V L R G Q A L R L L C D A D G	gi 2913995			
		290	300	310	320	
281		N P P A R L S W T W R S L T L Y P S Q P S N P L V L E L - Q V H L G D E G E F T	HDPFW68.aa			
268		N P P A H L S W F Q G F P A L N A T P I S N T G V L E L P Q V G S A E E G D F T	gi 2913995			
		330	340	350	360	
320		C R A Q N S L G S Q H V S L N L S L Q Q E Y T G K M R P V S G V L L G A V G G A	HDPFW68.aa			
308		C R A Q H P L G S L Q I S L S L F V H W K P E G R - - - - A G G V L G A V W G A	gi 2913995			
		370	380	390	400	
360		G A T A L V F L S F C V I F I V V R S C R K K S A R P A A D V G D I G M K D A N	HDPFW68.aa			
344		S I T T L V F L C V C F I F R V - K T R R K K A A Q P V Q N T D D V - - - - N	gi 2913995			
		410	420	430	440	
400		T I R G S A S Q G N L T E S W A D D N P R H H G L A A H S S G E E R E I Q Y A P	HDPFW68.aa			
378		P V M V S G S R G H Q H Q F Q T G I V S D H P A E A G P I S E D E Q E L H Y A V	gi 2913995			
		450	460			
440		L S F H K G E P Q D L S G Q E A T N N E Y S E I K I E K L	HDPFW68.aa			
418		L H F H K V Q P Q E - - - P K V T D T E Y S E I K I H - K	gi 2913995			

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 18



## FIG. 19A

1 GCCGCGCCGAGGAGGCTGCCGCTCTGGCTTGCCGCCCCCGCCGCGCTGCACACCGGAC 60

61 CCAGCCCGCGTGCCGCGGGCCATGGACCTGCCCAGGGGCTGGTGGTGGCCTGGGCGCTC 120  
1 M D L P R G L V V A W A L 13

121 AGCCTGTGGCCAGGCTTCACGGACACCTTCAACATGGACACCAGGAAGCCCCGGGTCATC 180  
14 S L W P G F T D T F N M D T R K P R V I 33

181 CCTGGCTCCAGGACCGCCTTCTTTGGCTACACAGTGCAGCAGCAGACATCAGTGGCAAT 240  
34 P G S R T A F F G Y T V Q Q H D I S G N 53

241 AAGTGGCTGGTTCGTGGCGCCCCACTGAAAACCAATGGCTACCAGAAGACGGGAGACGTG 300  
54 K W L V V G A P L E T N G Y Q K T G D V 73

301 TACAAGTGTCCAGTGATCCACGGAACTGCACCAAACCTCAACCTGGGAAGGGTCACCCTG 360  
74 Y K C P V I H G N C T K L N L G R V T L 93

361 TCCAACGTGTCCGAGCGGAAAGACAACATGCGCCTCGGCCTTAGTCTCGCCACCAACCCC 420  
94 S N V S E R K D N M R L G L S L A T N P 113

421 AAGGACAACAGCTTCCTGGCCTGCAGCCCCCTCTGGTCTCATGAGTGTGGGAGCTCCTAC 480  
114 K D N S F L A C S P L W S H E C G S S Y 133

481 TACACCACAGGGATGTGTTCAAGAGTCAACTCCAACCTCAGGTTCTCCAAGACCGTGGCC 540  
134 Y T T G M C S R V N S N F R F S K T V A 153

541 CCAGCTCTCAAAGGTGCCAGACCTACATGGACATCGTCATTGTCTCGGATGGCTCCAAC 600  
154 P A L Q R C Q T Y M D I V I V L D G S N 173

601 AGCATCTACCCCTGGGTGGAGGTTCAGCACTTCCTCATCAACATCCTGAAAAAGTTTAC 660  
174 S I Y P W V E V Q H F L I N I L K K F Y 193

661 ATTGGCCCAGGGCAGATCCAGGTGGAGTTGTGCAGTATGGCGAAGATGTGGTGCATGAG 720  
194 I G P G Q I Q V G V V Q Y G E D V V H E 213

721 TTTCACCTCAATGACTACAGGTCTGTAAAAGATGTGGTGGAAAGCTGCCAGCCACATGAG 780  
214 F H L N D Y R S V K D V V E A A S H I E 233

781 CAGAGAGGAGGAACAGAGACCCGACGGCATTGGCATTGAATTTGCACGCTCAGAGGCT 840  
234 Q R G G T E T R T A F G I E F A R S E A 253

FIG. 19B

841	TTCCAGAAGGGTGGAAAGGAAAGGAGCCAAAGAGGTGATGATTGTTCATCACAGATGGGGAG	900
254	F Q K G G R K G A K K V M I V I T D G E	273
901	TCCCACGACAGCCCAGACCTGGAGAAGGTGATCCAGCAAAGCGAAAGAGACAACGTAACA	960
274	S H D S P D L E K V I Q Q S E R D N V T	293
961	AGATATGCGGTGGCCGTCCTGGGCTACTACAACCGCAGGGGGATCAATCCAGAAACTTTT	1020
294	R Y A V A V L G Y Y N R R G I N P E T F	313
1021	CTAAATGAAATCAAATACATCGCCAGTGACCTGATGACAAGCACTTCTTCAATGTCACT	1080
314	L N E I K Y I A S D P D D K H F F N V T	333
1081	GATGAGGCTGCCTTGAAGGACATTGTGATGCCCTGGGGGACAGAATCTTCAGCCTGGAA	1140
334	D E A A L K D I V D A L G D R I F S L E	353
1141	GGCACCAACAAGAACGAGACCTCCTTTGGGCTGGAGATGTCACAGACGGGCTTTTCCTCG	1200
354	G T N K N E T S F G L E M S Q T G F S S	373
1201	CACGTGGTGGAGGATGGGGTTCTGCTGGGAGCCGTCGGTGCCTATGACTGGAATGGAGCT	1260
374	H V V E D G V L L G A V G A Y D W N G A	393
1261	GTGCTAAAGGAGACGAGTGCCGGGAAGGTCATTCTCTCCGCGAGTCTTACCTGAAAGAG	1320
394	V L K E T S A G K V I P L R E S Y L K E	413
1321	TTCCCCGAGGAGCTCAAGAACCATGGTGCATACCTGGGGTACACAGTCACATCGGTCGTC	1380
414	F P E E L K N H G A Y L G Y T V T S V V	433
1381	TCCTCCAGGCAGGGGCGAGTGACGTGGCCGGAGCCCCCGGTTCAACCACACGGGCAAG	1440
434	S S R Q G R V Y V A G A P R F N H T G K	453
1441	GTCATCCTGTTTCACCATGCACAACAACCGGAGCCTCACCATCCACCAGGCTATGCGGGGC	1500
454	V I L F T M H N N R S L T I H Q A M R G	473
1501	CAGCAGATAGGCTCTTACTTTGGGAGTGAAATCACCTCGGTGGACATCGACGGCGACGGC	1560
474	Q Q I G S Y F G S E I T S V D I D G D G	493
1561	GTGACTGATGTCCTGCTGGTGGGCGCACCCATGTACTTCAACGAGGGCCGTGAGCGAGGC	1620
494	V T D V L L V G A P M Y F N E G R E R G	513
1621	AAGGTGTACGTCTATGAGCTGAGACAGAACCGGTTTGTATTATAACGGAACGCTAAAGGAT	1680
514	K V Y V Y E L R Q N R F V Y N G T L K D	533

## FIG. 19C

1681	TCACACAGTTACCAGAATGCCCGATTGGGTCCTCCATTGCCTCAGTTCGAGACCTCAAC	1740
534	S H S Y Q N A R F G S S I A S V R D L N	553
1741	CAGGATTCTTACAATGACGTGGTGGTGGGAGCCCCCTGGAGGACAACCACGCAGGAGCC	1800
554	Q D S Y N D V V V G A P L E D N H A G A	573
1801	ATCTACATCTTCCACGGCTTCCGAGGCAGCATCTGAAGACACCTAAGCAGAGAATCACA	1860
574	I Y I F H G F R G S I L K T P K Q R I T	593
1861	GCCTCAGAGCTGGCTACCGGCTCCAGTATTTTGGCTGCAGCATCCACGGGCAATTGGAC	1920
594	A S E L A T G L Q Y F G C S I H G Q L D	613
1921	CTCAATGAGGATGGGCTCATCGACCTGGCAGTGGGAGCCCTTGGCAACGCTGTGATTCTG	1980
614	L N E D G L I D L A V G A L G N A V I L	633
1981	TGGTCCCGCCAGTGGTTCAGATCAATGCCAGCCTCCACTTTGAGCCATCCAAGATCAAC	2040
634	W S R P V V Q I N A S L H F E P S K I N	653
2041	ATCTTCCACAGAGACTGCAAGCGCAGTGGCAGGGATGCCACCTGCCTGGCCGCTTCCTC	2100
654	I F H R D C K R S G R D <u>A T C L A A F L</u>	673
2101	TGCTTCACGCCCATCTTCCTGGCACCCCATTTCCAAACAACAACCTGTTGGCATCAGATAC	2160
674	<u>C F T P I F L A P</u> H F Q T T T V G I R Y	693
2161	AACGCCACCATGGATGAGAGGGCGTATACACCGAGGGCCACCTGGACGAGGGCGGGGAC	2220
694	N A T M D E R R Y T P R A H L D E G G D	713
2221	CGATTACCAACAGAGCCGTACTGCTCTCTCCGCGCCAGGAGCTCTGTGAGCGGATCAAC	2280
714	R F T N R A V L L S S G Q E L C E R I N	733
2281	TTCCATGTCCTGGACACTGCTGACTACGTGAAGCCAGTGACCTTCTCAGTCGAGTATTC	2340
734	F H V L D T A D Y V K P V T F S V E Y S	753
2341	CTGGAGGACCCTGACCATGGCCCCATGCTGGACGACGGCTGGCCCACCACTCTCAGAGTC	2400
754	L E D P D H G P M L D D G W P T T L R V	773
2401	TCGGTGCCTTCTGGAACGGCTGCAATGAGGATGAGCACTGTGTCCCTGACCTTGTGTTG	2460
774	S V P F W N G C N E D E H C V P D L V L	793
2461	GATGCCCGGAGTGACCTGCCACGGCCATGGAGTACTGCCAGAGGGTGTGAGGAAGCCT	2520
794	D A R S D L P T A M E Y C Q R V L R K P	813

FIG. 19D

2521	GCGCAGGACTGCTCCGCATACACGCTGTCCTTCGACACCACAGTCTTCATCATAGAGAGC	2580
814	A Q D C S A Y T L S F D T T V F I I E S	833
2581	ACACGCCAGCGAGTGGCGGTGGAGGCCACACTGGAGAACAGGGGCGAGAACGCCTACAGC	2640
834	T R Q R V A V E A T L E N R G E N A Y S	853
2641	ACGGTCCTAAATATCTCGCAGTCAGCAAACCTGCAGTTTGCCAGCTTGATCCAGAAGGAC	2700
854	T V L N I S Q S A N L Q F A S L I Q K E	873
2701	GACTCAGACGGTAGCATTCAGTGTGTGAACGAGGAGAGGAGGCTCCAGAAGCAAGTCTGC	2760
874	D S D G S I E C V N E E R R L Q K Q V C	893
2761	AACGTCAGCTATCCCTTCTTCCGGGCCAAGGCCAAGGTGGCTTTCCGTCTTGATTTTGAG	2820
894	N V S Y P F F R A K A K V A F R L D F E	913
2821	TTCAAGCAATCCATCTTCCTACACCACCTGGAGATCGAGCTCGCTGCAGGCAGTGACAGT	2880
914	F S K S I F L H H L E I E L A A G S D S	933
2881	AATGAGCGGGACAGCACCAAGGAAGACAACGTGGCCCCCTTACGCTTCCACCTCAAATAC	2940
934	N E R D S T K E D N V A P L R F H L K Y	953
2941	GAGGCTGACGTCCTCTTCACCAGGAGCAGCAGCCTGAGCCACTACGAGGTCAAGCTCAAC	3000
954	E A D V L F T R S S S L S H Y E V K L N	973
3001	AGCTCGCTGGAGAGATACGATGGTATCGGGCCTCCCTTCAGCTGCATCTTCAGGATCCAG	3060
974	S S L E R Y D G I G P P F S C I F R I Q	993
3061	AACTTGGGCTTGTTCCTCCATCCACGGGATTATGATGAAGATCACCATTCCCATCGCCACC	3120
994	N L G L F P I H G I M M K I T I P I A T	1013
3121	AGGAGCGGCAACCGCTACTGAAGCTGAGGGACTTCCTCACGGACGAGGTAGCGAACACG	3180
1014	R S G N R L L K L R D F L T D E V A N T	1033
3181	TCCTGTAAATCTGGGGCAATAGCACTGAGTACCGGGCCACCCCACTGGAGGAAGACTTG	3240
1034	S C N I W G N S T E Y R P T P V E E D L	1053
3241	CGTCGTGCTCCACAGCTGAATCACAGCAACTCTGATGTGCTCTCCATCAACTGCAATATA	3300
1054	R R A P Q L N H S N S D V V S I N C N I	1073
3301	CGGCTGGTCCCCAACCGGAATCAATTTCCATCTACTGGGGAACCTGTGGTTGAGGTCC	3360
1074	R L V P N Q E I N F H L L G N L W L R S	1093

FIG. 19E

3361	CTAAAAGCACTCAAGTACAAATCCATGAAAATCATGGTCAACGCAGCCTTGCAGAGGCAG	3420
1094	L K A L K Y K S M K I M V N A A L Q R Q	1113
3421	TTCCACAGCCCCTTCATCTTCCGTGAGGAGGATCCCAGCCGCCAGATCGTGTTCAGATC	3480
1114	F H S P F I F R E E D P S R Q I V F E I	1133
3481	TCCAAGCAAGAGGACTGGCAGGTCCCCATCTGGATCATTTGTAGGCAGCACCCCTGGGGGGC	3540
1134	S K Q E D W Q V P I W <u>I I V G S T L G G</u>	1153
3541	CTCCTACTGCTGGCCCTGCTGGTCCTGGCACTGTGGAAGCTCGGCTTCTTTAGAACTGCC	3600
1154	<u>L L L L A L L V</u> L A L W K L G F F R S A	1173
3601	AGGCGCAGGAGGGAGCCTGGTCTGGACCCCAACCCCAAGTGTGGAGTGAGGCTCCAGA	3660
1174	R R R R E P G L D P T P K V L E *	1190
3661	GGAGACTTTGAGTTGATGGGGGCCAGGACACCAGTCCAGGTAGTCTTGAGACCCAGGCCT	3720
3721	GTGGCCCCACCGAGCTGGAGCGGAGAGGAAGCCAGCTGGCTTTGCACTTGACCTCATCTC	3780
3781	CCGAGCAATGGCGCCTGCTCCCTCCAGAATGGAAGTCAAGCTGGTTTAAAGTGGAAGTGC	3840
3841	CCTACTGGGAGACTGGGACACCTTTAACACAGACCCCTAGGGATTTAAAGGGACACCCCT	3900
3901	ACACACACCCAGGCCACGCCAAGGCCTCCCTCAGGCTCTGTGGAGGGCATTTGCTGCCC	3960
3961	CAGCTACTAAGGTGCTAGGAATTCGTAATCATCCCCATCCTCCAGAGAAACCCAGGGAGG	4020
4021	AAGACTGTAAATACGAACCCAATCTGCACACTCCAGGCCTCTAGTTCCAGAAGGATCCAA	4080
4081	GACAAAACAGATCTGAATTCTGCCCTTTTCTCTCACCCTATCCACCCCTCCATTGGCTCC	4140
4141	CAAGTCACACCCACTCCCTTCCCCATAGATAGGCCCTGGGGCTCCCGAAGAATGAACCC	4200
4201	AAGAGCAAGGGCTTGATGGTGACAGCTGCAAGCCAGGGATGAAGAAAGACTCTGAGATGT	4260
4261	GGAGACTGATGGCCAGGCAAGTGGGACCAGGATACTGCACGCTGTCTTGAGATGAGAGGT	4320
4321	AGCCGGGCTCTGCACCCACGTGCATTACATTGACCGCAACTCACACATTCCCCCACCAG	4380

FIG. 19F

4381 CTGCAGCCCCCTTGCTCTCAGCTGCCAACCCCTCCCGGGTCACTTTTGTTCCTCCAGGTACCTC 4440  
4441 ATGGGAAGCATGTGCATGACACAATCCCTGGGGCTGTGCATTCCCACGTCTTCTTGCTGC 4500  
4501 AGCCTGCCCCCTAGACATGGACGCACCGGCTGGCTGCAGCTGGGCAGCAGGGGTAGGGGT 4560  
4561 AGGGAGCCTCCCTCCCTGTATCACCCTCCCTACACACACACACACACACACACACACACAC 4620  
4621 ACACTGCCTCCCATCCTTCCCTCATGCCCGCCAGTGCACAGGGAAGGGCTTGCCAGCGC 4680  
4681 TGTTGAGGGGTCCCTCTGGAATGCACTGAATAAAGCACGTGCAAGGACTCCCGGAGCCT 4740  
4741 GTGCAGCCTTGGTGGCAAATATCTCATCTGCCGGCCCCCAGGACAAGTGGTATGACCAGT 4800  
4801 GATAATGCCCCAAGGACAAGGGGCGTGCCTGGCGCCCAGTGGAGTAATTTATGCCTTAGT 4860  
4861 CTTGTTTTGAGGTAGAAATGCAAGGGGGACACATGAAAGGCATCAGTCCCCCTGTGCATA 4920  
4921 GTACGACCTTTACTGTCGTATTTTTGAAAAATTAAAAATACAGTGTTTAAAAACAAAAAA 4980  
4981 AAAAAAAAAAAAAA 4995



FIG. 20A

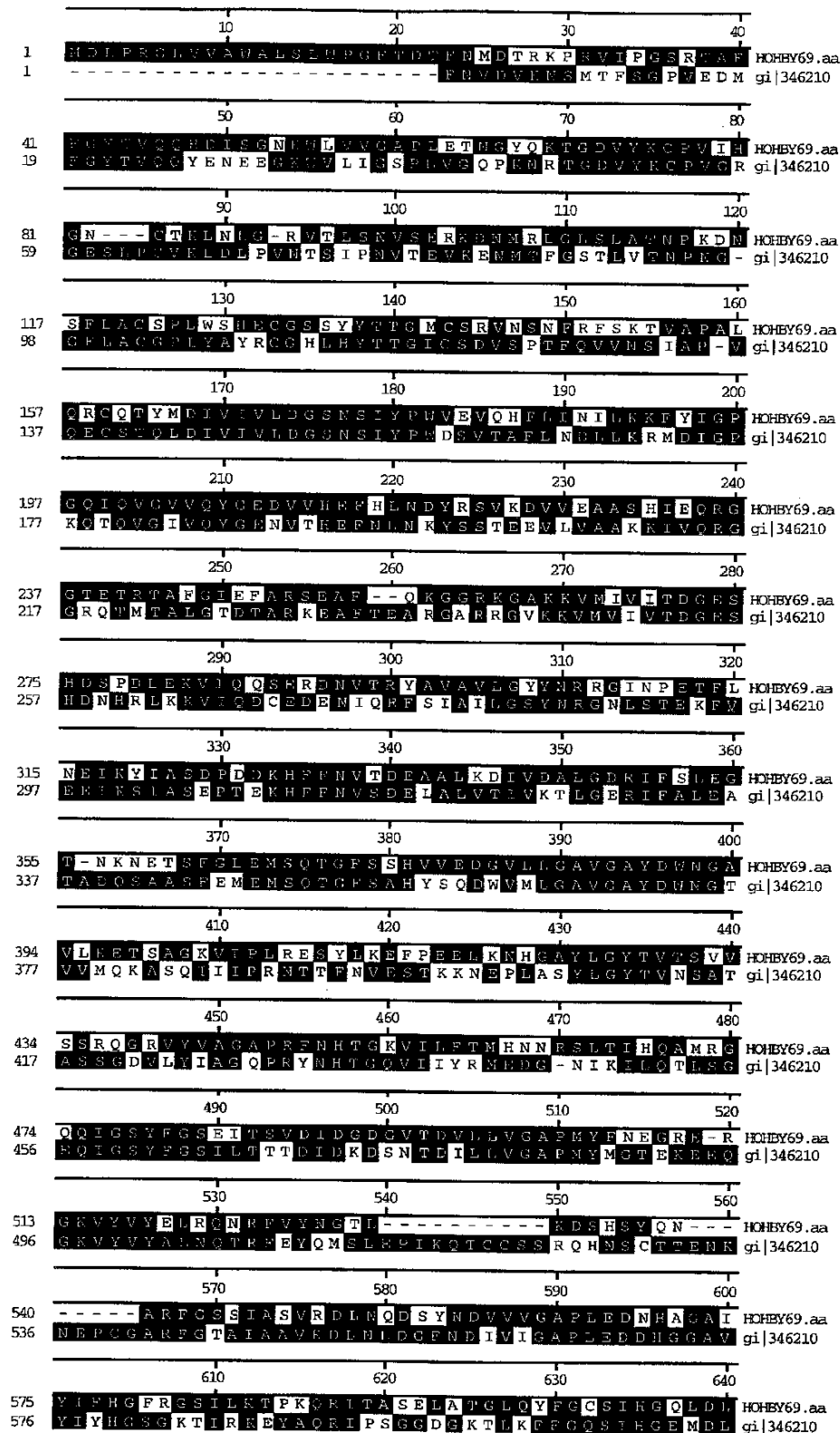
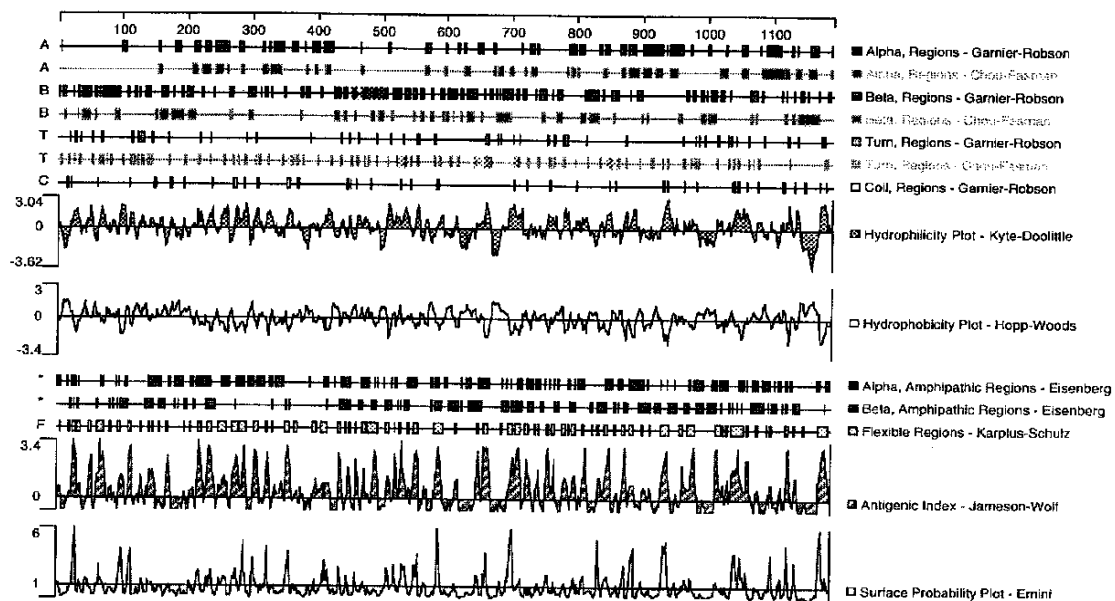


FIG. 20B

615	NEDGSLDPLAVGALGNVILVSEPVVQIINASLHFEPSKIHI	HOHEY69.aa
616	KGGGLTDVTTIGGIGGAAFFERRDVAVV KVTMKEFENKVT	gi 346210
655	FHRDCRRSGRDAITCLAAFLCFTPIFLAPHFOTTTVGIIRVN	HOHEY69.aa
656	QKNNCHMEGRKETWCINATVCTEVKHKSKEDTIYEADLOVR	gi 346210
695	ATMDERRYTFRALHDEGGDRFTNRAVILSSGQELCERINF	HOHEY69.aa
696	VTLDLDRQISRSFFSGTQERKVRNITVRKSE--CTKHSF	gi 346210
735	HVLDLTADYVKPVTFSVEYSLEDPEHGMLEDGWPPTLRLVS	HOHEY69.aa
734	YMLDKHDFQDSVRITLDDNLTDBENGCPVLDLDSLSEVHVEY	gi 346210
775	VPTFWNGCNEDERHCVFDLVLDARSDDLPTAHEVQQRVLRKPA	HOHEY69.aa
774	IPFAKDCGNKEKGISDLSLHVATTE-----	gi 346210
815	DDCSAYTISEDDTTVFIIESTRQRVAVEATLENRGENAYST	HOHEY69.aa
798	-----EKDLLIVRSQNDKFNVSLLTVKNTKDSAYNT	gi 346210
855	VLNISOSANLQFASL--IQKEDSDGSECVNEERRIQKQV	HOHEY69.aa
828	RTLVHYSPNLVFSGTEAICRDSCESN-----HNIT	gi 346210
893	CNVSYPPFRAKAKVAFRLDFEFSSKSIPLHHLIEIELAAGSD	HOHEY69.aa
858	CKVGYPELRRGEMVTFKILRQFNFSYLMFNVTIYLSATSD	gi 346210
933	SNRRDSTKEDNVAFRLRFHLKYEADVLFTRSSSSSHYEVKL	HOHEY69.aa
898	SEEPPEFISDMNVNISIIPVKYEVGLQFYSSAS--EYHISI	gi 346210
973	NS-----ERYDGGPPFSICIFRIQNLGLFPICIMMK	HOHEY69.aa
936	AANETVPEVINSTEDIGNEINIFYLIRKSQSTPMPELRKS	gi 346210
1007	ITIPATRSQNLLELRDFITDEVAANTSCHIWGNS---T	HOHEY69.aa
976	ISFPNMTSNGYPVLYPTGLSSSENANCRPHIEEPFSINS	gi 346210
1043	EYRPTPVEEDLRRAPQINHSNSDVVSNINIRLVPNQETIN	HOHEY69.aa
1016	GKKNPTSTHHLKRGTDLCNTCKFATITCNLTSSDISQVN	gi 346210
1083	FHLGNNHRSSTKALKYKSMKIMVNAALQRQEHSPFIFRE	HOHEY69.aa
1056	VSII--LVKPTFIKSYFSSINLTIRGEERSE--NASLVLES	gi 346210
1123	EDPSRQIVFEISKQE--EWQVPTWIIIVGSTLGGLLLLALLV	HOHEY69.aa
1093	SNQKRELAIQISKGLPSRVPLWVILLSAFAGLLLLMLLI	gi 346210
1162	LALWKLGFPRCAARRRRREPGLDPTPKVLE	HOHEY69.aa
1133	LALWKLGFPRRPKRRK-----MER	gi 346210

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 21



## FIG. 22A

1	GGCACGAGCTGTCATCCGTTTCCATGCCGTGAGGTCCATTTCACAGAACACATCCATGGCT	60
1	<u>M A</u>	2
61	CTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT	120
3	<u>L M L S L V L S L L K L G S G Q W Q V F</u>	22
121	GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGAGGACGCAGCATTCCTCTGTTTCCTG	180
23	G P D K P V Q A L V G E D A A F S C F L	42
181	TCTCCTAAGACCAATGCAGAGGCCATGGAAGTCCGGTTCTTCAGGGGCCAGTTCTCTAGC	240
43	S P K T N A E A M E V R F F R G Q F S S	62
241	GTGGTCCACCTCTACAGGGACGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAA	300
63	V V H L Y R D G K D Q P F M Q M P Q Y Q	82
301	GGCAGGACAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAA	360
83	G R T K L V K D S I A E G R I S L R L E	102
361	AACATTACTGTGTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTAC	420
103	N I T V L D A G L Y G C R I S S Q S Y Y	122
421	CAGAAGGCCATCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCCTCTCATTTCATC	480
123	Q K A I W E L Q V S A L G S V P L I S I	142
481	GCGGGATATGTTGATAGAGACATCCAGCTACTCTGTCACTCCTCGGGCTGGTCCCCCGG	540
143	A G Y V D R D I Q L L C Q S S G W F P R	162
541	CCCACAGCGAAGTGGAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAAC	600
163	P T A K W K G P Q G Q D L S T D S R T N	182
601	AGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGG	660
183	R D M H G L F D V E I S L T V Q E N A G	202
661	AGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAG	720
203	S I S C S M R H A H L S R E V E S R V Q	222
721	ATAGGAGACTGGAGAAGAAAGCACGGACAGGCAGGTAAAAGAAAATATTCCTCTTCACAC	780
223	I G D W R R K H G Q A G K R K Y S S S H	242
781	ATTTATGACTCCTTTCCAAGTCTCTCGTTTATGGATTTTATATCCTGAGGCCCCGTGGGT	840
243	I Y D S F P S L S F M D F Y I L R P V G	262

## FIG. 22B

841 CCCTGCAGAGCCAAGCTTGTGATGGGAACCTCTGAAATTGCAGATTCTGGGGGAGGTGCAT 900  
263 P C R A K L V M G T L K L Q I L G E V H 282

901 TTTGTAGAGAAGCCCCATAGCCTTCTTCAGATCTCTGGAGGGTCCACAACACTCAAAAAG 960  
283 F V E K P H S L L Q I S G G S T T L K K 302

961 GGTCCCAATCCTTGGTCTTTCCCTTCTCCCTGCGCCCTGTTTCCCACGTGAGCACGGAAC 1020  
303 G P N P W S F P S P C A L F P T \* 319

1021 TGCCTGCTCTCTCTGCTTTGCTTTCAGAATTGAGAGACGCCCCGAAACACGCAGGTACCAA 1080

1081 CGCCTGAGAGGGTAACAGTGGGCATGGAGTAGGAAGATGACCAGTGACAGATATGGAGCC 1140

1141 CATCCAGCTTGTAGACAGCAAATCTGTGATGCCCCAATCCACCCCAGGGTGCAGCTGCCT 1200

1201 CTAAATACACTTCTTGGCCCAGGACTTGAGGGGAAAAGCGTAGGGACTGGGTGAGCTAGG 1260

1261 AGGGGTCACAGGCAAGACGCCAGGGAAGTGGGGCATTAGTAGCTGGCTTCTAGGGGTCT 1320

1321 GTGCAAAGGGGAACGAAGTGAAGTTAGCAGGAAGTGGTGGGTGGAAGGAAGCTGAATCCT 1380

1381 GGAGTCACTCAAGGTCTCACAAAGTCAAATAGAGGGCTTACGTGGGAGGGCAGTGGTAGG 1440

1441 GCTGGGTGAACATCTCATGGTTGAGCATCTCCAAGCATCAGTGAGGCACGGGGGCTGCCC 1500

1501 TGGAGAAGGTACATGGCTGGTGGGATAGTGGGACTGGCCGGATCCTACCCGAGCCAGTC 1560

1561 TGCAGTGGGAGGGTCGACCTCTTGCTCCAGCCCAGATTTCTGCTTCAGTAACTCATGCTT 1620

1621 CCTCTCTCCCCACCGCACCCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGA 1680

1681 AGCTCTGCGTTTCTGATCTGAAACTGTAACCCATAGAAAAGCTCCTCAGGAGGTGCCTC 1740

1741 ACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGA 1800

1801 AACATTACTGGGAGGTGGACGTGGGACAAAATGTAGGGTGCTATGTGGGAGTCTGTCTGGG 1860

1861 ATGACGTAGACAGGGGGAAGAACAATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCC 1920

## FIG. 22C

1921 TCAGACTGACAACAGAACATTGTATTTCACATTCAATCCCCATTTTATCAGCCTCCCC 1980  
1981 CCAGCACCCCTCCTACACGAGTAGGGGTCTTCCTGGACTATGAGGGTGGGACCATCTCCT 2040  
2041 TCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGCTGACATGTCAGTTGAAGGCT 2100  
2101 TGTGAGACCCCTATATCCAGCATGCGATGTATGACGAGGAAAAGGGGACTCCCATATTCA 2160  
2161 TATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGCCCCACACCACA 2220  
2221 GACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGCCCCAGCTTCTCTCCGGAG 2280  
2281 CCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCCT 2340  
2341 GAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTG 2400  
2401 GGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGT 2460  
2461 TTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCA 2520  
2521 TTTGCTAGTCACGGACAGTGATTCCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATG 2580  
2581 TGAATCATGCTTGCAGGTTTGAGGGCCACAGTGTTTGCTAATGGATGTGTTTTATGATT 2640  
2641 ATACATTTTCCCCACCATAAAACTCTGTTTGCCTTAATTCCCACATTAATTTAACTTTTC 2700  
2701 CTCCTATACCCAAATCCACCCATGGAATAGTTAATTGGAACACCTGCCTTTGTGAGGCTC 2760  
2761 CAAAGAATAAAGAGGAGGTAGGATTTTTCACTGATTCTATAAGCCCAGCATTACCTGATA 2820  
2821 CCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCA 2880  
2881 TTAACACAGACACAAAAATTCTAAATAAAATTTTAACAAATTAACTAAACAATATATT 2940  
2941 AAAGATGATATATAACTACTCAGTGTGGTTTGTCCCACAAATGCAGAGTTGGTTTAATAT 3000  
3001 TTAAATATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAAAAAAAAAAAAAAAA 3059

FIG. 23

1	MA	10	20	30	40	
1	MAVF	PNSCLAGCLLI	IFIL	QLPK	LDSAP	FDVIGUQEPTLA
						HTTDB46.aa gi 162773
31	LV	50	60	70	80	
41	VV	GEDA	ELPC	RLSP	NVSA	KGMELRWFR
						HTTDB46.aa gi 162773
71	KD	90	100	110	120	
81	QD	QEGF	EMAEY	RGRV	SLVED	HIAEGSVAVRIQEVKASDDG
						HTTDB46.aa gi 162773
111	LY	130	140	150	160	
121	EY	RCFF	RQDEN	YREA	IVHL	KVAALGSDPHISM
						HTTDB46.aa gi 162773
151	QL	170	180	190	200	
161	GL	ECTS	VGWY	PEPQ	VQWR	THRGE
						HTTDB46.aa gi 162773
190	DV	210	220	230	240	
201	TV	RASV	IRDS	SMKN	VSCC	IRNLLL
						HTTDB46.aa gi 162773
226	---	250	260	270	280	
241	PR	LTPW	MVAV	AVLL	VVLGL	LTIGSIFFTWRL
						HTTDB46.aa gi 162773
236	RK	290	300	310	320	
281	NE	FSSK	EKLL	EELK	WKRA	TLHAVDVTLD
						HTTDB46.aa gi 162773
241	---	330	340	350	360	
321	DS	KSVR	LED	SRQK	LPEK	PEREDSWPCV
						HTTDB46.aa gi 162773
257	IL	370	380	390	400	
361	EV	EVGD	RTDW	ATGV	CR	ENVMKK
						HTTDB46.aa gi 162773
280	E	410	420	430	440	
401	NG	YWA	LTP	LRTE	LP	LAGP
						HTTDB46.aa gi 162773
303	GP	450	460	470	480	
441	GS	HTYT	FES	KASF	SGEL	RPF
						HTTDB46.aa gi 162773
315	---	490	500	510	520	
481	GVM	VVAD	AKDT	SKEI	PLSP	MGED
						HTTDB46.aa gi 162773
318	---					
521	PS	QGV				
						HTTDB46.aa gi 162773

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 24

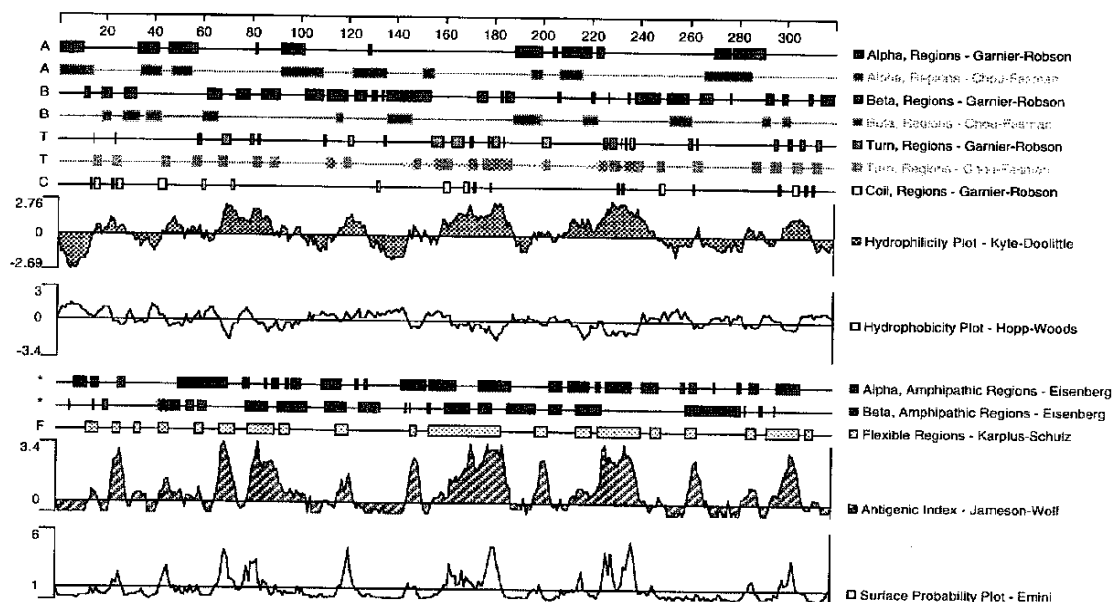






FIG. 25B

841 ATGGATTATGATTATGCCCTCCTGGAAC TCAAAAAGCCCCACAAGAGAAAATTTATGAAG 900  
243 M D Y D Y A L L E L K K P H K R K F M K 262

901 ATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACCTTCTCTGCTTAT 960  
263 I G V S P P A K Q L P G G R I H F S G Y 282

961 GACAATGACCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGACCTAT 1020  
283 D N D R P G N L V Y R F C D V K D E T Y 302

1021 GACTTGCTCTACCAACAATGCGATTCCCAGCCAGGGGCCAGCGGTCTGGGGTCTATGTG 1080  
303 D L L Y Q Q C D S Q P G A S G S G V Y V 322

1081 AGGATGTGGAAGAGACAACACCAGAAGTGGGAGCGGAAAATTATTGGCATGATTCAGGG 1140  
323 R M W K R Q H Q K W E R K I I G M I S G 342

1141 CACCACTGGGTGGACATGGATGGTTCCCCACAGGAATTCACACGTGGCTGTTTCAGAGATC 1200  
343 H Q W V D M D G S P Q E F T R G C S E I 362

1201 ACTCCTCTCCAATATATCCCAGATATATCTATTGGAGTATAAGGAAACTACCTGGATTGT 1260  
363 T P L Q Y I P D I S I G V \* 376

1261 AGGGAGGGGTGACACAGTGTCCCTCCTGCAGCAACTAAGGTCGTTCATGTTCTTATTTTAG 1320

1321 GAGAGGCCAAATTGTTTTTGTTCATTGCCGTGCACACGTGTGTGTGTGTGTGTGTGTGTG 1380

1381 TGTAAGGTGTCCTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACT 1440

1441 ATTTGAAAAC TGGTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATACTT 1500

1501 TTGCATAGAAAATAAAAAAAATACTGATTGTTGGGGCAATGAGGAATATTTGACAATTAAGTT 1560

1561 AATCTTCACGTTTTTGCAAAC TTTGATTTTTATTTTCATCTGAACTTGTTCAAAGATTTA 1620

1621 TATTAAATATTTGGCATACAAAAAAAAAAAAAAAAAACGGGGGGGCCCCGTACCCAATTGC 1680

1681 CCCTATAGTGAGGCGATAC 1699

FIG. 26

		10	20	30	40	
1	MAGIPGLIF	LLFFLLCAVGVSPYSAPWKPTWPA	YRLPVV	HUSAQ05.aa		
1	M--IRTL	LL-----	ST	gi 219620		
		50	60	70	80	
41	LPOST	LNLAKPDFGAEAKLEVSS	SCGP	QCHKGTPLPTYEE	HUSAQ05.aa	
10	LVAGAL	-----	SCGD	-----	PTYPP	gi 219620
		90	100	110	120	
81	AKQYLSYETLYANGSR	TETQVGIV	ILSSSGD	GAGHRD	SGS	HUSAQ05.aa
25	-----	-----	YVTRVVGGEE	ARPNS	---	gi 219620
		130	140	150	160	
121	SGKSRRKRQ	IYGYDSRFSIFGKDFLL	NYPFSTSV	KLSTGC	HUSAQ05.aa	
40	-----	WFWQV-----	SLQYSSNGK	WYHTC	gi 219620	
		170	180	190	200	
161	TGTLVAEK	HVLTAAHCH	HDGKTYVKG	TQKL	RVGFLKPKFK	HUSAQ05.aa
59	GGSLIAN	SWVLTAAHCH	ISSSRTY	-----	RVGLGRHNL	Y gi 219620
		210	220	230	240	
201	DGGRGAND	STSAMPEOMKFQW	IRVKRTHV	PKGWIKGNAND	HUSAQ05.aa	
92	VAESGSLA	-----	VSVSKI	VVHKDW---	NSNQ	gi 219620
		250	260	270	280	
241	IGMDYDY	ALLELKK	PHK--RK	FMKIGVSP	PAKQLPG---	HUSAQ05.aa
116	ISKGN	DIALLLKLANPV	SLTDKIQ	LACLP	PAGTILPN	NYPC gi 219620
		290	300	310	320	
275	-----	GRIHFSGYDND	--RPGNLV	---YREFCD	-----	HUSAQ05.aa
156	YVTGWGR	LQTN	GAVPDV	LQQGRLL	VVDYATC	SSSAWWGSS gi 219620
		330	340	350	360	
297	VKDETY	---DLLYQQ	CD	SOPGASG	SGVYVRMW	KRQHOKW HUSAQ05.aa
196	VKTS	MI	VAGGDGV	ISSCNG	DSGGPLNC	---QASDGRW gi 219620
		370	380	390	400	
333	ERK	IGMISGHQ	WVDM	DGSPQ	EFTRG	CSEITPLQYIPDIS HUSAQ05.aa
230	QVHG	IVSFGSR	LGCN	YYHKPS	VFTRV	SNYI---DWINSV- gi 219620
		370	380	390	400	
373	IGV					HUSAQ05.aa
266	IANN					gi 219620

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 27

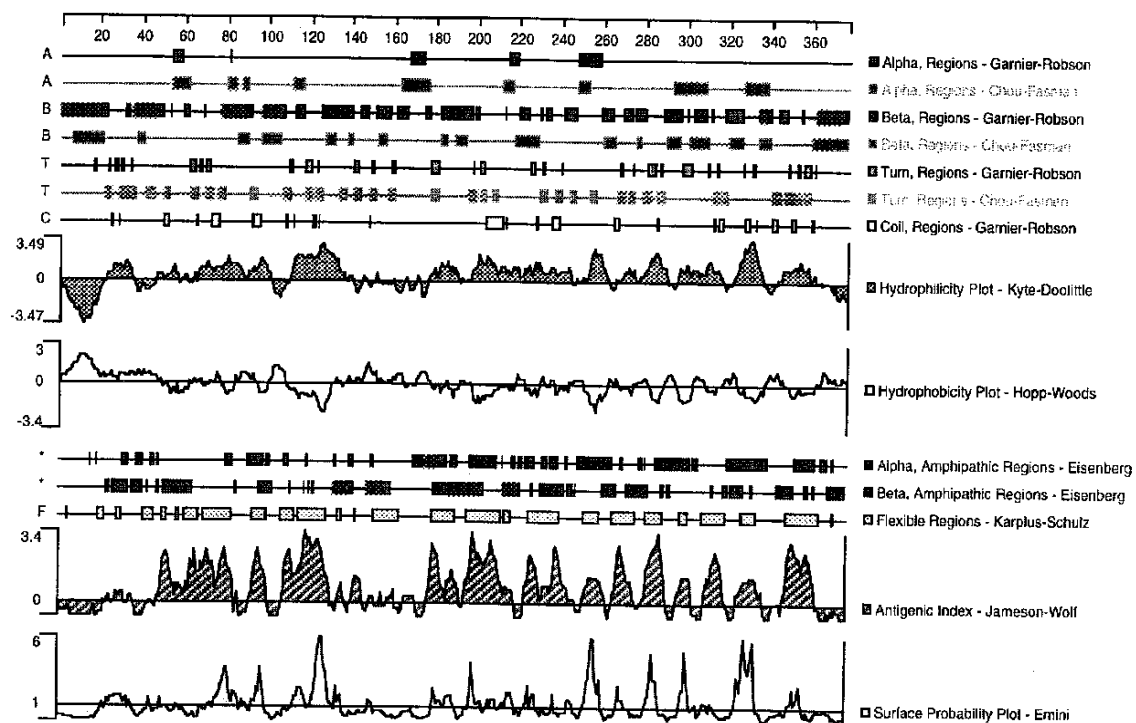




FIG. 28B

841 GCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATGATGAAATGCCTCAACACGCCCGT 900  
273 P Q P V M V T W V R V D D E M P Q H A V 292

901 ACTGTCTGGGCCCAACCTGTTTCATCAATAACCTAAACAAAACAGATAATGGTACATACCG 960  
293 L S G P N L F I N N L N K T D N G T Y R 312

961 CTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTATATGCTGTATGTATACGA 1020  
313 C E A S N I V G K A H S D Y M L Y V Y D 332

1021 TCCCCCACAACCTATCCCTCCTCCCAACAACCAACCACCACCACCACCACCACCACCACCAC 1080  
333 P P T T I P P P T T T T T T T T T T T T 352

1081 CACCATCCTTACCATCATCACAGATTCGCGAGCCAGGTGAAGAAGGCTCGATCAGGGCAG 1140  
353 T I L T I I T D S R A R \* 365

1141 TGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCATGCTGTGCTTGC 1200

1201 TCATCATTTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTCATGAAGCCA 1260

1261 AAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGAGGACAGA 1320

1321 ACAACTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTGTGTTCAATGAGGT 1380

1381 GTCCAACTGGCCCTATTTAGATGATAAAGAGACAGTGATATGGAACTTGCGAGAAATTC 1440

1441 GTGTGT'TTTTTATGAATGGGTGGAAGGTGTGAGACTGGGAAGGCTTGGGATTGCTGT 1500

1501 GTAAAAAAAAAAAAAAAAAAAA 1520

1	MA	10	20	30	40	
1	MA	AAAL	LDPS	RS	---	HOUDJ81.aa
1	M	WWR	VL	---	---	gi 1524088
1	M	TFTT	VL	---	---	WO9634102
				---	---	gb AAB88491.1
				---	---	
39	T	PTSG	GGH	ETTD	VTV	HOUDJ81.aa
32	---	Q	IVRV	QVLP	EV	gi 1524088
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21	G	AG	SET	---	---	gb AAB88491.1
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				---	---	
78	N	PNK	LT	---	---	HOUDJ81.aa
69	T	WQ	LP	DA	PAN	gi 1524088
47	S	LOW	LP	PS	GFT	WO9634102
48	T	KQ	WLN	PR	GFT	gb AAB88491.1
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				---	---	
106	---	---	---	---	---	HOUDJ81.aa
109	K	OST	GQD	TEA	EL	gi 1524088
80	---	---	---	---	---	WO9634102
81	---	---	---	---	---	gb AAB88491.1
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				---	---	
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149	S	VR	GM	W	LR	gi 1524088
105	V	ST	KE	V	KVI	WO9634102
106	F	RS	KM	TT	VE	gb AAB88491.1
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170	A	SK	PAT	T	I	HOUDJ81.aa
187	E	GR	B	P	ART	gi 1524088
145	R	SK	P	P	Q	WO9634102
142	G	C	EP	Q	P	gb AAB88491.1
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				---	---	
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227	P	S	G	R	A	gi 1524088
185	I	L	S	Y	G	WO9634102
182	V	L	A	Y	G	gb AAB88491.1
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249	N	T	Y	F	L	HOUDJ81.aa
267	G	Y	D	D	N	gi 1524088
218	---	---	---	---	---	WO9634102
216	R	T	V	A	N	gb AAB88491.1
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				---	---	
288	P	O	H	A	V	HOUDJ81.aa
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233	---	---	---	---	---	WO9634102
245	A	E	S	D	L	gb AAB88491.1
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				---	---	
328	I	V	Y	T	E	HOUDJ81.aa
344	I	F	M	R	E	gi 1524088
241	---	---	---	---	---	WO9634102
283	---	---	---	---	---	gb AAB88491.1
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				---	---	
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384	Q	O	R	K	E	gi 1524088
274	A	N	P	O	Y	WO9634102
321	Q	D	V	K	S	gb AAB88491.1
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				---	---	
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424	L	F	I	I	V	gi 1524088
348	L	L	I	I	V	WO9634102
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462	E	T	S	S	E	gi 1524088
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365	E	E	E	Y	L	HOUDJ81.aa
502	K	E	---	---	---	gi 1524088
373	K	E	---	---	---	WO9634102
418	N	P	---	---	---	gb AAB88491.1

Decoration 'Decoration #1': Shade (with solid black) residues that match HOUDJ81.aa exactly.

FIG. 30

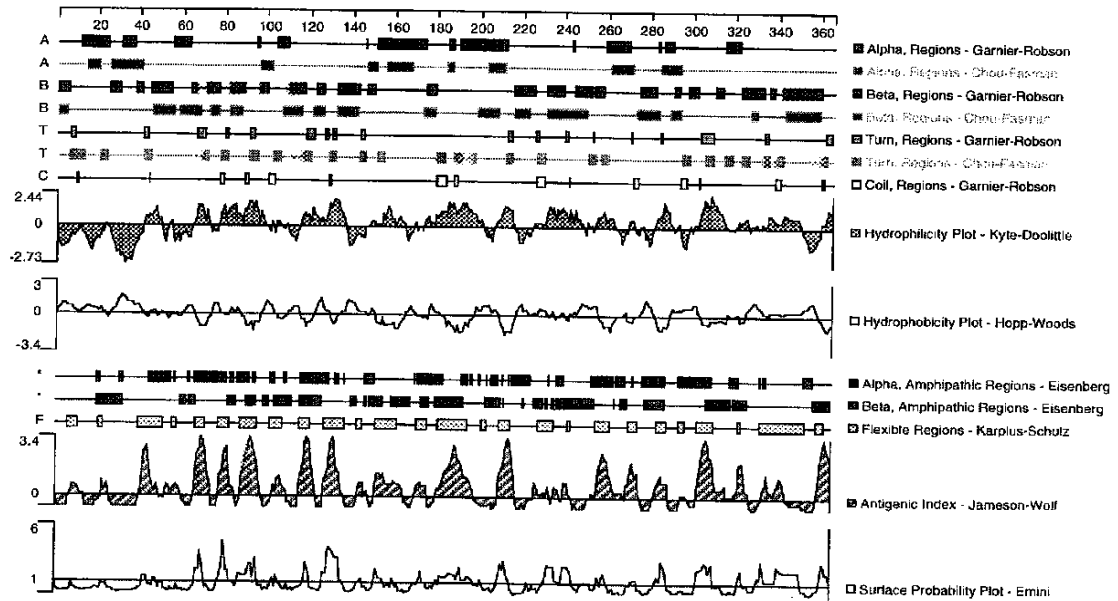
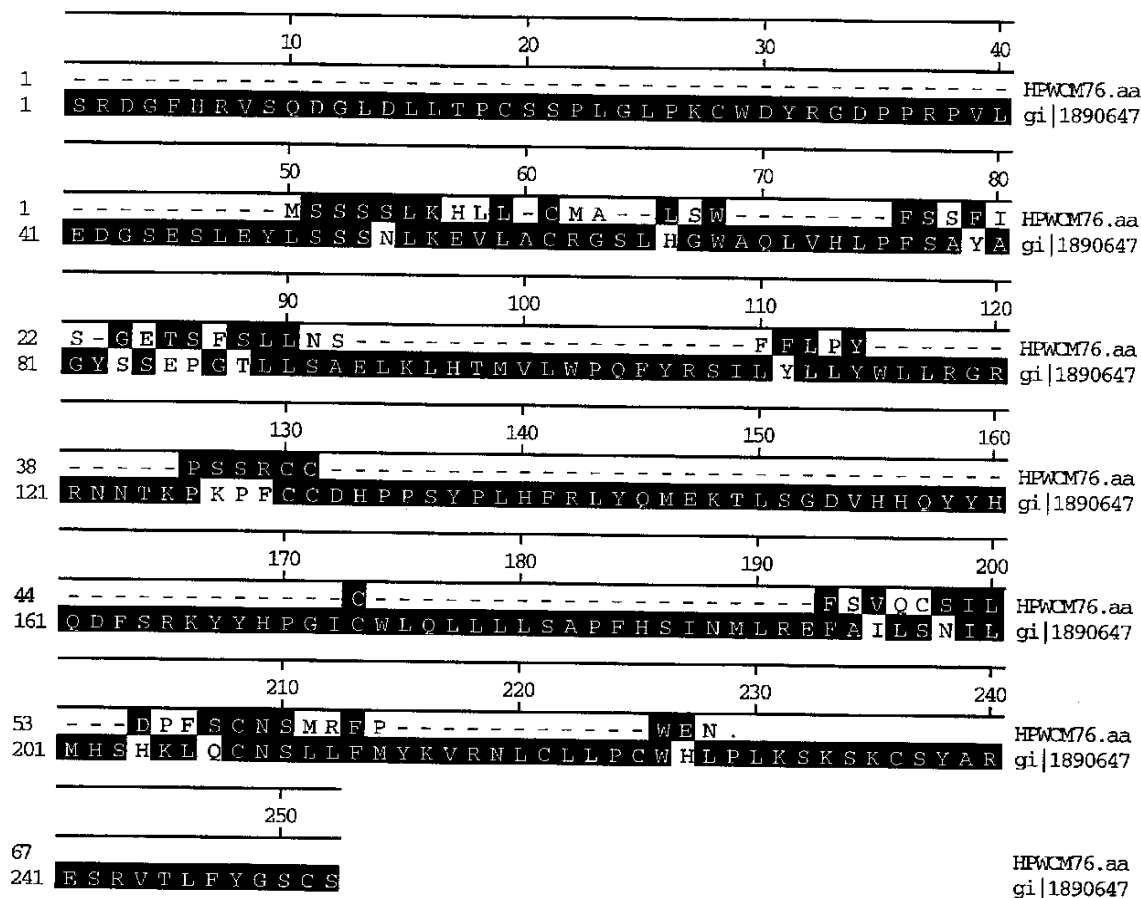




FIG. 31

1 TTTT TTTT TTTT GAGACGGAGTCTCGCTCTTTCACCCAGGCCAGACTGAAGTGGCGCAGTC 60  
61 TCGGATCACTGAAAAGCTCAGCCTCACGGGATCAGGACCATTCCTCTGCCCTCAGCCTCCC 120  
121 GAGTGGCTGGGACTAAAGGCGCCCGCCACCGACGCCCGGACTAATTTTGTATTATATAG 180  
181 TAGAGACGGGGTTTACCCGTGTTAGCCAAGATGGTCTCGATCTCTTGAACTCGTGATCCG 240  
241 CCCGCGTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACAGCGCCCGGCCTGTA 300  
301 AAGATTTCTTGAGCAAATGAATGAGTAAATGAAAGGAGTGCTCAAATTTCTTTTATTCTA 360  
361 AAAAATGTTCCCTTTTGTAGAAAATGCTCTGTAGCTTTTGTAGGTCTTCTCCTGCACTCA 420  
421 AACATCCACTCCTTACCCTTTCCAATCTCCCTTTTCTTCTCAACCCATAGAATGTACTTC 480  
481 CATGTCTACCATTCACCAGAACTACTCTAACCAAGGCTACCCAGGATATCCTTATTTCT 540  
541 TTCAACTTCTTTGACATGCTCAGTCGCATTGGGCACTGTTAATGTCTTCTCCTCCTTTGA 600  
1 M S S S S L K 7  
601 AACACCTCCTTTGCAATGGCACTATCCTGGTTTTCTTCCTTCATTTTCAGGAGAACTTCAT 660  
8 H L L C M A L S W F S S F I S G E T S F 27  
661 TCTCCTTACTGAATTCTTTCTCCTCCCTATCCATCATCTAGATGTTGTTGTTTCTCAG 720  
28 S L L N S F F L P Y P S S R C C C F S V 47  
721 TGCAGTGTTC AATCCTAGACCCCTTTTCATGTAAC TCAATGCGTTTTCCTTGGGAGAATT 780  
48 Q C S I L D P F S C N S M R F P W E N \* 67  
781 AATCCCTTCCCTGGTGTCACTNTGCC 807

FIG. 32



Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 33

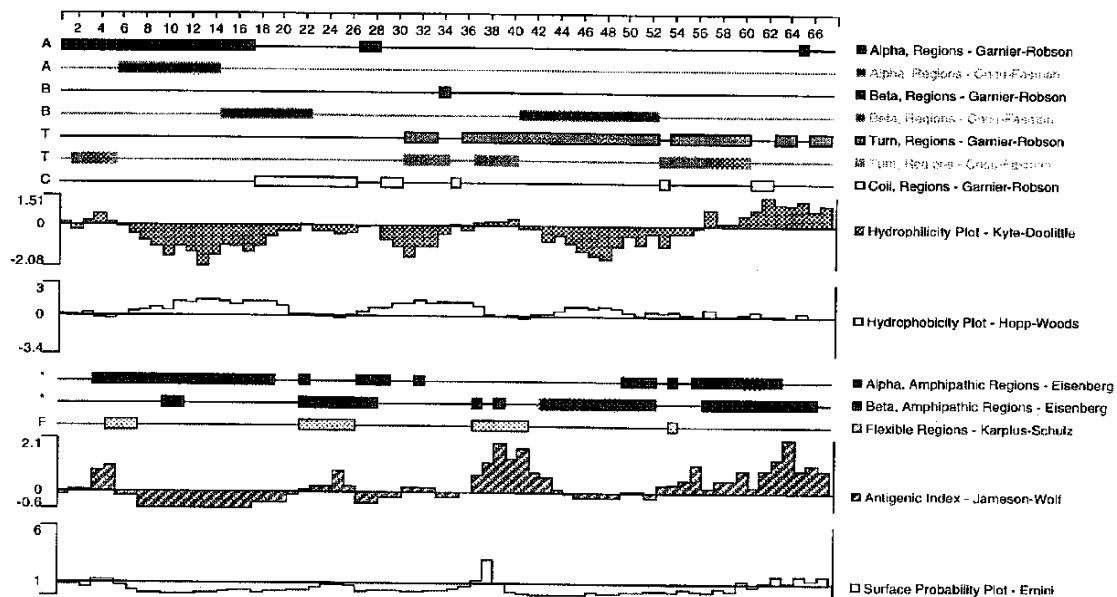
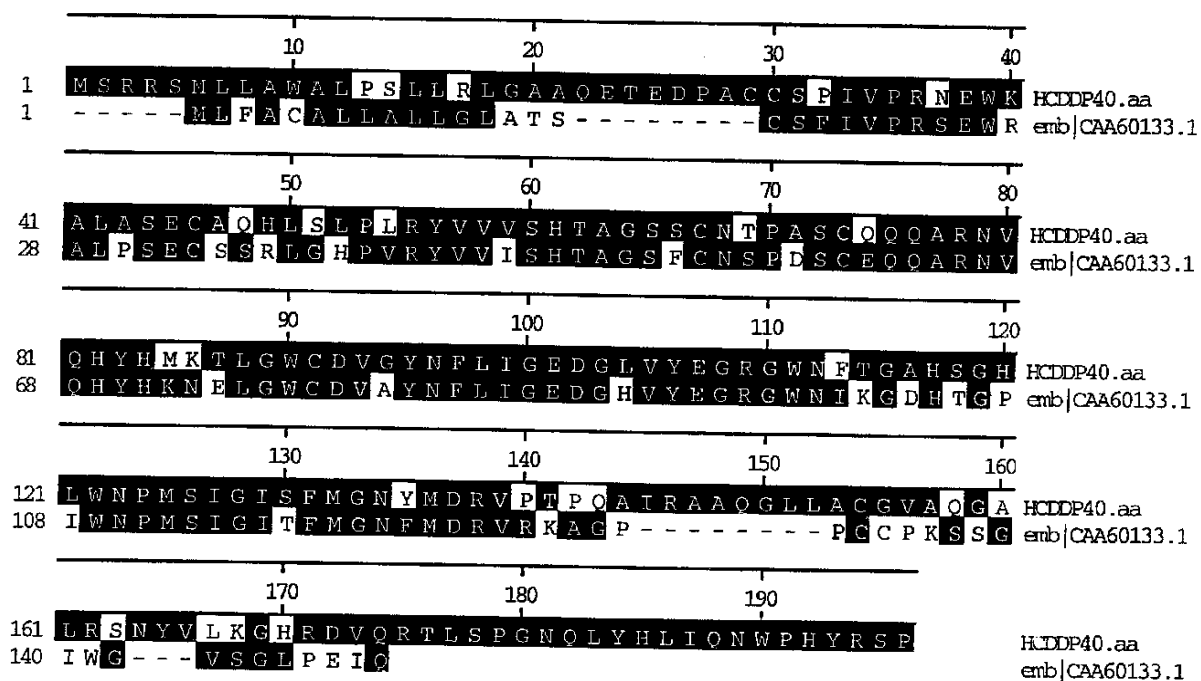


FIG. 34

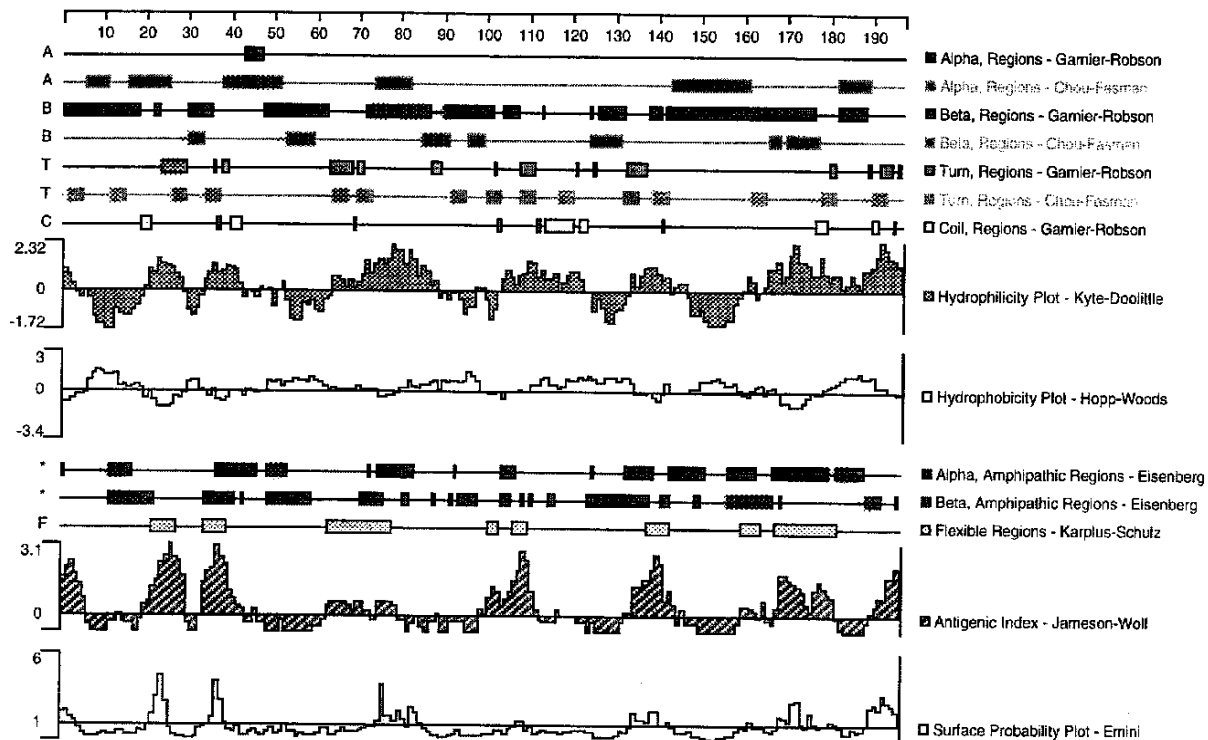
1	GGCACGAGCCGGACCCCTGCCGCCCTGCCACTATGTCCCGCCGCTCTATGCTGCTTGCCTG	60
1	<u>M S R R S M L L A W</u>	10
61	GGCTCTCCCCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTG	120
11	<u>A L P S L L R L G A A Q E T E D P A C C</u>	30
121	CAGCCCCATAGTCCCCCGGAACGAGTGGAGGCCCTGGCATCAGAGTGCGCCCCAGCACCT	180
31	<u>S P I V P R N E W K A L A S E C A O H L</u>	50
181	GAGCCTGCCCTTACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCC	240
51	<u>S L P L R Y V V V S H T A G S S C N T P</u>	70
241	CGCCTCGTGCCAGCAGCAGGCCCCGAATGTGCAGCACTACCACATGAAGACACTGGGCTG	300
71	<u>A S C O O O A R N V O H Y H M K T L G W</u>	90
301	GTGCGACGTGGGCTACAACCTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGG	360
91	<u>C D V G Y N F L I G E D G L V Y E G R G</u>	110
361	CTGGAACCTTCACGGGTGCCCACTCAGGTCACTTATGGAACCCCATGTCCATTGGCATCAG	420
111	<u>W N F T G A H S G H L W N P M S I G I S</u>	130
421	CTTCATGGGCAACTACATGGATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCCAGGG	480
131	<u>F M G N Y M D R V P T P Q A I R A A Q G</u>	150
481	TCTACTGGCCTGCGGTGTGGCTCAGGGAGCCCTGAGGTCCAACCTATGTGCTCAAAGGACA	540
151	<u>L L A C G V A Q G A L R S N Y V L K G H</u>	170
541	CCGGGATGTGCAGCGTACACTCTCTCCAGGCAACCAGCTCTACCACCTCATCCAGAATTG	600
171	<u>R D V Q R T L S P G N Q L Y H L I Q N W</u>	190
601	GCCACACTACCGCTCCCCCTGAGGCCCTGCTGATCCGCACCCCATTCCTCCCCTCCCATG	660
191	<u>P H Y R S P *</u>	197
661	GCCAAAAACCCCACTGTCTCCTTCTCCAATAAAGATGTAGCTCAAAAAAAAAAAAAAAAAA	720
721	AAAAAA 726	

FIG. 35



Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 36



<110> Human Genome Sciences, Inc.

<120> 12 Human Secreted Proteins

<130> PF489

<140> Unassigned

<141> 1999-10-26

<150> 60/105,971

<151> 1998-10-28

<160> 147

<170> PatentIn Ver. 2.0

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&lt;211&gt; 27

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&lt;213&gt; Homo sapiens

&lt;400&gt; 4

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&lt;210&gt; 5

&lt;211&gt; 271

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

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&lt;211&gt; 31

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&lt;400&gt; 7

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&lt;210&gt; 8

&lt;211&gt; 12

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;210&gt; 9

&lt;211&gt; 73

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



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 ccattctcaat tag 73

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&lt;210&gt; 12

&lt;211&gt; 2499

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

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&lt;210&gt; 13

&lt;211&gt; 1339

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 13

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&lt;211&gt; 1389

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

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&lt;210&gt; 15

&lt;211&gt; 2295

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

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&lt;211&gt; 1748

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

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&lt;210&gt; 17

&lt;211&gt; 4995

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

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&lt;210&gt; 18

&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

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&lt;210&gt; 19

&lt;211&gt; 3059

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

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10

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&lt;210&gt; 20

&lt;211&gt; 1699

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

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&lt;210&gt; 21

&lt;211&gt; 1520

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

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&lt;210&gt; 22

&lt;211&gt; 807

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (803)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 22

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&lt;210&gt; 23

&lt;211&gt; 2522

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 23

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&lt;210&gt; 24

&lt;211&gt; 1344

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 24

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&lt;210&gt; 25

&lt;211&gt; 4631

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

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&lt;210&gt; 26

&lt;211&gt; 2008

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 26

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&lt;210&gt; 27

&lt;211&gt; 1654

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 27

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&lt;210&gt; 28

&lt;211&gt; 1508

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

ggcagcagga	catggcgtag	tgtagtgctg	ccgagcggat	cccagtgtgc	ggcggcagcg	60
gcggcgcgcg	cgcctcccgg	gctccggctc	cggcttctgc	tggtgtctct	ctccgcgcgc	120
gcactgatcc	ccacaggtga	tgggcagaat	ctgtttacga	aagacgtgac	agtgatcgag	180
ggagaggttg	cgaccatcag	ttgccaaagt	aataagagtg	acgactctgt	gattcagcta	240
ctgaatccca	acaggcagac	cattttatttc	agggacttca	ggcctttgaa	ggacagcagg	300
tttcagttgc	tgaatttttc	tagcagtga	ctcaaagtat	cattgacaaa	cgtctcaatt	360
tctgatgaag	gaagatactt	ttgccagctc	tataccgatc	ccccacagga	aagttacacc	420
accatcacag	tccctggctcc	accacgtaat	ctgatgatcg	atatccagaa	agacactgcg	480
gtggaagggtg	aggagattga	agtcaactgc	actgctatgg	ccagcaagcc	agccacgact	540
atcaggtggt	tcaaaggga	cacagagcta	aaaggcaaat	cggaggtgga	agagtgggtc	600
gacatgtaca	ctgtgaccag	tcagctgatg	ctgaagggtc	acaaggagga	cgatgggggtc	660
ccagtgatct	gccaggtgga	gcaccctgcg	gtcactggaa	acctgcagac	ccagcggtat	720
ctagaagtac	agtataagcc	tcaagtgcac	attcagatga	cttatcctct	acaaggctta	780
acccggaag	gggacgcgct	tgagtttaaca	tgtgaagcca	tcgggaagcc	ccagcctgtg	840
atggtaactt	gggtgagagt	cgatgatgaa	atgcctcaac	acgcctgact	gtctgggccc	900
aacctgttca	tcaataacct	aaacaaaaca	gataatggta	cataccgctg	tgaagcttca	960
aacatagttg	ggaaagctca	ctcggattat	atgctgtatg	tatacgatcc	ccccacaact	1020
atccctcctc	ccacaacaac	caccaccacc	accaccacca	ccaccaccac	catccttacc	1080
atcatcacag	attccccgag	ccaggtgaag	aaggctcgat	cagggcagtg	gatcatgccg	1140
tgatcggtgg	cgtcgtggcg	gtgggtggtg	tcgccatgct	gtgcttgctc	atcattcttg	1200
ggcgctattt	tgccagacat	aaaggtacat	acttcaactca	tgaagccaaa	ggagccgatg	1260

17

acgcagcaga	cgcagacaca	gctataatca	atgcagaagg	aggacagaac	aactccgaag	1320
aaaagaaaga	gtacttcate	tagatcagcc	tttttgtttc	aatgaggtgt	ccaactggcc	1380
ctattttagat	gataaagaga	cagtgatatt	ggaacttgcg	agaaattcgt	gtgttttttt	1440
atgaatgggt	ggaaaggtgt	gagactggga	aggcttggga	tttgctgtgt	aaaaaaaaaa	1500
aaaaaaaaa						1508

&lt;210&gt; 29

&lt;211&gt; 529

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 29

Met	Val	Ala	Gln	Asp	Pro	Gln	Gly	Cys	Leu	Gln	Leu	Cys	Leu	Ser	Glu
1				5					10					15	
Val	Ala	Asn	Gly	Leu	Arg	Asn	Pro	Val	Ser	Met	Val	His	Ala	Gly	Asp
			20					25					30		
Gly	Thr	His	Arg	Phe	Phe	Val	Ala	Glu	Gln	Val	Gly	Val	Val	Trp	Val
		35					40					45			
Tyr	Leu	Pro	Asp	Gly	Ser	Arg	Leu	Glu	Gln	Pro	Phe	Leu	Asp	Leu	Lys
	50					55					60				
Asn	Ile	Val	Leu	Thr	Thr	Pro	Trp	Ile	Gly	Asp	Glu	Arg	Gly	Phe	Leu
65					70					75					80
Gly	Leu	Ala	Phe	His	Pro	Lys	Phe	Arg	His	Asn	Arg	Lys	Phe	Tyr	Ile
				85					90					95	
Tyr	Tyr	Ser	Cys	Leu	Asp	Lys	Lys	Lys	Val	Glu	Lys	Ile	Arg	Ile	Ser
		100					105						110		
Glu	Met	Lys	Val	Ser	Arg	Ala	Asp	Pro	Asn	Lys	Ala	Asp	Leu	Lys	Ser
		115					120					125			
Glu	Arg	Val	Ile	Leu	Glu	Ile	Glu	Glu	Pro	Ala	Ser	Asn	His	Asn	Gly
	130					135					140				
Gly	Gln	Leu	Leu	Phe	Gly	Leu	Asp	Gly	Tyr	Met	Tyr	Ile	Phe	Thr	Gly
145					150				155						160
Asp	Gly	Gly	Gln	Ala	Gly	Asp	Pro	Phe	Gly	Leu	Phe	Gly	Asn	Ala	Gln
			165						170					175	
Asn	Lys	Ser	Ser	Leu	Leu	Gly	Lys	Val	Leu	Arg	Ile	Asp	Val	Asn	Arg
		180					185						190		
Ala	Gly	Ser	His	Gly	Lys	Arg	Tyr	Arg	Val	Pro	Ser	Asp	Asn	Pro	Phe
		195					200					205			
Val	Ser	Glu	Pro	Gly	Ala	His	Pro	Ala	Ile	Tyr	Ala	Tyr	Gly	Ile	Arg
	210					215					220				
Asn	Met	Trp	Arg	Cys	Ala	Val	Asp	Arg	Gly	Asp	Pro	Ile	Thr	Arg	Gln
225					230					235					240

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Pro



&lt;210&gt; 30

&lt;211&gt; 494

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

Met Arg Pro Pro Gly Phe Arg Asn Phe Leu Leu Leu Ala Ser Ser Leu  
 1 5 10 15

Leu Phe Ala Gly Leu Ser Ala Val Pro Gln Ser Phe Ser Pro Ser Leu  
 20 25 30

Arg Ser Trp Pro Gly Ala Ala Cys Arg Leu Ser Arg Ala Glu Ser Glu  
 35 40 45

Arg Arg Cys Arg Ala Pro Gly Gln Pro Pro Gly Ala Ala Leu Cys His  
 50 55 60

Gly Arg Gly Arg Cys Asp Cys Gly Val Cys Ile Cys His Val Thr Glu  
 65 70 75 80

Pro Gly Met Phe Phe Gly Pro Leu Cys Glu Cys His Glu Trp Val Cys  
 85 90 95

Glu Thr Tyr Asp Gly Ser Thr Cys Ala Gly His Gly Lys Cys Asp Cys  
 100 105 110

Gly Lys Cys Lys Cys Asp Gln Gly Trp Tyr Gly Asp Ala Cys Gln Tyr  
 115 120 125

Pro Thr Asn Cys Asp Leu Thr Lys Lys Lys Ser Asn Gln Met Cys Lys  
 130 135 140

Asn Ser Gln Asp Ile Ile Cys Ser Asn Ala Gly Thr Cys His Cys Gly  
 145 150 155 160

Arg Cys Lys Cys Asp Asn Ser Asp Gly Ser Gly Leu Val Tyr Gly Lys  
 165 170 175

Phe Cys Glu Cys Asp Asp Arg Glu Cys Ile Asp Asp Glu Thr Glu Glu  
 180 185 190

Ile Cys Gly Gly His Gly Lys Cys Tyr Cys Gly Asn Cys Tyr Cys Lys  
 195 200 205

Ala Gly Trp His Gly Asp Lys Cys Glu Phe Gln Cys Asp Ile Thr Pro  
 210 215 220

Trp Glu Ser Lys Arg Arg Cys Thr Ser Pro Asp Gly Lys Ile Cys Ser  
 225 230 235 240

Asn Arg Gly Thr Cys Val Cys Gly Glu Cys Thr Cys His Asp Val Asp  
 245 250 255

Pro Thr Gly Asp Trp Gly Asp Ile His Gly Asp Thr Cys Glu Cys Asp  
 260 265 270

Glu Arg Asp Cys Arg Ala Val Tyr Asp Arg Tyr Ser Asp Asp Phe Cys

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<400> 31
Met Glu Thr Gly Ala Leu Arg Arg Pro Gln Leu Leu Pro Leu Leu Leu
  1             5             10             15
Leu Leu Cys Gly Gly Cys Pro Arg Ala Gly Gly Cys Asn Glu Thr Gly
      20             25             30
Met Leu Glu Arg Leu Pro Leu Cys Gly Lys Ala Phe Ala Asp Met Met
    35             40             45
Gly Lys Val Asp Val Trp Lys Trp Cys Asn Leu Ser Glu Phe Ile Val

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50 21 60  
 Tyr Tyr Glu Ser Phe Thr Asn Cys Thr Glu Met Glu Ala Asn Val Val  
 65 70 75 80  
 Gly Cys Tyr Trp Pro Asn Pro Leu Ala Gln Gly Phe Ile Thr Gly Ile  
 85 90 95  
 His Arg Gln Phe Phe Ser Asn Cys Thr Val Asp Arg Val His Leu Glu  
 100 105 110  
 Asp Pro Pro Asp Glu Val Leu Ile Pro Leu Ile Val Ile Pro Val Val  
 115 120 125  
 Leu Thr Val Ala Met Ala Gly Leu Val Val Trp Arg Ser Lys Arg Thr  
 130 135 140  
 Asp Thr Leu Leu  
 145

<210> 32  
 <211> 332  
 <212> PRT  
 <213> Homo sapiens

<400> 32  
 Met Arg Leu Leu Ala Phe Leu Ser Leu Leu Ala Leu Val Leu Gln Glu  
 1 5 10 15  
 Thr Gly Thr Ala Ser Leu Pro Arg Lys Glu Arg Lys Arg Arg Glu Glu  
 20 25 30  
 Gln Met Pro Arg Glu Gly Asp Ser Phe Glu Val Leu Pro Leu Arg Asn  
 35 40 45  
 Asp Val Leu Asn Pro Asp Asn Tyr Gly Glu Val Ile Asp Leu Ser Asn  
 50 55 60  
 Tyr Glu Glu Leu Thr Asp Tyr Gly Asp Gln Leu Pro Glu Val Lys Val  
 65 70 75 80  
 Thr Ser Leu Ala Pro Ala Thr Ser Ile Ser Pro Ala Lys Ser Thr Thr  
 85 90 95  
 Ala Pro Gly Thr Pro Ser Ser Asn Pro Thr Met Thr Arg Pro Thr Thr  
 100 105 110  
 Ala Gly Leu Leu Leu Ser Ser Gln Pro Asn His Gly Leu Pro Thr Cys  
 115 120 125  
 Leu Val Cys Val Cys Leu Gly Ser Ser Val Tyr Cys Asp Asp Ile Asp  
 130 135 140  
 Leu Glu Asp Ile Pro Pro Leu Pro Arg Arg Thr Ala Tyr Leu Tyr Ala  
 145 150 155 160  
 Arg Phe Asn Arg Ile Ser Arg Ile Arg Ala Glu Asp Phe Lys Gly Leu

165 22 175  
 170  
 Thr Lys Leu Lys Arg Ile Asp Leu Ser Asn Asn Leu Ile Ser Ser Ile  
 180 185 190  
 Asp Asn Asp Ala Phe Arg Leu Leu His Ala Leu Gln Asp Leu Ile Leu  
 195 200 205  
 Pro Glu Asn Gln Leu Glu Ala Leu Pro Val Leu Pro Ser Gly Ile Glu  
 210 215 220  
 Phe Leu Asp Val Arg Leu Asn Arg Leu Gln Ser Ser Gly Ile Gln Pro  
 225 230 235 240  
 Ala Ala Phe Arg Ala Met Glu Lys Leu Gln Phe Leu Tyr Leu Ser Asp  
 245 250 255  
 Asn Leu Leu Asp Ser Ile Pro Gly Pro Leu Pro Pro Ser Leu Arg Ser  
 260 265 270  
 Val His Leu Gln Asn Asn Leu Ile Glu Thr Met Gln Arg Asp Val Phe  
 275 280 285  
 Cys Asp Pro Glu Glu His Lys His Thr Arg Arg Gln Leu Glu Asp Ile  
 290 295 300  
 Arg Leu Asp Gly Asn Pro Ile Asn Leu Ser Leu Phe Pro Ser Ala Tyr  
 305 310 315 320  
 Phe Cys Leu Pro Arg Leu Pro Ile Gly Arg Phe Thr  
 325 330

&lt;210&gt; 33

&lt;211&gt; 639

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

Met Leu Leu Pro Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln Ala  
 1 5 10 15  
 Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro  
 20 25 30  
 Glu Ala Cys Asp Ile Ser Val Pro Cys Ser Phe Ser Tyr Pro Arg Gln  
 35 40 45  
 Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp Phe Lys Ala Val  
 50 55 60  
 Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr Asn His Gln Ser Arg  
 65 70 75 80  
 Glu Val Glu Met Ser Thr Arg Gly Arg Phe Gln Leu Thr Gly Asp Pro  
 85 90 95  
 Ala Lys Gly Asn Cys Ser Leu Val Ile Arg Asp Ala Gln Met Gln Asp

23

100	105	110
Glu Ser Gln Tyr Phe Phe Arg Val Glu Arg Gly Ser Tyr Val Arg Tyr		
115	120	125
Asn Phe Met Asn Asp Gly Phe Phe Leu Lys Val Thr Val Leu Ser Phe		
130	135	140
Thr Pro Arg Pro Gln Asp His Asn Thr Asp Leu Thr Cys His Val Asp		
145	150	155
Phe Ser Arg Lys Gly Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val		
165	170	175
Ala Tyr Ala Pro Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr		
180	185	190
Pro Ala Leu Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala		
195	200	205
Gln Lys Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro		
210	215	220
Pro Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser		
225	230	235
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val Lys		
245	250	255
Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg Leu Gly		
260	265	270
Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro Pro Glu Asn		
275	280	285
Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val Leu Glu Asn Leu		
290	295	300
Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly Gln Ser Leu Cys Leu		
305	310	315
Val Cys Val Thr His Ser Ser Pro Pro Ala Arg Leu Ser Trp Thr Gln		
325	330	335
Arg Gly Gln Val Leu Ser Pro Ser Gln Pro Ser Asp Pro Gly Val Leu		
340	345	350
Glu Leu Pro Arg Val Gln Val Glu His Glu Gly Glu Phe Thr Cys His		
355	360	365
Ala Arg His Pro Leu Gly Ser Gln His Val Ser Leu Ser Leu Ser Val		
370	375	380
His Tyr Ser Pro Lys Leu Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu		
385	390	395
Gly Leu His Cys Ser Cys Ser Ser Gln Ala Ser Pro Ala Pro Ser Leu		
405	410	415

Arg Trp Trp Leu Gly Glu Glu Leu Leu Glu Gly Asn Ser Ser Gln Asp  
 420 425 430  
 Ser Phe Glu Val Thr Pro Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser  
 435 440 445  
 Leu Ser Leu His Gly Gly Leu Ser Ser Gly Leu Arg Leu Arg Cys Glu  
 450 455 460  
 Ala Trp Asn Val His Gly Ala Gln Ser Gly Ser Ile Leu Gln Leu Pro  
 465 470 475 480  
 Asp Lys Lys Gly Leu Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu  
 485 490 495  
 Gly Ile Gly Ile Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile  
 500 505 510  
 Met Lys Ile Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro  
 515 520 525  
 Arg Phe Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro  
 530 535 540  
 Thr Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn  
 545 550 555 560  
 Ser Pro Arg Thr Pro Leu Pro Pro Gly Ala Pro Ser Pro Glu Ser Lys  
 565 570 575  
 Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu Pro Lys  
 580 585 590  
 Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu Glu Leu His  
 595 600 605  
 Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg Pro Glu Ala Arg  
 610 615 620  
 Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu Val Lys Phe Gln  
 625 630 635

&lt;210&gt; 34

&lt;211&gt; 467

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

Met Leu Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Val  
 1 5 10 15  
 Glu Gly Gln Lys Ser Asn Arg Lys Asp Tyr Ser Leu Thr Met Gln Ser  
 20 25 30  
 Ser Val Thr Val Gln Glu Gly Met Cys Val His Val Arg Cys Ser Phe  
 35 40 45

Ser Tyr Pro Val Asp Ser Gln Thr Asp Ser Asp Pro Val His Gly Tyr  
 50 55 60  
 Trp Phe Arg Ala Gly Asn Asp Ile Ser Trp Lys Ala Pro Val Ala Thr  
 65 70 75 80  
 Asn Asn Pro Ala Trp Ala Val Gln Glu Glu Thr Arg Asp Arg Phe His  
 85 90 95  
 Leu Leu Gly Asp Pro Gln Thr Lys Asn Cys Thr Leu Ser Ile Arg Asp  
 100 105 110  
 Ala Arg Met Ser Asp Ala Gly Arg Tyr Phe Phe Arg Met Glu Lys Gly  
 115 120 125  
 Asn Ile Lys Trp Asn Tyr Lys Tyr Asp Gln Leu Ser Val Asn Val Thr  
 130 135 140  
 Ala Leu Thr His Arg Pro Asn Ile Leu Ile Pro Gly Thr Leu Glu Ser  
 145 150 155 160  
 Gly Cys Phe Gln Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln  
 165 170 175  
 Gly Thr Pro Pro Met Ile Ser Trp Met Gly Thr Ser Val Ser Pro Leu  
 180 185 190  
 His Pro Ser Thr Thr Arg Ser Ser Val Leu Thr Leu Ile Pro Gln Pro  
 195 200 205  
 Gln His His Gly Thr Ser Leu Thr Cys Gln Val Thr Leu Pro Gly Ala  
 210 215 220  
 Gly Val Thr Thr Asn Arg Thr Ile Gln Leu Asn Val Ser Tyr Pro Pro  
 225 230 235 240  
 Gln Asn Leu Thr Val Thr Val Phe Gln Gly Glu Gly Thr Ala Ser Thr  
 245 250 255  
 Ala Leu Gly Asn Ser Ser Ser Leu Ser Val Leu Glu Gly Gln Ser Leu  
 260 265 270  
 Arg Leu Val Cys Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Trp  
 275 280 285  
 Thr Trp Arg Ser Leu Thr Leu Tyr Pro Ser Gln Pro Ser Asn Pro Leu  
 290 295 300  
 Val Leu Glu Leu Gln Val His Leu Gly Asp Glu Gly Glu Phe Thr Cys  
 305 310 315 320  
 Arg Ala Gln Asn Ser Leu Gly Ser Gln His Val Ser Leu Asn Leu Ser  
 325 330 335  
 Leu Gln Gln Glu Tyr Thr Gly Lys Met Arg Pro Val Ser Gly Val Leu  
 340 345 350

26

Leu Gly Ala Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe Leu Ser  
 355 360 365

Phe Cys Val Ile Phe Ile Val Val Arg Ser Cys Arg Lys Lys Ser Ala  
 370 375 380

Arg Pro Ala Ala Asp Val Gly Asp Ile Gly Met Lys Asp Ala Asn Thr  
 385 390 395 400

Ile Arg Gly Ser Ala Ser Gln Gly Asn Leu Thr Glu Ser Trp Ala Asp  
 405 410 415

Asp Asn Pro Arg His His Gly Leu Ala Ala His Ser Ser Gly Glu Glu  
 420 425 430

Arg Glu Ile Gln Tyr Ala Pro Leu Ser Phe His Lys Gly Glu Pro Gln  
 435 440 445

Asp Leu Ser Gly Gln Glu Ala Thr Asn Asn Glu Tyr Ser Glu Ile Lys  
 450 455 460

Ile Pro Lys  
 465

&lt;210&gt; 35

&lt;211&gt; 1189

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 35

Met Asp Leu Pro Arg Gly Leu Val Val Ala Trp Ala Leu Ser Leu Trp  
 1 5 10 15

Pro Gly Phe Thr Asp Thr Phe Asn Met Asp Thr Arg Lys Pro Arg Val  
 20 25 30

Ile Pro Gly Ser Arg Thr Ala Phe Phe Gly Tyr Thr Val Gln Gln His  
 35 40 45

Asp Ile Ser Gly Asn Lys Trp Leu Val Val Gly Ala Pro Leu Glu Thr  
 50 55 60

Asn Gly Tyr Gln Lys Thr Gly Asp Val Tyr Lys Cys Pro Val Ile His  
 65 70 75 80

Gly Asn Cys Thr Lys Leu Asn Leu Gly Arg Val Thr Leu Ser Asn Val  
 85 90 95

Ser Glu Arg Lys Asp Asn Met Arg Leu Gly Leu Ser Leu Ala Thr Asn  
 100 105 110

Pro Lys Asp Asn Ser Phe Leu Ala Cys Ser Pro Leu Trp Ser His Glu  
 115 120 125

Cys Gly Ser Ser Tyr Tyr Thr Thr Gly Met Cys Ser Arg Val Asn Ser  
 130 135 140



27

Asn Phe Arg Phe Ser Lys Thr Val Ala Pro Ala Leu Gln Arg Cys Gln  
 145 150 155 160  
 Thr Tyr Met Asp Ile Val Ile Val Leu Asp Gly Ser Asn Ser Ile Tyr  
 165 170 175  
 Pro Trp Val Glu Val Gln His Phe Leu Ile Asn Ile Leu Lys Lys Phe  
 180 185 190  
 Tyr Ile Gly Pro Gly Gln Ile Gln Val Gly Val Val Gln Tyr Gly Glu  
 195 200 205  
 Asp Val Val His Glu Phe His Leu Asn Asp Tyr Arg Ser Val Lys Asp  
 210 215 220  
 Val Val Glu Ala Ala Ser His Ile Glu Gln Arg Gly Gly Thr Glu Thr  
 225 230 235 240  
 Arg Thr Ala Phe Gly Ile Glu Phe Ala Arg Ser Glu Ala Phe Gln Lys  
 245 250 255  
 Gly Gly Arg Lys Gly Ala Lys Lys Val Met Ile Val Ile Thr Asp Gly  
 260 265 270  
 Glu Ser His Asp Ser Pro Asp Leu Glu Lys Val Ile Gln Gln Ser Glu  
 275 280 285  
 Arg Asp Asn Val Thr Arg Tyr Ala Val Ala Val Leu Gly Tyr Tyr Asn  
 290 295 300  
 Arg Arg Gly Ile Asn Pro Glu Thr Phe Leu Asn Glu Ile Lys Tyr Ile  
 305 310 315 320  
 Ala Ser Asp Pro Asp Asp Lys His Phe Phe Asn Val Thr Asp Glu Ala  
 325 330 335  
 Ala Leu Lys Asp Ile Val Asp Ala Leu Gly Asp Arg Ile Phe Ser Leu  
 340 345 350  
 Glu Gly Thr Asn Lys Asn Glu Thr Ser Phe Gly Leu Glu Met Ser Gln  
 355 360 365  
 Thr Gly Phe Ser Ser His Val Val Glu Asp Gly Val Leu Leu Gly Ala  
 370 375 380  
 Val Gly Ala Tyr Asp Trp Asn Gly Ala Val Leu Lys Glu Thr Ser Ala  
 385 390 395 400  
 Gly Lys Val Ile Pro Leu Arg Glu Ser Tyr Leu Lys Glu Phe Pro Glu  
 405 410 415  
 Glu Leu Lys Asn His Gly Ala Tyr Leu Gly Tyr Thr Val Thr Ser Val  
 420 425 430  
 Val Ser Ser Arg Gln Gly Arg Val Tyr Val Ala Gly Ala Pro Arg Phe  
 435 440 445  
 Asn His Thr Gly Lys Val Ile Leu Phe Thr Met His Asn Asn Arg Ser

					28										
450					455					460					
Leu 465	Thr	Ile	His	Gln	Ala 470	Met	Arg	Gly	Gln	Gln 475	Ile	Gly	Ser	Tyr	Phe 480
Gly	Ser	Glu	Ile	Thr 485	Ser	Val	Asp	Ile	Asp 490	Gly	Asp	Gly	Val	Thr 495	Asp
Val	Leu	Leu	Val 500	Gly	Ala	Pro	Met	Tyr 505	Phe	Asn	Glu	Gly	Arg 510	Glu	Arg
Gly	Lys 515	Val	Tyr	Val	Tyr	Glu 520	Leu	Arg	Gln	Asn	Arg	Phe 525	Val	Tyr	Asn
Gly	Thr 530	Leu	Lys	Asp	Ser	His 535	Ser	Tyr	Gln	Asn	Ala 540	Arg	Phe	Gly	Ser
Ser 545	Ile	Ala	Ser	Val	Arg 550	Asp	Leu	Asn	Gln	Asp 555	Ser	Tyr	Asn	Asp	Val 560
Val	Val	Gly	Ala	Pro 565	Leu	Glu	Asp	Asn	His 570	Ala	Gly	Ala	Ile	Tyr 575	Ile
Phe	His	Gly	Phe 580	Arg	Gly	Ser	Ile	Leu 585	Lys	Thr	Pro	Lys	Gln 590	Arg	Ile
Thr	Ala 595	Ser	Glu	Leu	Ala	Thr	Gly 600	Leu	Gln	Tyr	Phe	Gly 605	Cys	Ser	Ile
His 610	Gly	Gln	Leu	Asp	Leu 615	Asn	Glu	Asp	Gly	Leu	Ile 620	Asp	Leu	Ala	Val
Gly 625	Ala	Leu	Gly	Asn 630	Ala	Val	Ile	Leu	Trp	Ser 635	Arg	Pro	Val	Val	Gln 640
Ile	Asn	Ala	Ser	Leu 645	His	Phe	Glu	Pro	Ser 650	Lys	Ile	Asn	Ile	Phe 655	His
Arg	Asp	Cys	Lys 660	Arg	Ser	Gly	Arg	Asp 665	Ala	Thr	Cys	Leu	Ala 670	Ala	Phe
Leu	Cys 675	Phe	Thr	Pro	Ile	Phe	Leu 680	Ala	Pro	His	Phe	Gln 685	Thr	Thr	Thr
Val	Gly 690	Ile	Arg	Tyr	Asn 695	Ala	Thr	Met	Asp	Glu	Arg 700	Arg	Tyr	Thr	Pro
Arg 705	Ala	His	Leu	Asp 710	Glu	Gly	Gly	Asp	Arg	Phe 715	Thr	Asn	Arg	Ala	Val 720
Leu	Leu	Ser	Ser	Gly 725	Gln	Glu	Leu	Cys	Glu 730	Arg	Ile	Asn	Phe	His 735	Val
Leu	Asp	Thr	Ala 740	Asp	Tyr	Val	Lys	Pro 745	Val	Thr	Phe	Ser	Val 750	Glu	Tyr
Ser	Leu 755	Glu	Asp	Pro	Asp	His	Gly 760	Pro	Met	Leu	Asp	Asp 765	Gly	Trp	Pro

Thr Thr Leu Arg Val Ser Val Pro Phe Trp Asn Gly Cys Asn Glu Asp  
 770 775 780  
 Glu His Cys Val Pro Asp Leu Val Leu Asp Ala Arg Ser Asp Leu Pro  
 785 790 795 800  
 Thr Ala Met Glu Tyr Cys Gln Arg Val Leu Arg Lys Pro Ala Gln Asp  
 805 810 815  
 Cys Ser Ala Tyr Thr Leu Ser Phe Asp Thr Thr Val Phe Ile Ile Glu  
 820 825 830  
 Ser Thr Arg Gln Arg Val Ala Val Glu Ala Thr Leu Glu Asn Arg Gly  
 835 840 845  
 Glu Asn Ala Tyr Ser Thr Val Leu Asn Ile Ser Gln Ser Ala Asn Leu  
 850 855 860  
 Gln Phe Ala Ser Leu Ile Gln Lys Glu Asp Ser Asp Gly Ser Ile Glu  
 865 870 875 880  
 Cys Val Asn Glu Glu Arg Arg Leu Gln Lys Gln Val Cys Asn Val Ser  
 885 890 895  
 Tyr Pro Phe Phe Arg Ala Lys Ala Lys Val Ala Phe Arg Leu Asp Phe  
 900 905 910  
 Glu Phe Ser Lys Ser Ile Phe Leu His His Leu Glu Ile Glu Leu Ala  
 915 920 925  
 Ala Gly Ser Asp Ser Asn Glu Arg Asp Ser Thr Lys Glu Asp Asn Val  
 930 935 940  
 Ala Pro Leu Arg Phe His Leu Lys Tyr Glu Ala Asp Val Leu Phe Thr  
 945 950 955 960  
 Arg Ser Ser Ser Leu Ser His Tyr Glu Val Lys Leu Asn Ser Ser Leu  
 965 970 975  
 Glu Arg Tyr Asp Gly Ile Gly Pro Pro Phe Ser Cys Ile Phe Arg Ile  
 980 985 990  
 Gln Asn Leu Gly Leu Phe Pro Ile His Gly Ile Met Met Lys Ile Thr  
 995 1000 1005  
 Ile Pro Ile Ala Thr Arg Ser Gly Asn Arg Leu Leu Lys Leu Arg Asp  
 1010 1015 1020  
 Phe Leu Thr Asp Glu Val Ala Asn Thr Ser Cys Asn Ile Trp Gly Asn  
 1030 1035 1040  
 Ser Thr Glu Tyr Arg Pro Thr Pro Val Glu Glu Asp Leu Arg Arg Ala  
 1045 1050 1055  
 Pro Gln Leu Asn His Ser Asn Ser Asp Val Val Ser Ile Asn Cys Asn  
 1060 1065 1070

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30

Ile Arg Leu Val Pro Asn Gln Glu Ile Asn Phe His Leu Leu Gly Asn  
1075 1080 1085

Leu Trp Leu Arg Ser Leu Lys Ala Leu Lys Tyr Lys Ser Met Lys Ile  
1090 1095 1100

Met Val Asn Ala Ala Leu Gln Arg Gln Phe His Ser Pro Phe Ile Phe  
1110 1115 1120

Arg Glu Glu Asp Pro Ser Arg Gln Ile Val Phe Glu Ile Ser Lys Gln  
1125 1130 1135

Glu Asp Trp Gln Val Pro Ile Trp Ile Ile Val Gly Ser Thr Leu Gly  
1140 1145 1150

Gly Leu Leu Leu Leu Ala Leu Leu Val Leu Ala Leu Trp Lys Leu Gly  
1155 1160 1165

Phe Phe Arg Ser Ala Arg Arg Arg Arg Glu Pro Gly Leu Asp Pro Thr  
1170 1175 1180

Pro Lys Val Leu Glu

<210> 36

<211> 196

<212> PRT

<213> Homo sapiens

<400> 36

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu Leu  
1 5 10 15

Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys Ser Pro  
20 25 30

Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu Cys Ala Gln  
35 40 45

His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser His Thr Ala Gly  
50 55 60

Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln Gln Ala Arg Asn Val  
65 70 75 80

Gln His Tyr His Met Lys Thr Leu Gly Trp Cys Asp Val Gly Tyr Asn  
85 90 95

Phe Leu Ile Gly Glu Asp Gly Leu Val Tyr Glu Gly Arg Gly Trp Asn  
100 105 110

Phe Thr Gly Ala His Ser Gly His Leu Trp Asn Pro Met Ser Ile Gly  
115 120 125

Ile Ser Phe Met Gly Asn Tyr Met Asp Arg Val Pro Thr Pro Gln Ala  
130 135 140

Ile Arg Ala Ala Gln Gly Leu Leu Ala Cys Gly Val Ala Gln Gly Ala  
 145 150 155 160  
 Leu Arg Ser Asn Tyr Val Leu Lys Gly His Arg Asp Val Gln Arg Thr  
 165 170 175  
 Leu Ser Pro Gly Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His  
 180 185 190  
 Tyr Arg Ser Pro  
 195

<210> 37  
 <211> 319  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SITE  
 <222> (319)  
 <223> Xaa equals stop translation

<400> 37  
 Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly Ser  
 1 5 10 15  
 Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala Leu Val  
 20 25 30  
 Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys Thr Asn Ala  
 35 40 45  
 Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe Ser Ser Val Val  
 50 55 60  
 His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe Met Gln Met Pro Gln  
 65 70 75 80  
 Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp Ser Ile Ala Glu Gly Arg  
 85 90 95  
 Ile Ser Leu Arg Leu Glu Asn Ile Thr Val Leu Asp Ala Gly Leu Tyr  
 100 105 110  
 Gly Cys Arg Ile Ser Ser Gln Ser Tyr Tyr Gln Lys Ala Ile Trp Glu  
 115 120 125  
 Leu Gln Val Ser Ala Leu Gly Ser Val Pro Leu Ile Ser Ile Ala Gly  
 130 135 140  
 Tyr Val Asp Arg Asp Ile Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe  
 145 150 155 160  
 Pro Arg Pro Thr Ala Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser  
 165 170 175  
 Thr Asp Ser Arg Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu

**PCT/US99/25031**

	180						185					32	190				
Ile Ser Leu Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met 195 200 205																	
Arg His Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly 210 215 220																	
Asp Trp Arg Arg Lys His Gly Gln Ala Gly Lys Arg Lys Tyr Ser Ser 225 230 235 240																	
Ser His Ile Tyr Asp Ser Phe Pro Ser Leu Ser Phe Met Asp Phe Tyr 245 250 255																	
Ile Leu Arg Pro Val Gly Pro Cys Arg Ala Lys Leu Val Met Gly Thr 260 265 270																	
Leu Lys Leu Gln Ile Leu Gly Glu Val His Phe Val Glu Lys Pro His 275 280 285																	
Ser Leu Leu Gln Ile Ser Gly Gly Ser Thr Thr Leu Lys Lys Gly Pro 290 295 300																	
Asn Pro Trp Ser Phe Pro Ser Pro Cys Ala Leu Phe Pro Thr Xaa 305 310 315																	
<210> 38																	
<211> 375																	
<212> PRT																	
<213> Homo sapiens																	
<400> 38																	
Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys 1 5 10 15																	
Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp 20 25 30																	
Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu 35 40 45																	
Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser 50 55 60																	
Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu 65 70 75 80																	
Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg 85 90 95																	
Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly 100 105 110																	
Ala Gln His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg 115 120 125																	
Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe																	

PCT/US99/25031

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<210> 39
<211> 364
<212> PRT
<213> Homo sapiens
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<400> 39
Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala Ala
 1           5           10           15
```

Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu Leu

20 25 34 30  
 Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe  
 35 40 45  
 Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys  
 50 55 60  
 Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn  
 65 70 75 80  
 Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg  
 85 90 95  
 Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr  
 100 105 110  
 Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr  
 115 120 125  
 Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro  
 130 135 140  
 Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu  
 145 150 155 160  
 Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr  
 165 170 175  
 Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val  
 180 185 190  
 Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys  
 195 200 205  
 Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His  
 210 215 220  
 Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln  
 225 230 235 240  
 Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu  
 245 250 255  
 Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys  
 260 265 270  
 Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro  
 275 280 285  
 Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn  
 290 295 300  
 Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly  
 305 310 315 320  
 Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr  
 325 330 335



35

Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr  
                   340                                  345                                  350

Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Arg  
           355                                  360

&lt;210&gt; 40

&lt;211&gt; 66

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 40

Met Ser Ser Ser Ser Leu Lys His Leu Leu Cys Met Ala Leu Ser Trp  
   1                                  5                                  10                                  15

Phe Ser Ser Phe Ile Ser Gly Glu Thr Ser Phe Ser Leu Leu Asn Ser  
                   20                                  25                                  30

Phe Phe Leu Pro Tyr Pro Ser Ser Arg Cys Cys Cys Phe Ser Val Gln  
           35                                  40                                  45

Cys Ser Ile Leu Asp Pro Phe Ser Cys Asn Ser Met Arg Phe Pro Trp  
   50                                  55                                  60

Glu Asn  
   65

&lt;210&gt; 41

&lt;211&gt; 469

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 41

Met Arg Pro Pro Gly Phe Arg Asn Phe Leu Leu Leu Ala Ser Ser Leu  
   1                                  5                                  10                                  15

Leu Phe Ala Gly Leu Ser Ala Val Pro Gln Ser Phe Ser Pro Ser Leu  
                   20                                  25                                  30

Arg Ser Trp Pro Gly Ala Ala Cys Arg Leu Ser Arg Ala Glu Ser Glu  
           35                                  40                                  45

Arg Arg Cys Arg Ala Pro Gly Gln Pro Pro Gly Ala Ala Leu Cys His  
   50                                  55                                  60

Gly Arg Gly Arg Cys Asp Cys Gly Val Cys Ile Cys His Val Thr Glu  
   65                                  70                                  75                                  80

Pro Gly Met Phe Phe Gly Pro Leu Cys Glu Cys His Glu Trp Val Cys  
                   85                                  90                                  95

Glu Thr Tyr Asp Gly Ser Thr Cys Ala Gly His Gly Lys Cys Asp Cys  
           100                                  105                                  110

Gly Lys Cys Lys Cys Asp Gln Gly Trp Tyr Gly Asp Ala Cys Gln Tyr

36

115	120	125
Pro Thr Asn Cys Asp Leu Thr Lys Lys Lys Ser Asn Gln Met Cys Lys 130 135 140		
Asn Ser Gln Asp Ile Ile Cys Ser Asn Ala Gly Thr Cys His Cys Gly 145 150 155 160		
Arg Cys Lys Cys Asp Asn Ser Asp Gly Ser Gly Leu Val Tyr Gly Lys 165 170 175		
Phe Cys Glu Cys Asp Asp Arg Glu Cys Ile Asp Asp Glu Thr Glu Glu 180 185 190		
Ile Cys Gly Gly His Gly Lys Cys Tyr Cys Gly Asn Cys Tyr Cys Lys 195 200 205		
Ala Gly Trp His Gly Asp Lys Cys Glu Phe Gln Cys Asp Ile Thr Pro 210 215 220		
Trp Glu Ser Lys Arg Arg Cys Thr Ser Pro Asp Gly Lys Ile Cys Ser 225 230 235 240		
Ser Arg Gly Thr Cys Val Cys Gly Glu Cys Thr Cys His Asp Val Asp 245 250 255		
Pro Thr Gly Asp Trp Gly Asp Ile His Gly Asp Thr Cys Glu Cys Asp 260 265 270		
Glu Arg Asp Cys Arg Ala Val Tyr Asp Arg Tyr Ser Asp Asp Phe Cys 275 280 285		
Ser Gly His Gly Gln Cys Asn Cys Gly Arg Cys Asp Cys Lys Ala Gly 290 295 300		
Trp Tyr Gly Lys Lys Cys Glu His Pro Gln Ser Cys Thr Leu Ser Ala 305 310 315 320		
Glu Glu Ser Ile Arg Lys Cys Gln Gly Ser Ser Asp Leu Pro Cys Ser 325 330 335		
Gly Arg Gly Lys Cys Glu Cys Gly Lys Cys Thr Cys Tyr Pro Pro Gly 340 345 350		
Asp Arg Arg Val Tyr Gly Lys Thr Cys Glu Cys Asp Asp Arg Arg Cys 355 360 365		
Glu Asp Leu Asp Gly Val Val Cys Gly Gly His Gly Thr Cys Ser Cys 370 375 380		
Gly Arg Cys Val Cys Glu Arg Gly Trp Phe Gly Lys Leu Cys Gln His 385 390 395 400		
Pro Arg Lys Cys Asn Met Thr Glu Glu Gln Ser Lys Asn Leu Cys Glu 405 410 415		
Ser Ala Asp Gly Ile Leu Cys Ser Gly Lys Gly Ser Cys His Cys Gly 420 425 430		

Lys Cys Ile Cys Ser Ala Glu Glu Trp Tyr Ile Ser Gly Glu Phe Cys  
 435 440 445

Asp Cys Asp Asp Arg Asp Cys Asp Lys His Asp Gly Leu Ile Cys Thr  
 450 455 460

Arg Glu Trp Asn Met  
 465

<210> 42

<211> 127

<212> PRT

<213> Homo sapiens

<400> 42

Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln Ala  
 1 5 10 15

Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro  
 20 25 30

Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr Pro Arg Gln  
 35 40 45

Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp Phe Lys Ala Val  
 50 55 60

Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr Asn His Gln Ser Arg  
 65 70 75 80

Glu Val Glu Met Ser Thr Arg Gly Arg Phe Pro Gly Ser Leu Gly Asp  
 85 90 95

Pro Ala Lys Gly Asn Cys Ser Leu Val Ile Arg Arg Arg Ala Asp Ala  
 100 105 110

Arg Met Ser His Ser Thr Ser Phe Gly Trp Arg Glu Glu Ala Met  
 115 120 125

<210> 43

<211> 1034

<212> PRT

<213> Homo sapiens

<400> 43

Met Asp Leu Pro Arg Gly Leu Val Val Ala Trp Ala Leu Ser Leu Trp  
 1 5 10 15

Pro Gly Phe Thr Asp Thr Phe Asn Met Asp Thr Arg Lys Pro Arg Val  
 20 25 30

Ile Pro Gly Ser Arg Thr Ala Phe Phe Gly Tyr Thr Val Gln Gln His  
 35 40 45

Asp Ile Ser Gly Asn Lys Trp Leu Val Val Gly Ala Pro Leu Glu Thr

50 55 38 60  
 Asn Gly Tyr Gln Lys Thr Gly Asp Val Tyr Lys Cys Pro Val Ile His  
 65 70 75 80  
 Gly Asn Cys Thr Lys Leu Asn Leu Gly Arg Val Thr Leu Ser Asn Val  
 85 90 95  
 Ser Glu Arg Lys Asp Asn Met Arg Leu Gly Leu Ser Leu Ala Thr Asn  
 100 105 110  
 Pro Lys Asp Asn Ser Phe Leu Ala Cys Ser Pro Leu Trp Ser His Glu  
 115 120 125  
 Cys Gly Ser Ser Tyr Tyr Thr Thr Gly Met Cys Ser Arg Val Asn Ser  
 130 135 140  
 Asn Phe Arg Phe Ser Lys Thr Val Ala Pro Ala Leu Gln Arg Cys Gln  
 145 150 155 160  
 Thr Tyr Met Asp Ile Val Ile Val Leu Asp Gly Ser Asn Ser Ile Tyr  
 165 170 175  
 Pro Trp Val Glu Val Gln His Phe Leu Ile Asn Ile Leu Lys Lys Phe  
 180 185 190  
 Tyr Ile Gly Pro Gly Gln Ile Gln Val Gly Val Val Gln Tyr Gly Glu  
 195 200 205  
 Asp Val Val His Glu Phe His Leu Asn Asp Tyr Arg Ser Val Lys Asp  
 210 215 220  
 Val Val Glu Ala Ala Ser His Ile Glu Gln Arg Gly Gly Thr Glu Thr  
 225 230 235 240  
 Arg Thr Ala Phe Gly Ile Glu Phe Ala Arg Ser Glu Ala Phe Gln Lys  
 245 250 255  
 Gly Gly Arg Lys Gly Ala Lys Lys Val Met Ile Val Ile Thr Asp Gly  
 260 265 270  
 Glu Ser His Asp Ser Pro Asp Leu Glu Lys Val Ile Gln Gln Ser Glu  
 275 280 285  
 Arg Asp Asn Val Thr Arg Tyr Ala Val Ala Val Leu Gly Tyr Tyr Asn  
 290 295 300  
 Arg Arg Gly Ile Asn Pro Glu Thr Phe Leu Asn Glu Ile Lys Tyr Ile  
 305 310 315 320  
 Ala Ser Asp Pro Asp Asp Lys His Phe Phe Asn Val Thr Asp Glu Ala  
 325 330 335  
 Ala Leu Lys Asp Ile Val Asp Ala Leu Gly Asp Arg Ile Phe Ser Leu  
 340 345 350  
 Glu Gly Thr Asn Lys Asn Glu Thr Ser Phe Gly Leu Glu Met Ser Gln  
 355 360 365

Thr Gly Phe Ser Ser His Val Val Glu Asp Gly Val Leu Leu Gly Ala  
 370 375 380  
 Val Gly Ala Tyr Asp Trp Asn Gly Ala Val Leu Lys Glu Thr Ser Ala  
 385 390 395 400  
 Gly Lys Val Ile Pro Leu Arg Glu Ser Tyr Leu Lys Glu Phe Pro Glu  
 405 410 415  
 Glu Leu Lys Asn His Gly Ala Tyr Leu Gly Tyr Thr Val Thr Ser Val  
 420 425 430  
 Val Ser Ser Arg Gln Gly Arg Val Tyr Val Ala Gly Ala Pro Arg Phe  
 435 440 445  
 Asn His Thr Gly Lys Val Ile Leu Phe Thr Met His Asn Asn Arg Ser  
 450 455 460  
 Leu Thr Ile His Gln Ala Met Arg Gly Gln Gln Ile Gly Ser Tyr Phe  
 465 470 475 480  
 Gly Ser Glu Ile Thr Ser Val Asp Ile Asp Gly Asp Gly Val Thr Asp  
 485 490 495  
 Val Leu Leu Val Gly Ala Pro Met Tyr Phe Asn Glu Gly Arg Glu Arg  
 500 505 510  
 Gly Lys Val Tyr Val Tyr Glu Leu Arg Gln Asn Arg Phe Val Tyr Asn  
 515 520 525  
 Gly Thr Leu Lys Asp Ser His Ser Tyr Gln Asn Ala Arg Phe Gly Ser  
 530 535 540  
 Ser Ile Ala Ser Val Arg Asp Leu Asn Gln Asp Ser Tyr Asn Asp Val  
 545 550 555 560  
 Val Val Gly Ala Pro Leu Glu Asp Asn His Ala Gly Ala Ile Tyr Ile  
 565 570 575  
 Phe His Gly Phe Arg Gly Ser Ile Leu Lys Thr Pro Lys Gln Arg Ile  
 580 585 590  
 Thr Ala Ser Glu Leu Ala Thr Gly Leu Gln Tyr Phe Gly Cys Ser Ile  
 595 600 605  
 His Gly Gln Leu Asp Leu Asn Glu Asp Gly Leu Ile Asp Leu Ala Val  
 610 615 620  
 Gly Ala Leu Gly Asn Ala Val Ile Leu Trp Ser Arg Pro Val Val Gln  
 625 630 635 640  
 Ile Asn Ala Ser Leu His Phe Glu Pro Ser Lys Ile Asn Ile Phe His  
 645 650 655  
 Arg Asp Cys Lys Arg Ser Gly Arg Asp Ala Thr Cys Leu Ala Ala Phe  
 660 665 670

40

Leu Cys Phe Thr Pro Ile Phe Leu Ala Pro His Phe Gln Thr Thr Thr  
675 680 685

Val Gly Ile Arg Tyr Asn Ala Thr Met Asp Glu Lys Arg Tyr Thr Pro  
690 695 700

Arg Ala His Leu Asp Glu Gly Gly Asp Arg Phe Thr Asn Arg Ala Val  
705 710 715 720

Leu Leu Ser Ser Gly Gln Glu Leu Cys Glu Arg Ile Asn Phe His Val  
725 730 735

Leu Asp Thr Ala Asp Tyr Val Lys Pro Val Thr Phe Ser Val Glu Tyr  
740 745 750

Ser Leu Glu Asp Pro Asp His Gly Pro Met Leu Asp Asp Gly Trp Pro  
755 760 765

Thr Thr Leu Arg Val Ser Val Pro Phe Trp Asn Gly Cys Asn Glu Asp  
770 775 780

Glu His Cys Val Pro Asp Leu Val Leu Asp Ala Arg Ser Asp Leu Pro  
785 790 795 800

Thr Ala Met Glu Tyr Cys Gln Arg Val Leu Arg Lys Pro Ala Gln Asp  
805 810 815

Cys Ser Ala Tyr Thr Leu Ser Phe Asp Thr Thr Val Phe Ile Ile Glu  
820 825 830

Ser Thr Arg Gln Arg Val Ala Val Glu Ala Thr Leu Glu Asn Arg Gly  
835 840 845

Glu Asn Ala Tyr Ser Thr Val Leu Asn Ile Ser Gln Ser Ala Asn Leu  
850 855 860

Gln Phe Ala Ser Leu Ile Gln Lys Glu Asp Ser Asp Gly Ser Ile Glu  
865 870 875 880

Cys Val Asn Glu Glu Arg Arg Leu Gln Lys Gln Val Cys Asn Val Ser  
885 890 895

Tyr Pro Phe Phe Arg Ala Lys Ala Lys Val Ala Phe Arg Leu Asp Phe  
900 905 910

Glu Phe Ser Lys Ser Ile Phe Leu His His Leu Glu Ile Glu Leu Ala  
915 920 925

Ala Gly Ser Asp Ser Asn Glu Arg Asp Ser Thr Lys Glu Asp Asn Val  
930 935 940

Ala Pro Leu Arg Phe His Leu Lys Tyr Glu Ala Asp Val Leu Phe Thr  
945 950 955 960

Arg Ser Ser Ser Leu Ser His Tyr Glu Val Lys Leu Asn Ser Ser Leu  
965 970 975

Glu Arg Tyr Asp Gly Ile Gly Pro Pro Phe Ser Cys Ile Phe Arg Ile

41

980	985	990
Gln Asn Leu Gly Leu Phe Pro Ile His Gly Ile Met Met Lys Ile Thr		
995	1000	1005
Ile Pro Ile Ala Thr Arg Ser Gly Asn Arg Leu Leu Lys Leu Arg Asp		
1010	1015	1020
Phe Leu Thr Asp Glu Gly Glu His Val Leu		
1030		

<210> 44  
 <211> 461  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SITE  
 <222> (234)  
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>  
 <221> SITE  
 <222> (236)  
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 44

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly Ser		
1	5	10 15
Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala Leu Val		
20	25	30
Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys Thr Asn Ala		
35	40	45
Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe Ser Ser Val Val		
50	55	60
His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe Met Gln Met Pro Gln		
65	70	75 80
Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp Ser Ile Ala Glu Gly Arg		
85	90	95
Ile Ser Leu Arg Leu Glu Asn Ile Thr Val Leu Asp Ala Gly Leu Tyr		
100	105	110
Gly Cys Arg Ile Ser Ser Gln Ser Tyr Tyr Gln Lys Ala Ile Trp Glu		
115	120	125
Leu Gln Val Ser Ala Leu Gly Ser Val Pro Leu Ile Ser Ile Thr Gly		
130	135	140
Tyr Val Asp Arg Asp Ile Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe		
145	150	155 160

42

Pro	Arg	Pro	Thr	Ala	Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	165	170	175	
Thr	Asp	Ser	Arg	Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	180	185	190	
Ile	Ser	Leu	Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	195	200	205	
Arg	His	Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	210	215	220	
Asp	Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	Xaa	Leu	Xaa	Thr	Lys	Val	Leu	225	230	235	240
Gly	Ile	Leu	Cys	Cys	Gly	Leu	Phe	Phe	Gly	Ile	Val	Gly	Leu	Lys	Ile	245	250	255	
Phe	Phe	Ser	Lys	Phe	Gln	Trp	Lys	Ile	Gln	Ala	Glu	Leu	Asp	Trp	Arg	260	265	270	
Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys	His	Ala	Val	275	280	285	
Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys	Leu	Cys	Val	Ser	290	295	300	
Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro	Gln	Glu	Val	Pro	His	305	310	315	320
Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	Val	Ala	Ser	Gln	Ser	Phe	325	330	335	
Gln	Ala	Gly	Lys	His	Tyr	Trp	Glu	Val	Asp	Gly	Gly	His	Asn	Lys	Arg	340	345	350	
Trp	Arg	Val	Gly	Val	Cys	Arg	Asp	Asp	Val	Asp	Arg	Arg	Lys	Glu	Tyr	355	360	365	
Val	Thr	Leu	Ser	Pro	Asp	His	Gly	Tyr	Trp	Val	Leu	Arg	Leu	Asn	Gly	370	375	380	
Glu	His	Leu	Tyr	Phe	Thr	Leu	Asn	Pro	Arg	Phe	Ile	Ser	Val	Phe	Pro	385	390	395	400
Arg	Thr	Pro	Pro	Thr	Lys	Ile	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Cys	Gly	405	410	415	
Thr	Ile	Ser	Phe	Phe	Asn	Ile	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	420	425	430	
Thr	Cys	Arg	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Glu	Tyr	Pro	Ser	435	440	445	
Tyr	Asn	Glu	Gln	Asn	Gly	Thr	Pro	Arg	Asp	Lys	Gln	Gln				450	455	460	



43

&lt;210&gt; 45

&lt;211&gt; 383

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 45

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Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys
 1             5             10             15

Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp
      20             25             30

Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu
      35             40             45

Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser
      50             55             60

Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu
      65             70             75             80

Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg
      85             90             95

Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly
      100            105            110

Ala Gln His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg
      115            120            125

Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe
      130            135            140

Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys
      145            150            155            160

Thr Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys
      165            170            175

Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val
      180            185            190

Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp
      195            200            205

Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val
      210            215            220

Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
      225            230            235            240

Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His
      245            250            255

Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu
      260            265            270

Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly

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44

275                                      280                                      285  
 Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu  
     290                                      295                                      300  
 Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val  
     305                                      310                                      315                                      320  
 Tyr Val Arg Met Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile  
                                     325                                      330                                      335  
 Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro  
                                     340                                      345                                      350  
 Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln  
                                     355                                      360                                      365  
 Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly  
     370                                      375                                      380  
  
 <210> 46  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 46  
 Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu Glu Ile Glu  
     1                                      5                                      10                                      15  
 Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr Ile Arg Trp  
                                     20                                      25                                      30  
 Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val Glu Glu Trp  
                                     35                                      40                                      45  
 Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys Val His Lys  
     50                                      55                                      60  
 Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His Pro Ala Val  
     65                                      70                                      75                                      80  
 Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln Tyr Lys Pro  
                                     85                                      90                                      95  
 Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu Thr Arg Glu  
                                     100                                      105                                      110  
 Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys Pro Gln Pro  
     115                                      120                                      125  
 Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro Gln His Ala  
     130                                      135                                      140  
 Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn Lys Thr Asp  
     145                                      150                                      155                                      160  
 Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly Lys Ala His

165 45 175  
 170  
 Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr Ile Pro Pro  
 180 185 190  
 Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Ile Leu  
 195 200 205  
 Thr Ile Ile Thr Asp Ser Pro Ser Gln Val Lys Lys Ala Arg Ser Gly  
 210 215 220  
 Gln Trp Ile Met Pro  
 225  
 <210> 47  
 <211> 724  
 <212> PRT  
 <213> Homo sapiens  
 <400> 47  
 Met Leu Arg Thr Ser Thr Pro Asn Leu Cys Gly Gly Leu His Cys Arg  
 1 5 10 15  
 Ala Pro Trp Leu Ser Ser Gly Ile Leu Cys Leu Cys Leu Ile Phe Leu  
 20 25 30  
 Leu Gly Gln Val Gly Leu Leu Gln Gly His Pro Gln Cys Leu Asp Tyr  
 35 40 45  
 Gly Pro Pro Phe Gln Pro Pro Leu His Leu Glu Phe Cys Ser Asp Tyr  
 50 55 60  
 Glu Ser Phe Gly Cys Cys Asp Gln His Lys Asp Arg Arg Ile Ala Ala  
 65 70 75 80  
 Arg Tyr Trp Asp Ile Met Glu Tyr Phe Asp Leu Lys Arg His Glu Leu  
 85 90 95  
 Cys Gly Asp Tyr Ile Lys Asp Ile Leu Cys Gln Glu Cys Ser Pro Tyr  
 100 105 110  
 Ala Ala His Leu Tyr Asp Ala Glu Asn Thr Gln Thr Pro Leu Arg Asn  
 115 120 125  
 Leu Pro Gly Leu Cys Ser Asp Tyr Cys Ser Ala Phe His Ser Asn Cys  
 130 135 140  
 His Ser Ala Ile Ser Leu Leu Thr Asn Asp Arg Gly Leu Gln Glu Ser  
 145 150 155 160  
 His Gly Arg Asp Gly Thr Arg Phe Cys His Leu Leu Asp Leu Pro Asp  
 165 170 175  
 Lys Asp Tyr Cys Phe Pro Asn Val Leu Arg Asn Asp Tyr Leu Asn Arg  
 180 185 190  
 His Leu Gly Met Val Ala Gln Asp Pro Gln Gly Cys Leu Gln Leu Cys

195	200	205
Leu Ser Glu Val Ala Asn Gly Leu Arg Asn Pro Val Ser Met Val His		
210	215	220
Ala Gly Asp Gly Thr His Arg Phe Phe Val Ala Glu Gln Val Gly Val		
225	230	235 240
Val Trp Val Tyr Leu Pro Asp Gly Ser Arg Leu Glu Gln Pro Phe Leu		
	245	250 255
Asp Leu Lys Asn Ile Val Leu Thr Thr Pro Trp Ile Gly Asp Glu Arg		
	260	265 270
Gly Phe Leu Gly Leu Ala Phe His Pro Lys Phe Arg His Asn Arg Lys		
	275	280 285
Phe Tyr Ile Tyr Tyr Ser Cys Leu Asp Lys Lys Lys Val Glu Lys Ile		
	290	295 300
Arg Ile Ser Glu Met Lys Val Ser Arg Ala Asp Pro Asn Lys Ala Asp		
305	310	315 320
Leu Lys Ser Glu Arg Val Ile Leu Glu Ile Glu Glu Pro Ala Ser Asn		
	325	330 335
His Asn Gly Gly Gln Leu Leu Phe Gly Leu Asp Gly Tyr Met Tyr Ile		
	340	345 350
Phe Thr Gly Asp Gly Gly Gln Ala Gly Asp Pro Phe Gly Leu Phe Gly		
	355	360 365
Asn Ala Gln Asn Lys Ser Ser Leu Leu Gly Lys Val Leu Arg Ile Asp		
	370	375 380
Val Asn Arg Ala Gly Ser His Gly Lys Arg Tyr Arg Val Pro Ser Asp		
385	390	395 400
Asn Pro Phe Val Ser Glu Pro Gly Ala His Pro Ala Ile Tyr Ala Tyr		
	405	410 415
Gly Ile Arg Asn Met Trp Arg Cys Ala Val Asp Arg Gly Asp Pro Ile		
	420	425 430
Thr Arg Gln Gly Arg Gly Arg Ile Phe Cys Gly Asp Val Gly Gln Asn		
	435	440 445
Arg Phe Glu Glu Val Asp Leu Ile Leu Lys Gly Gly Asn Tyr Gly Trp		
	450	455 460
Arg Ala Lys Glu Gly Phe Ala Cys Tyr Asp Lys Lys Leu Cys His Asn		
465	470	475 480
Ala Ser Leu Asp Asp Val Leu Pro Ile Tyr Ala Tyr Gly His Ala Val		
	485	490 495
Gly Lys Ser Val Thr Gly Gly Tyr Val Tyr Arg Gly Cys Glu Ser Pro		
	500	505 510

Asn Leu Asn Gly Leu Tyr Ile Phe Gly Asp Phe Met Ser Gly Arg Leu  
 515 520 525  
 Met Ala Leu Gln Glu Asp Arg Lys Asn Lys Lys Trp Lys Lys Gln Asp  
 530 535 540  
 Leu Cys Leu Gly Ser Thr Thr Ser Cys Ala Phe Pro Gly Leu Ile Ser  
 545 550 555 560  
 Thr His Ser Lys Phe Ile Ile Ser Phe Ala Glu Asp Glu Ala Gly Glu  
 565 570 575  
 Leu Tyr Phe Leu Ala Thr Ser Tyr Pro Ser Ala Tyr Ala Pro Arg Gly  
 580 585 590  
 Ser Ile Tyr Lys Phe Val Asp Pro Ser Arg Arg Ala Pro Pro Gly Lys  
 595 600 605  
 Cys Lys Tyr Lys Pro Val Pro Val Arg Thr Lys Ser Lys Arg Ile Pro  
 610 615 620  
 Phe Arg Pro Leu Ala Lys Thr Val Leu Asp Leu Leu Lys Glu Gln Ser  
 625 630 635 640  
 Glu Lys Ala Ala Arg Lys Ser Ser Ser Ala Thr Leu Ala Ser Gly Pro  
 645 650 655  
 Ala Gln Gly Leu Ser Glu Lys Gly Ser Ser Lys Lys Leu Ala Ser Pro  
 660 665 670  
 Thr Ser Ser Lys Asn Thr Leu Arg Gly Pro Gly Thr Lys Lys Lys Ala  
 675 680 685  
 Arg Val Gly Pro His Val Arg Gln Gly Lys Arg Arg Lys Ser Leu Lys  
 690 695 700  
 Ser His Ser Gly Arg Met Arg Pro Ser Ala Glu Gln Lys Arg Ala Gly  
 705 710 715 720  
 Arg Ser Leu Pro

<210> 48  
 <211> 995  
 <212> PRT  
 <213> Homo sapiens

<400> 48

Met Pro Lys Pro Thr Pro Asn Ser Glu Arg Val Ser Val Arg Phe Pro  
 1 5 10 15  
 Gly Cys Arg Thr Gly Met His Met Ile Ser Val Ser Leu Arg Leu Val  
 20 25 30  
 Phe Cys Ser Phe Ile Phe Lys Ala Gly Val Leu Leu Gly His Pro Gln  
 35 40 45

Cys Leu Asp Tyr Gly Pro Pro Phe Lys Pro Leu Val His Leu Glu Phe  
 50 55 60  
 Cys Ser Glu Tyr Glu Thr Phe Gly Cys Cys Asp Gln Asp Arg Asp Asn  
 65 70 75 80  
 Val Ile Ala Glu Lys Tyr Trp Ser Ile Met Asp Tyr Phe Asp Leu Asn  
 85 90 95  
 Asn Tyr His Ile Cys Gly Gly Tyr Ile Lys Asp Ile Leu Cys Gln Glu  
 100 105 110  
 Cys Ser Pro Tyr Ala Ala His Leu Tyr Asp Ala Glu Asp Pro His Thr  
 115 120 125  
 Pro Leu Arg Val Ile Pro Gly Leu Cys Phe Asn Tyr Cys Ser Glu Phe  
 130 135 140  
 His Leu Lys Cys Gln Asn Ser Ile Thr Leu Leu Thr Glu Asp Lys Gln  
 145 150 155 160  
 Ile Arg Glu Ser Cys Asp Lys Gly Arg Asp Leu Phe Cys Ser Leu Leu  
 165 170 175  
 Asn Leu Pro Asp Glu Asp Tyr Cys Phe Pro Asn Val Leu His Asn Thr  
 180 185 190  
 Glu Leu Asn Asn Asn Leu Gly Ser Val Val Glu Asp Pro Glu Gly Cys  
 195 200 205  
 Ile Lys Leu Cys Leu Ile Glu Val Ala Asn Gly Leu Arg Asn Pro Val  
 210 215 220  
 Leu Met Leu His Ala Asn Asp Gly Thr His Arg Met Phe Val Ala Glu  
 225 230 235 240  
 Gln Ile Gly Phe Val Trp Val Tyr Leu Pro Asp Gly Ser Arg Leu Tyr  
 245 250 255  
 Glu Pro Phe Leu Asn Leu Arg Arg Thr Val Leu Ala Thr Pro Trp Leu  
 260 265 270  
 Gly Asp Glu Arg Gly Leu Leu Gly Met Ala Phe His Pro Lys Tyr Gln  
 275 280 285  
 Asn Asn Arg Lys Phe Tyr Val Tyr Tyr Ser Ile Met Asp Glu Tyr Arg  
 290 295 300  
 Asn Glu Lys Ile Arg Ile Ser Glu Phe Gln Val Glu Glu His Asp Ile  
 305 310 315 320  
 Asn Lys Ala Asp Pro Tyr Ser Glu Arg Arg Ile Leu Glu Ile Glu Glu  
 325 330 335  
 Pro Ala Ala Asn His Asn Gly Gly Gln Ile Leu Phe Gly Lys Asp Gly  
 340 345 350

49

Tyr Leu Tyr Ile Phe Thr Gly Asp Gly Gly Lys Ala Gly Asp Pro Phe  
 355 360 365

Gly Arg Phe Gly Asn Ala Gln Asn Lys Ser Val Leu Leu Gly Lys Val  
 370 375 380

Leu Arg Ile Asp Val Asp Gly Arg Arg Ala Asn Gly Lys Pro Tyr Gly  
 385 390 395 400

Ile Pro Ser Asp Asn Pro Phe Leu Ser Glu Arg Gly Ala Ala Pro Glu  
 405 410 415

Val His Ala Tyr Gly Val Arg Asn Met Trp Arg Cys Ser Val Asp Gln  
 420 425 430

Gly Asp Pro Val Thr Gly Arg Gly Lys Gly Arg Ile Phe Cys Gly Asp  
 435 440 445

Val Gly Gln Asn Arg Phe Gly Glu Asp Asp Ile Ile Val Ile Gly Gly  
 450 455 460

Asn Tyr Gly Trp Arg Ala Lys Glu Gly Phe Glu Cys Phe Asp Leu Lys  
 465 470 475 480

Leu Cys Gln Asn Ser Ser Leu Asp Asp Ile Leu Pro Ile Phe Ala Tyr  
 485 490 495

Gly His Gln Val Gly Lys Ser Val Thr Gly Gly Tyr Val Tyr Arg Gly  
 500 505 510

Cys Glu Ser Pro Asn Leu Asn Gly Val Tyr Ile Phe Gly Asp Phe Met  
 515 520 525

Asn Gly Arg Leu Met Ala Leu Gln Glu Asp Gly Val Thr Gly Thr Trp  
 530 535 540

Lys Lys Gln Asp Ile Cys Met Gly Asp Ser Thr Ile Cys Ala Phe Pro  
 545 550 555 560

Arg Leu Ile Asn Lys Tyr Ser Lys Phe Ile Ile Ser Phe Gly Glu Asp  
 565 570 575

Glu Ala Gly Glu Leu Leu Phe Leu Ser Thr Ser Gln Ala Ser Ala Tyr  
 580 585 590

Ser Pro Gln Gly Ser Ile Tyr Lys Leu Val Asp Pro Ser Arg Arg Ala  
 595 600 605

Ala Pro Gly Lys Cys Lys Tyr Lys Pro Val Pro Val Lys Thr Arg Ser  
 610 615 620

Lys Leu Val Pro Phe Ile Pro Lys Glu Lys Thr Val Leu Glu Ile Val  
 625 630 635 640

Asn Glu Ser Val Lys Pro Thr Lys Ala Pro Arg Lys Lys Thr Pro Thr  
 645 650 655

Lys Phe Pro Thr Lys Val Pro Pro Thr Pro Thr Lys Phe Pro Thr Lys

50

660	665	670
Val Pro Pro Thr Pro Thr Gln Phe Pro Thr Lys Val Pro Pro Ile Pro		
675	680	685
Thr Lys Val Pro Ser Lys Val Pro Pro Thr Pro Thr Gln Phe Pro Thr		
690	695	700
Lys Val Pro Pro Thr Pro Thr Lys Val Ser Thr Lys Val Leu Ser Thr		
705	710	715
Pro Thr Ile Ala His Thr Lys Val Ser Pro Thr Ser Thr Lys Leu Pro		
725	730	735
Ser Lys Ala Pro Ser Thr Gln Thr Met Val Pro Thr Lys Val His Pro		
740	745	750
Thr Pro Thr Lys Leu Pro Thr Lys Val Pro Pro Ile Thr Thr Lys Val		
755	760	765
Ser Asn Lys Val Leu Leu Thr Ser Pro Glu Leu Pro Thr Lys Val Pro		
770	775	780
Pro Thr Pro Thr Lys Leu Pro Thr Asn Ala Pro Pro Thr Ser Ile Leu		
785	790	795
Leu Ser Pro Thr Pro Ile Lys Leu Pro Thr Lys Ile Ser Leu Thr Leu		
805	810	815
Thr Ser Val Pro Ile Lys Asn Gln Leu Thr Ser Ala Lys Leu Leu Thr		
820	825	830
Thr Thr Leu Pro Ile Ser Thr Lys Arg Ala Thr Lys Leu Pro Ser Thr		
835	840	845
Ser Thr Ser Val Pro Ser Asn Thr Ser Cys Ile Leu Thr His Val Gln		
850	855	860
Pro Lys Met Leu Pro Thr Glu Thr Arg Val Pro Asn Lys Met Pro Pro		
865	870	875
Lys Pro Thr Arg Ile Pro Thr Met Ser Met Tyr Ile Thr Lys Lys Pro		
885	890	895
Pro Leu Lys Lys Asn Ser Ala Lys Lys Val Thr Asp Lys Arg Pro Thr		
900	905	910
Lys Ser Pro Lys Thr Thr Lys Pro Pro Lys Pro Pro Lys Ser Lys Thr		
915	920	925
Ser Val Val Asn Gln Pro Lys Lys Lys Glu Thr Lys Thr Gly Val Asn		
930	935	940
Asn Lys Thr Lys Asn Leu Pro Pro Lys Ala Lys Glu Pro Lys Lys Glu		
945	950	955
Lys Lys Thr Ile Lys Val Lys Gln Pro Val Ser His Tyr Phe Pro Pro		
965	970	975



Gln Lys Pro Lys Lys Gln Lys Ile Lys Lys Met Gln Lys Glu Gly Asn  
 980 985 990

Glu Lys Ser  
 995

<210> 49

<211> 700

<212> PRT

<213> Homo sapiens

<400> 49

Met Leu Lys Met Leu Ser Phe Lys Leu Leu Leu Leu Ala Val Ala Leu  
 1 5 10 15

Gly Phe Phe Glu Gly Asp Ala Lys Phe Gly Glu Arg Ser Glu Gly Ser  
 20 25 30

Gly Ala Arg Arg Arg Arg Cys Leu Asn Gly Asn Pro Pro Lys Arg Leu  
 35 40 45

Lys Arg Arg Asp Arg Arg Val Met Ser Gln Leu Glu Leu Leu Ser Gly  
 50 55 60

Gly Glu Ile Leu Cys Gly Gly Phe Tyr Pro Arg Val Ser Cys Cys Leu  
 65 70 75 80

Gln Ser Asp Ser Pro Gly Leu Gly Arg Leu Glu Asn Lys Ile Phe Ser  
 85 90 95

Ala Thr Asn Asn Ser Glu Cys Ser Arg Leu Leu Glu Glu Ile Gln Cys  
 100 105 110

Ala Pro Cys Ser Pro His Ser Gln Ser Leu Phe Tyr Thr Pro Glu Arg  
 115 120 125

Asp Val Leu Asp Gly Asp Leu Ala Leu Pro Leu Leu Cys Lys Asp Tyr  
 130 135 140

Cys Lys Glu Phe Phe Tyr Thr Cys Arg Gly His Ile Pro Gly Leu Leu  
 145 150 155 160

Gln Thr Thr Ala Asp Glu Phe Cys Phe Tyr Tyr Ala Arg Lys Asp Ala  
 165 170 175

Gly Leu Cys Phe Pro Asp Phe Pro Arg Lys Gln Val Arg Gly Pro Ala  
 180 185 190

Ser Asn Tyr Leu Gly Gln Met Glu Asp Tyr Glu Lys Val Gly Gly Ile  
 195 200 205

Ser Arg Lys His Lys His Asn Cys Leu Cys Val Gln Glu Val Met Ser  
 210 215 220

Gly Leu Arg Gln Pro Val Ser Ala Val His Ser Gly Asp Gly Ser His  
 225 230 235 240

Arg Leu Phe Ile Leu Glu Lys Glu Gly Tyr Val Lys Ile Leu Thr Pro  
 245 250 255  
 Glu Gly Glu Leu Phe Lys Glu Pro Tyr Leu Asp Ile His Lys Leu Val  
 260 265 270  
 Gln Ser Gly Ile Lys Gly Gly Asp Glu Arg Gly Leu Leu Ser Leu Ala  
 275 280 285  
 Phe His Pro Asn Tyr Lys Lys Asn Gly Lys Leu Tyr Val Ser Tyr Thr  
 290 295 300  
 Thr Asn Gln Glu Arg Trp Ala Ile Gly Pro His Asp His Ile Leu Arg  
 305 310 315 320  
 Val Val Glu Tyr Thr Val Ser Arg Lys Asn Pro His Gln Val Asp Val  
 325 330 335  
 Arg Thr Ala Arg Val Phe Leu Glu Val Ala Glu Leu His Arg Lys His  
 340 345 350  
 Leu Gly Gly Gln Leu Leu Phe Gly Pro Asp Gly Phe Leu Tyr Ile Ile  
 355 360 365  
 Leu Gly Asp Gly Met Ile Thr Leu Asp Asp Met Glu Glu Met Asp Gly  
 370 375 380  
 Leu Ser Asp Phe Thr Gly Ser Val Leu Arg Leu Asp Val Asp Thr Asp  
 385 390 395 400  
 Met Cys Asn Val Pro Tyr Ser Ile Pro Arg Ser Asn Pro His Phe Asn  
 405 410 415  
 Ser Thr Asn Gln Pro Pro Glu Val Phe Ala His Gly Leu His Asp Pro  
 420 425 430  
 Gly Arg Cys Ala Val Asp Arg His Pro Thr Asp Ile Asn Ile Asn Leu  
 435 440 445  
 Thr Ile Leu Cys Ser Asp Ser Asn Gly Lys Asn Arg Ser Ser Ala Arg  
 450 455 460  
 Ile Leu Gln Ile Ile Lys Gly Arg Asp Tyr Glu Ser Glu Pro Ser Leu  
 465 470 475 480  
 Leu Glu Phe Lys Pro Phe Ser Asn Gly Pro Leu Val Gly Gly Phe Val  
 485 490 495  
 Tyr Arg Gly Cys Gln Ser Glu Arg Leu Tyr Gly Ser Tyr Val Phe Gly  
 500 505 510  
 Asp Arg Asn Gly Asn Phe Leu Thr Leu Gln Gln Ser Pro Val Thr Lys  
 515 520 525  
 Gln Trp Gln Glu Lys Pro Leu Cys Leu Gly Ala Ser Ser Ser Cys Arg  
 530 535 540

53

Gly Tyr Phe Ser Gly His Ile Leu Gly Phe Gly Glu Asp Glu Leu Gly  
 545 550 555 560

Glu Val Tyr Ile Leu Ser Ser Ser Lys Ser Met Thr Gln Thr His Asn  
 565 570 575

Gly Lys Leu Tyr Lys Ile Val Asp Pro Lys Arg Pro Leu Met Pro Glu  
 580 585 590

Glu Cys Arg Val Thr Val Gln Pro Ala Gln Pro Leu Thr Ser Asp Cys  
 595 600 605

Ser Arg Leu Cys Arg Asn Gly Tyr Tyr Thr Pro Thr Gly Lys Cys Cys  
 610 615 620

Cys Ser Pro Gly Trp Glu Gly Asp Phe Cys Arg Ile Ala Lys Cys Glu  
 625 630 635 640

Pro Ala Cys Arg His Gly Gly Val Cys Val Arg Pro Asn Lys Cys Leu  
 645 650 655

Cys Lys Lys Gly Tyr Leu Gly Pro Gln Cys Glu Gln Val Asp Arg Asn  
 660 665 670

Val Arg Arg Val Thr Arg Ala Gly Ile Leu Asp Gln Ile Ile Asp Met  
 675 680 685

Thr Ser Tyr Leu Leu Asp Leu Thr Ser Tyr Ile Val  
 690 695 700

&lt;210&gt; 50

&lt;211&gt; 567

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

Thr Ser Thr Pro Pro Arg Ala Val Pro Leu Pro Lys Ser Ser Gln Ala  
 1 5 10 15

Ala His Gln Arg Asn Cys Asn Ser Gly Trp Ser Pro Gly Pro Ala Ser  
 20 25 30

Leu Gly Val Arg Gly Ser Val Cys Pro Ala Ile Cys Trp Trp His Leu  
 35 40 45

Ser Leu Leu Pro Pro Pro Ser Val Asn Pro Thr Leu Gln Lys Cys Ser  
 50 55 60

Ser Pro Gly Ala Ala Gln Glu Leu Ser Met Arg Pro Pro Gly Phe Arg  
 65 70 75 80

Asn Phe Leu Leu Leu Ala Ser Ser Leu Leu Phe Ala Gly Leu Ser Ala  
 85 90 95

Val Pro Gln Ser Phe Ser Pro Ser Leu Arg Ser Trp Pro Gly Ala Ala  
 100 105 110

54

Cys Arg Leu Ser Arg Ala Glu Ser Glu Arg Arg Cys Arg Ala Pro Gly  
 115 120 125  
 Gln Pro Pro Gly Ala Ala Leu Cys His Gly Arg Gly Arg Cys Asp Cys  
 130 135 140  
 Gly Val Cys Ile Cys His Val Thr Glu Pro Gly Met Phe Phe Gly Pro  
 145 150 155 160  
 Leu Cys Glu Cys His Glu Trp Val Cys Glu Thr Tyr Asp Gly Ser Thr  
 165 170 175  
 Cys Ala Gly His Gly Lys Cys Asp Cys Gly Lys Cys Lys Cys Asp Gln  
 180 185 190  
 Gly Trp Tyr Gly Asp Ala Cys Gln Tyr Pro Thr Asn Cys Asp Leu Thr  
 195 200 205  
 Lys Lys Lys Ser Asn Gln Met Cys Lys Asn Ser Gln Asp Ile Ile Cys  
 210 215 220  
 Ser Asn Ala Gly Thr Cys His Cys Gly Arg Cys Lys Cys Asp Asn Ser  
 225 230 235 240  
 Asp Gly Ser Gly Leu Val Tyr Gly Lys Phe Cys Glu Cys Asp Asp Arg  
 245 250 255  
 Glu Cys Ile Asp Asp Glu Thr Glu Glu Ile Cys Gly Gly His Gly Lys  
 260 265 270  
 Cys Tyr Cys Gly Asn Cys Tyr Cys Lys Ala Gly Trp His Gly Asp Lys  
 275 280 285  
 Cys Glu Phe Gln Cys Asp Ile Thr Pro Trp Glu Ser Lys Arg Arg Cys  
 290 295 300  
 Thr Ser Pro Asp Gly Lys Ile Cys Ser Asn Arg Gly Thr Cys Val Cys  
 305 310 315 320  
 Gly Glu Cys Thr Cys His Asp Val Asp Pro Thr Gly Asp Trp Gly Asp  
 325 330 335  
 Ile His Gly Asp Thr Cys Glu Cys Asp Glu Arg Asp Cys Arg Ala Val  
 340 345 350  
 Tyr Asp Arg Tyr Ser Asp Asp Phe Cys Ser Gly His Gly Gln Cys Asn  
 355 360 365  
 Cys Gly Arg Cys Asp Cys Lys Ala Gly Trp Tyr Gly Lys Lys Cys Glu  
 370 375 380  
 His Pro Gln Ser Cys Thr Leu Ser Ala Glu Glu Ser Ile Arg Lys Cys  
 385 390 395 400  
 Gln Gly Ser Ser Asp Leu Pro Cys Ser Gly Arg Gly Lys Cys Glu Cys  
 405 410 415  
 Gly Lys Cys Thr Cys Tyr Pro Pro Gly Asp Arg Arg Val Tyr Gly Lys

55

420                      425                      430

Thr Cys Glu Cys Asp Asp Arg Arg Cys Glu Asp Leu Asp Gly Val Val  
                  435                      440                      445

Cys Gly Gly His Gly Thr Cys Ser Cys Gly Arg Cys Val Cys Glu Arg  
                  450                      455                      460

Gly Trp Phe Gly Lys Leu Cys Gln His Pro Arg Lys Cys Asn Met Thr  
                  465                      470                      475                      480

Glu Glu Gln Ser Lys Asn Leu Cys Glu Ser Ala Asp Gly Ile Leu Cys  
                                  485                      490                      495

Ser Gly Lys Gly Ser Cys His Cys Gly Lys Cys Ile Cys Ser Ala Glu  
                                  500                      505                      510

Glu Trp Tyr Ile Ser Gly Glu Phe Cys Asp Cys Asp Asp Arg Asp Cys  
                                  515                      520                      525

Asp Lys His Asp Gly Leu Ile Cys Thr Gly Asn Gly Ile Cys Ser Cys  
                                  530                      535                      540

Gly Asn Cys Glu Cys Trp Asp Gly Trp Asn Gly Asn Ala Cys Glu Ile  
                                  545                      550                      555                      560

Trp Leu Gly Ser Glu Tyr Pro  
                                  565

<210> 51  
 <211> 29  
 <212> PRT  
 <213> Homo sapiens

<400> 51  
 Gly Lys Cys Asp Cys Gly Lys Cys Lys Cys Asp Gln Gly Trp Tyr Gly  
   1                                 5                                 10                                 15

Asp Ala Cys Gln Tyr Pro Thr Asn Cys Asp Leu Thr Lys  
                                  20                                 25

<210> 52  
 <211> 29  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Gly Gly His Gly Lys Cys Tyr Cys Gly Asn Cys Tyr Cys Lys Ala Gly  
   1                                 5                                 10                                 15

Trp His Gly Asp Lys Cys Glu Phe Gln Cys Asp Ile Thr  
                                  20                                 25

<210> 53  
 <211> 29

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 53

His Gly Gln Cys Asn Cys Gly Arg Cys Asp Cys Lys Ala Gly Trp Tyr  
1 5 10 15

Gly Lys Lys Cys Glu His Pro Gln Ser Cys Thr Leu Ser  
20 25

&lt;210&gt; 54

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 54

His Gly Thr Cys Ser Cys Gly Arg Cys Val Cys Glu Arg Gly Trp Phe  
1 5 10 15

Gly Lys Leu Cys Gln His Pro Arg Lys Cys Asn Met Thr  
20 25

&lt;210&gt; 55

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 55

Gly Asn Gly Ile Cys Ser Cys Gly Asn Cys Glu Cys Trp Asp Gly Trp  
1 5 10 15

Asn Gly Asn Ala Cys Glu Ile Trp Leu Gly Ser Glu Tyr  
20 25

&lt;210&gt; 56

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 56

Gly Asn Gly Ile Cys Ser Cys Gly Asn Cys Glu Cys Trp Asp Gly Trp  
1 5 10 15

Asn Gly Asn Ala Cys Glu Ile Trp Leu Gly Ser Glu Tyr  
20 25

&lt;210&gt; 57

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 57

Gly Asn Gly Ile Cys Ser Cys Gly Asn Cys Glu Cys Trp Asp Gly Trp  
1 5 10 15

Asn Gly Asn Ala Cys Glu Ile Trp Leu Gly Ser Glu Tyr  
                   20                  25

<210> 58

<211> 33

<212> PRT

<213> Homo sapiens

<400> 58

Glu Thr Tyr Asp Gly Ser Thr Cys Ala Gly His Gly Lys Cys Asp Cys  
   1                  5                  10                  15

Gly Lys Cys Lys Cys Asp Gln Gly Trp Tyr Gly Asp Ala Cys Gln Tyr  
                   20                  25                  30

Pro

<210> 59

<211> 34

<212> PRT

<213> Homo sapiens

<400> 59

Met Cys Lys Asn Ser Gln Asp Ile Ile Cys Ser Asn Ala Gly Thr Cys  
   1                  5                  10                  15

His Cys Gly Arg Cys Lys Cys Asp Asn Ser Asp Gly Ser Gly Leu Val  
                   20                  25                  30

Tyr Gly

<210> 60

<211> 31

<212> PRT

<213> Homo sapiens

<400> 60

Ile Asp Asp Glu Thr Glu Glu Ile Cys Gly Gly His Gly Lys Cys Tyr  
   1                  5                  10                  15

Cys Gly Asn Cys Tyr Cys Lys Ala Gly Trp His Gly Asp Lys Cys  
                   20                  25                  30

<210> 61

<211> 34

<212> PRT

<213> Homo sapiens

<400> 61

Lys Arg Arg Cys Thr Ser Pro Asp Gly Lys Ile Cys Ser Asn Arg Gly  
   1                  5                  10                  15

Thr Cys Val Cys Gly Glu Cys Thr Cys His Asp Val Asp Pro Thr Gly  
                   20                                  25                                  30

Asp Trp

<210> 62  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<400> 62  
 Asp Arg Tyr Ser Asp Asp Phe Cys Ser Gly His Gly Gln Cys Asn Cys  
   1                  5                                  10                                  15

Gly Arg Cys Asp Cys Lys Ala Gly Trp Tyr Gly Lys Lys Cys Glu His  
                   20                                  25                                  30

Pro Gln

<210> 63  
 <211> 33  
 <212> PRT  
 <213> Homo sapiens

<400> 63  
 Cys Gln Gly Ser Ser Asp Leu Pro Cys Ser Gly Arg Gly Lys Cys Glu  
   1                  5                                  10                                  15

Cys Gly Lys Cys Thr Cys Tyr Pro Pro Gly Asp Arg Arg Val Tyr Gly  
                   20                                  25                                  30

Lys

<210> 64  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Cys Glu Asp Leu Asp Gly Val Val Cys Gly Gly His Gly Thr Cys Ser  
   1                  5                                  10                                  15

Cys Gly Arg Cys Val Cys Glu Arg Gly Trp Phe Gly Lys Leu Cys  
                   20                                  25                                  30

<210> 65  
 <211> 32  
 <212> PRT  
 <213> Homo sapiens



59

&lt;400&gt; 65

Ser Ala Asp Gly Ile Leu Cys Ser Gly Lys Gly Ser Cys His Cys Gly  
 1 5 10 15

Lys Cys Ile Cys Ser Ala Glu Glu Trp Tyr Ile Ser Gly Glu Phe Cys  
 20 25 30

&lt;210&gt; 66

&lt;211&gt; 33

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

Cys Asp Lys His Asp Gly Leu Ile Cys Thr Gly Asn Gly Ile Cys Ser  
 1 5 10 15

Cys Gly Asn Cys Glu Cys Trp Asp Gly Trp Asn Gly Asn Ala Cys Glu  
 20 25 30

Ile

&lt;210&gt; 67

&lt;211&gt; 769

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 67

Met Cys Gly Ser Ala Leu Ala Phe Phe Thr Ala Ala Phe Val Cys Leu  
 1 5 10 15

Gln Asn Asp Arg Arg Gly Pro Ala Ser Phe Leu Trp Ala Ala Trp Val  
 20 25 30

Phe Ser Leu Val Leu Gly Leu Gly Gln Gly Glu Asp Asn Arg Cys Ala  
 35 40 45

Ser Ser Asn Ala Ala Ser Cys Ala Arg Cys Leu Ala Leu Gly Pro Glu  
 50 55 60

Cys Gly Trp Cys Val Gln Glu Asp Phe Ile Ser Gly Gly Ser Arg Ser  
 65 70 75 80

Glu Arg Cys Asp Ile Val Ser Asn Leu Ile Ser Lys Gly Cys Ser Val  
 85 90 95

Asp Ser Ile Glu Tyr Pro Ser Val His Val Ile Ile Pro Thr Glu Asn  
 100 105 110

Glu Ile Asn Thr Gln Val Thr Pro Gly Glu Val Ser Ile Gln Leu Arg  
 115 120 125

Pro Gly Ala Glu Ala Asn Phe Met Leu Lys Val His Pro Leu Lys Lys

130		135	60	140
Tyr 145	Pro Val Asp Leu	Tyr 150	Tyr Leu Val Asp 155	Val Ser Ala Ser Met His 160
Asn 165	Asn Ile Glu Lys Leu	Asn 170	Ser Val Gly Asn Asp Leu Ser	Arg Lys 175
Met 180	Ala Phe Phe Ser Arg Asp Phe Arg	Leu 185	Gly Phe Gly Ser Tyr Val	190
Asp 195	Lys Thr Val Ser Pro Tyr Ile Ser	Ile 200	His Pro Glu Arg Ile His	205
Asn 210	Gln Cys Ser Asp Tyr Asn Leu Asp Cys Met	215	Pro Pro His Gly Tyr	220
Ile 225	His Val Leu Ser Leu Thr Glu Asn Ile Thr Glu Phe Glu Lys Ala	230	235	240
Val 245	His Arg Gln Lys Ile Ser Gly Asn Ile Asp Thr Pro Glu Gly Gly	250	255	
Phe 260	Asp Ala Met Leu Gln Ala Ala Val Cys Glu Ser His Ile Gly Trp	265	270	
Arg 275	Lys Glu Ala Lys Arg Leu Leu Leu Val Met Thr Asp Gln Thr Ser	280	285	
His 290	Leu Ala Leu Asp Ser Lys Leu Ala Gly Ile Val Val Pro Asn Asp	295	300	
Gly 305	Asn Cys His Leu Lys Asn Asn Val Tyr Val Lys Ser Thr Thr Met	310	315	320
Glu 325	His Pro Ser Leu Gly Gln Leu Ser Glu Lys Leu Ile Asp Asn Asn	330	335	
Ile 340	Asn Val Ile Phe Ala Val Gln Gly Lys Gln Phe His Trp Tyr Lys	345	350	
Asp 355	Leu Leu Pro Leu Leu Pro Gly Thr Ile Ala Gly Glu Ile Glu Ser	360	365	
Lys 370	Ala Ala Asn Leu Asn Asn Leu Val Val Glu Ala Tyr Gln Lys Leu	375	380	
Ile 385	Ser Glu Val Lys Val Gln Val Glu Asn Gln Val Gln Gly Ile Tyr	390	395	400
Phe 405	Asn Ile Thr Ala Ile Cys Pro Asp Gly Ser Arg Lys Pro Gly Met	410	415	
Glu 420	Gly Cys Arg Asn Val Thr Ser Asn Asp Glu Val Leu Phe Asn Val	425	430	
Thr 435	Val Thr Met Lys Lys Cys Asp Val Thr Gly Gly Lys Asn Tyr Ala	440	445	

Ile Ile Lys Pro Ile Gly Phe Asn Glu Thr Ala Lys Ile His Ile His  
 450 455 460  
 Arg Asn Cys Ser Cys Gln Cys Glu Asp Asn Arg Gly Pro Lys Gly Lys  
 465 470 475 480  
 Cys Val Asp Glu Thr Phe Leu Asp Ser Lys Cys Phe Gln Cys Asp Glu  
 485 490 495  
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 500 505 510  
 Ser His Lys Asp Gln Pro Val Cys Ser Gly Arg Gly Val Cys Val Cys  
 515 520 525  
 Gly Lys Cys Ser Cys His Lys Ile Lys Leu Gly Lys Val Tyr Gly Lys  
 530 535 540  
 Tyr Cys Glu Lys Asp Asp Phe Ser Cys Pro Tyr His His Gly Asn Leu  
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 Cys Ala Gly His Gly Glu Cys Glu Ala Gly Arg Cys Gln Cys Phe Ser  
 565 570 575  
 Gly Trp Glu Gly Asp Arg Cys Gln Cys Pro Ser Ala Ala Ala Gln His  
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 595 600 605  
 Cys Gly Arg Cys Glu Cys Thr Asp Pro Arg Ser Ile Gly Arg Phe Cys  
 610 615 620  
 Glu His Cys Pro Thr Cys Tyr Thr Ala Cys Lys Glu Asn Trp Asn Cys  
 625 630 635 640  
 Met Gln Cys Leu His Pro His Asn Leu Ser Gln Ala Ile Leu Asp Gln  
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 Cys Lys Thr Ser Cys Ala Leu Met Glu Gln Gln His Tyr Val Asp Gln  
 660 665 670  
 Thr Ser Glu Cys Phe Ser Ser Pro Ser Tyr Leu Arg Ile Phe Phe Ile  
 675 680 685  
 Ile Phe Ile Val Thr Phe Leu Ile Gly Leu Leu Lys Val Leu Ile Ile  
 690 695 700  
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 705 710 715 720  
 Asp Tyr Arg Val Ser Ala Ser Lys Lys Asp Lys Leu Ile Leu Gln Ser  
 725 730 735  
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AATAACAGAG GGACTTGTGT ATGTGGTGAA TGTACCTGTC ACGATGTTGA TCCGACTGGG 180  
GACTGGGGAG ATATTCATGG GGACACCTGT GAATGTGATG AGAGGGACTG TAGAGCTGTC 240  
TATGACCGAT ATTCTGATGA CTTCTGTTCA GGTCATGGAC AGTGTAAATG CGGAAGATGT 300  
GACTGCAAAG CAGGCTGGTT ATGGGAAGAA GTGTGAGCAC CCACAGTCCT GCACGCTGTC 360  
AGCTGAGGAG AGCATCAGGA AGTGCCAAGG AAGCTCGGAT CTGCCCTTGCT CTGGGAAGGG 420  
TAAATGTGAA TGTGGCAAAT GCACNTGGTA TCCTCCAGGN GNTCCGCCGG GTGTATNGGC 480  
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 ATGAAATCCG AGTACCTATT AGAAATGAAG TTATGCAAAT TTAGATGCAA ATAACATTAG 180  
 AAAAAAAGA TTCTTCCATA ATTAACATAA GTGGTTCCTA ACGAGAGCAA TTTTTCACC 240  
 CAAAAGTCAT TTGGCAANAT CTACAGACCA TTTTGTGATT TCACACTGGG GTCGGGTAGG 300  
 ANGTATGCTG CCAGACATTT NGGTGGGGTA GAGGGCCNGG GATGCTGCNN GGCNTCCNC 360  
 CNNTTGTTC AGGCCGGNCC CCCCANNNAA GGGANTTTTT NCCCGGCCCC AAATGGCCCA 420  
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69

CATTTNTTCT GCTGAGGAGT GGTATATTTT TGGGGAGTTC TGTGAACTGT GAATGACACA 180  
GNACTGCGAC ANACATGGAT GGTCTCATTT GTACAGGGAA TGGAATATGT AGCTGTGGGA 240  
AACTGTGNAA TGCTGGGGAT GGATGGGAAT GGGAAATGCA TGTGAAAATC TGGGCTTGGG 300  
CTCCAGAATA TCCCTTTAAC CATTTACATG AGGAGAGGGT CTTGGATTCT TAATTTTTTC 360  
CTGGGGGGCCN TTAGGGNCCN TTAAATGNC GGGGGGAANC CTGTTNTNTT TNCNCCCTGG 420  
GGGNCGGTTT AAAAAGCCCC NTGNNTNTTT TTCCCTTTNC GGANTNNNGG GTNAAAACCN 480  
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&lt;211&gt; 495

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TGNAATCCG NGTNACCTAT TAGAAATGGG TTATGCANAT TTAGATGCAA ATAACATTAG 180  
AAAAAAAAGA TTCTTCCATA ATTAACATAA GTGGTTCCTA ACGNGAGCAA TTTTTCNCC 240  
CTNAAGTCAT TTGGCAANTC TACAGACNAT TTTGGTTGTC ACACTGGGTC GCGTAGGAAG 300  
GTATGCTGGC AGNCATTTNG TGGGTANAGG GCCCTGGNNT GCTGTTGAAG CATCCCCNAG 360  
TGTANCAGGN NCGNGCNCCA NACCANGGGG NTTNATCCCN GCCCCAANTG CCCATGGGGG 420  
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NGCAAGTGTG ACCAGGGATG GTATGGGGAT GCTTGCCAGT ACCCAACTAA CTGTGACTTG 180

ACAANGAAGA AAAGTAACCA AATGTGGCAA GAATTCACAA GACATCATCT GCTCTAATTC 240

AGGTACATGT CACTGTGGCA GTGTAANTGT GATAGATTCA GATGGAANTG GGACNTGGTG 300

TATGGGNNA TTTGTGG 317

&lt;210&gt; 73

&lt;211&gt; 36

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

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Ala	Gly	Trp	His	Gly	Asp	Lys	Cys	Glu	Phe	Gln	Cys	Asp	Ile	Thr	Pro
			20					25					30		

Trp	Glu	Ser	Lys
			35

&lt;210&gt; 74

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens



75

&lt;400&gt; 74

Gly Gln Pro Pro Gly Ala Ala Leu Cys His Gly Arg Gly Arg Cys Asp  
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Cys Gly Val Cys Ile Cys His Val Thr Glu Pro Gly Met Phe Phe Gly  
 20 25 30

Pro Leu Cys  
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&lt;210&gt; 75

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 75

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Leu Ala His His Leu Phe Met Val Thr Ala Cys Arg Asp Pro Asp Tyr  
 20 25 30

Gly Thr Leu Ile Gln Glu Leu Cys Leu Ser Arg Phe Lys Glu Asn Met  
 35 40 45

Glu Thr Ile Gly Lys Thr Leu Trp Cys Asp Trp Gly Lys Thr Ile Gln  
 50 55 60

Ser Tyr Gly Glu Leu Thr Tyr Cys Thr Lys His Val Ala His Thr Ile  
 65 70 75 80

Gly Cys Phe Trp Pro Asn Pro Glu Val Asp Arg Phe Phe Ile Ala Val  
 85 90 95

His His Arg Tyr Phe Ser Lys Cys Pro Ile Ser Gly Arg Ala Leu Arg  
 100 105 110

Asp Pro Pro Asn Ser Ile Leu Cys Pro Phe Ile Ala Leu Pro Ile Thr  
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Glu Gly Ile Val  
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<220>  
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77

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (424)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (448)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (454)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (459)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (465)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (472)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (485)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (487)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (498)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (501)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 76

AATTCGGCAN AGCTGGTCAT GGGCAGACCC CTCCCTTCCT GGGCTGACCT GCTCCCTCGA 60

GGCCAGCCTG CTCCCTGGCT GAGGCTCAGG CTATCCGCCC AAGCTCTTTG CTCATTCTAG 120

GGCCAGTGGA GGAAAATGTG ATAAGGCCAG AGCTTGTGTG CTGGGCAAGN AAATCACCTG 180

CTGCATCCTG TGCTCCGCAG CTGGGCCGNA GCCTCTGCCC GCAGTTTCTA TGCTGTTTCT	240
TAGCACAGAA TCCAGCCTAG CCTTAGCCGC AGTCTAGGCC CTGNTTGGGA CTAGGACTCC	300
TTGNTTGACC CCATCTTTGG TTCCTGCCTG GTTCCTGNAA CAGCCCNAGT TCTGGNTAAA	360
TCCAGGNAGA AAGTTAGGNA AGGGTTTTTG GAAGAAGTTC CGTGNTTTGA ACTTNGGAGN	420
CTTNTTGGTG GGAAGAAAAT TGGAAAGNTT GGGNAGGANA AAGGNGGGTT TNGGGGTTTC	480
AAGGNGNATG GGGGGTTNAA NA	502

&lt;210&gt; 77

&lt;211&gt; 505

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (11)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (14)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (67)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (208)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (247)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (250)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (267)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (299)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (320)

<223> n equals a,t,g, or c

<220>

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<222> (321)

<223> n equals a,t,g, or c

<220>

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<222> (339)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (349)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (364)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (384)

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<220>

<221> SITE

<222> (386)

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<220>

<221> SITE

<222> (406)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (417)

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<220>

<221> SITE

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<223> n equals a,t,g, or c

<220>

<221> SITE

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<220>  
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<220>  
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<220>  
<221> SITE  
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<223> n equals a,t,g, or c

<220>  
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<222> (484)  
<223> n equals a,t,g, or c

<220>  
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<222> (488)  
<223> n equals a,t,g, or c

<220>  
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<222> (490)  
<223> n equals a,t,g, or c

<220>  
<221> SITE  
<222> (497)  
<223> n equals a,t,g, or c

<220>  
<221> SITE  
<222> (504)  
<223> n equals a,t,g, or c

<400> 77  
GAATTCGGCA NAGNCTGCGG CCGGCCAGCC ATGGAGACTG GAGCGCTGCG ACGCCGCAAC 60  
TTCTCCNGTT GCTGCTGCTG CTCTGCGGTG GGTGTCCCAG AGCAGGCGGC TGCAACGAGA 120  
CAGGCATGTT GGAGAGGCTG CCCCTGTGTG GGAAAGGCTT TCGCAGACAT GATGGGCAAG 180  
GTGGACGTCT GGGAAATGGTG CAACTGTNCC GAGTTCATCG TGTACTATGA GAAGTTTCAC 240  
CAACTGNCAN CGAGATGGAG GCCAATNTCG TGGGCTGCTT ACTGGCCCAA CCCCCTGGNC 300  
CCAGGGCTTT CATCACCGN NTCCACAGGC AGTTTTTTNT TCCAACGNA ACGTGGACAA 360  
GGTNCATTTG GAGGGACCCC CCANANGAGG TTTTAATCCG TTGATNGTTA TTACCGNGGT 420

TTTNATTTGG GCATGGTTGN CTGGTNGNTT TGGGGAAAAA GGAACGNAAA GTTNTTTTAG 480

GGTNCCGNTN AATTGGNTTG GGTNA 505

<210> 78

<211> 101

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (101)

<223> n equals a,t,g, or c

<400> 78

AATTCGGCAC GAGGTGAGGG GCCCTCTGGA ATGGCATCCC ATGAGCTTGT GGCCTCTATC 60

TGCTACCATC TGTGTTTAT CTGAGTAAAG TTACCTTACT N 101

<210> 79

<211> 322

<212> PRT

<213> Homo sapiens

<400> 79

Met Gly Met Leu Ala Arg Val Ala Leu Gly Leu Ile Ile Ile Asp Ala  
1 5 10 15

Val Leu Ala Ala Pro Thr Thr Glu Leu Phe Asn Tyr Asp Ser Glu Val  
20 25 30

Tyr Asp Ala Ile Leu Glu Asp Thr Gly Thr Phe Tyr Asn Tyr Glu His  
35 40 45

Ile Pro Asp Asn His Val Glu Asn Glu Lys Val Ser Glu Arg Leu Ser  
50 55 60

Gly Asn Arg Glu Leu Leu Thr Pro Gly Pro Gln Leu Gly Asp Asn Gln  
65 70 75 80

Asp Glu Asp Lys Asp Glu Glu Ser Thr Pro Arg Leu Ile Asp Gly Ser  
85 90 95

Ser Pro Gln Glu Pro Glu Phe Pro Gly Leu Leu Gly Pro His Thr Asn  
100 105 110

Glu Asp Phe Pro Thr Cys Leu Leu Cys Thr Cys Ile Ser Thr Thr Val  
115 120 125

Tyr Cys Asp Asp His Glu Leu Asp Ala Ile Pro Pro Leu Pro Lys Lys  
130 135 140

Thr Thr Tyr Phe Tyr Ser Arg Phe Asn Arg Ile Lys Lys Ile Asn Lys

145                      150                      82                      155                      160  
 Asn Asp Phe Ala Ser Leu Asn Asp Leu Lys Arg Ile Asp Leu Thr Ser  
                                  165                                   170                                   175  
 Asn Leu Ile Ser Glu Ile Asp Glu Asp Ala Phe Arg Lys Leu Pro His  
                                  180                                   185                                   190  
 Leu Gln Glu Leu Val Leu Arg Asp Asn Lys Ile Lys Gln Leu Pro Glu  
                                  195                                   200                                   205  
 Leu Pro Asn Thr Leu Thr Phe Ile Asp Ile Ser Asn Asn Arg Leu Gly  
                                  210                                   215                                   220  
 Arg Lys Gly Ile Lys Gln Glu Ala Phe Lys Asp Met Tyr Asp Leu His  
                                  225                                   230                                   235                                   240  
 His Leu Tyr Ile Thr Asp Asn Ser Leu Asp His Ile Pro Leu Pro Leu  
                                  245                                   250                                   255  
 Pro Glu Ser Leu Arg Ala Leu His Leu Gln Asn Asn Asp Ile Leu Glu  
                                  260                                   265                                   270  
 Met His Glu Asp Thr Phe Cys Asn Val Lys Asn Leu Thr Tyr Val Arg  
                                  275                                   280                                   285  
 Lys Ala Leu Glu Asp Ile Arg Leu Asp Gly Asn Pro Ile Asn Leu Ser  
                                  290                                   295                                   300  
 Arg Thr Pro Gln Ala Tyr Met Cys Leu Pro Arg Leu Pro Ile Gly Ser  
                                  305                                   310                                   315                                   320  
 Phe Ile

<210> 80  
 <211> 435  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> SITE  
 <222> (85)  
 <223> n equals a,t,g, or c

<220>  
 <221> SITE  
 <222> (248)  
 <223> n equals a,t,g, or c

<400> 80  
 GGCAGAGCCA CCTTCTGGA AGCTGCAGGG CTCTCCATCC AGGATCCAGA AGCATTGAAG 60  
 GGGACCAGCC GCTGAAGGGA TTCTNAGTCC CATCTGACTC CCCATGAGGC TCCTGGCTTT 120  
 CCTGAGTCTG CTGGCCTTGG TGCTGCAGGA GACAGGGACA GCTTCTCTCC CAAGGAAGGA 180



83

GAGGAAGAGG AGAGAGGAGC AGATGCCCAG GGAAGGCGAT TCCTTTGAAG TTCTGCCTCT 240  
 GCGGAATNAT GTCCTGAACC CAGACAATA TGGTGAAGTC ATTGACCTGA GCAACTATGA 300  
 GGAGCTCACA GATTATGGGG ACCAACTCCC CGAGGTTAAG GTGACTAGCC TCGCTCCTGC 360  
 AACCAGCATC AGTCCCGCCA AGAGCACTAC GGCTCCAGGG ACAACCTCGT CAAACCCAC 420  
 GGATGACCCA GACCT 435

<210> 81  
 <211> 449  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> SITE  
 <222> (57)  
 <223> n equals a,t,g, or c

<220>  
 <221> SITE  
 <222> (98)  
 <223> n equals a,t,g, or c

<220>  
 <221> SITE  
 <222> (391)  
 <223> n equals a,t,g, or c

<220>  
 <221> SITE  
 <222> (433)  
 <223> n equals a,t,g, or c

<400> 81  
 GACAGCCTCC ACCAGAGTCC CCACCTTTTT GGAAGCTGCA GGGCTCTCCA TCCAGGNTCC 60  
 AGAAGCATTG AAGGGGACCA GCCGCTGAAG GGATTCTNAG TCCCATCTGA CTCCCCATGA 120  
 GGCTCCTGGC TTTCCTGAGT CTGCTGGCCT TGGTGTCTGCA GGAGACAGGG ACAGCTTCTT 180  
 TCCCAAGGAA GGAGAGGAAG AGGAGAGAGG AGCAGATGCC CAGGGAAGGC GATTCCTTTG 240  
 AAGTTCTGCC TCTGCGGAAT GATGTCTCTGA ACCCAGACAA CTATGGTGAA GTCATTGACC 300  
 TGAGCAACTA TGAGGAGCTC ACAGATTATG GGGACCAACT CCCCAGGTT AAGGTGACTA 360  
 GCCTCGCTCC TGCAACCAGC ATCAGTCCCG NCAAGAGCAC TACGGGCTTC AGGGGACAAC 420  
 CTCGTCAAAC CCNACGGTGA CCAGACCTA 449

<210> 82  
 <211> 331

<212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> SITE  
 <222> (29)  
 <223> n equals a,t,g, or c

<220>  
 <221> SITE  
 <222> (70)  
 <223> n equals a,t,g, or c

<220>  
 <221> SITE  
 <222> (152)  
 <223> n equals a,t,g, or c

<400> 82  
 CTGGAAGCTG CAGGGCTCTC CATCCAGGNT CCAGAAGCAT TGAAGGGGAC CAGCCGCTGA 60  
 AGGGATTCTN AGTCCCATCT GACTCCCCAT GAGGCTCCTG GCTTTCCTGA GTCTGCTGGC 120  
 CTTGGTGCTG CAGGAGACAG GGACAGCTTC TNTCCCAAGG AAGGAGAGGA AGAGGAGAGA 180  
 GGAGCAGATG CCCAGGGAAG GCGATTCCTT TGAAGTTCTG CCTCTGCGGA ATGATGTCCT 240  
 GAACCCAGAC AACTATGGTG AAGTCATTGA CCTGAGCAAC TATGAGGAGC TCACAGATTA 300  
 TGGGGACCAA CTCCCCGAGG TTAAGGTGAC T 331

<210> 83  
 <211> 280  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> SITE  
 <222> (19)  
 <223> n equals a,t,g, or c

<220>  
 <221> SITE  
 <222> (58)  
 <223> n equals a,t,g, or c

<220>  
 <221> SITE  
 <222> (115)  
 <223> n equals a,t,g, or c

<400> 83  
 CTGGCTTTCC TGAGTCTGNT GGCCTTGGTG CTGCAGGAGA CAGGGACAGC TTCTTTTNCA 60  
 AGGAAGGAGA GGAAGAGGAG AGAGGAGCAG ATGCCCAGGG AAGGCGATTC CTTTNAAGTT 120

85

CTGCCTCTGC GGAATGATGT CCTGAACCCA GACAACTATG GTGAAGTCAT TGACCTGAGC 180  
AACTATGAGG AGCTCACAGA TTATGGGGAC CAACTCCCCG AGGTAAAGGT GACTAGCCTC 240  
GCTCCTGCAA CCAGCATCAG TCCCGCCAAG AGCACTACGG 280

<210> 84  
<211> 211  
<212> DNA  
<213> Homo sapiens

<220>  
<221> SITE  
<222> (93)  
<223> n equals a,t,g, or c

<400> 84  
CTTGGACCAG CGGGCATCAC ATTCTCCAGC AGCCGCCATC TCACACGCCT CCCTCCTGTG 60  
GCCGCCGGCA GCATGGACAA AGGTCTCCAT GCNNGGGGAG GAGGCCTGCT TCTTTCCCCA 120  
CAGCTCTCAC GTCTCCCTTC TCCCTGCGGG TGACAAAGAA GCCCAAGGAC CACCTCCTTC 180  
CTGCCTCATTT GTAATAAAAT TCCCCACACT G 211

<210> 85  
<211> 208  
<212> DNA  
<213> Homo sapiens

<220>  
<221> SITE  
<222> (56)  
<223> n equals a,t,g, or c

<220>  
<221> SITE  
<222> (117)  
<223> n equals a,t,g, or c

<220>  
<221> SITE  
<222> (140)  
<223> n equals a,t,g, or c

<400> 85  
CTGGATGGCA ACCCCATCAA CCTCAGCCTC TTCCCCAGCG CCTACTTCTG CCTGCNTCGG 60  
CTCCCCATCG GCCGCTTCAC GTAGCTCGGA GCCCTTCCAC TCCTCCCAGG TCATCTNTTG 120  
GACCAGCGGG CATCACATTN TCCAGCAGCC GCCATCTCAC ACGCCTCCCT CCTGTGGCCG 180  
CCGGCAGCAT GGACAAAGGT CTCCATGC 208

<210> 86  
<211> 73  
<212> DNA  
<213> Homo sapiens

<400> 86  
CGACCCACGC GTCCGCCGCC TTCGGCTTCC CCTTCTGCCA AGAGCCCTGA GCCACTCACA 60  
GCACGACCAG AGA 73

<210> 87  
<211> 305  
<212> DNA  
<213> Homo sapiens

<400> 87  
GTATGGAATG GGGTGGGAAC CCCTGCCTCT CACACTGGGG AGGGACCCTG GGGACAGCCT 60  
ATGGGCTGAG CAGAGAGGGC TCTCAGGGAC CCCTGCAGCA CAAGAATCTC CCACCACGGT 120  
CTCTGTCCCA GCCCTGACTC AGAAGCCTGA TGTCTACATC CCCGAGACCC TGGAGCCCCGG 180  
GCAGCCGGTG ACGGTCATCT GTGTGTTTAA CTGGGCCTTT GAGGAATGTC CACCCCCTTC 240  
TTTCTCCTGG ACGGGGGCTG CCCTCTCCTC CCAAGGAACC AAACCAACGA CCTCCCCTT 300  
CTCAG 305

<210> 88  
<211> 175  
<212> DNA  
<213> Homo sapiens

<400> 88  
ATCCTCCAGA GAACCTGAGA GTGATGGTTT CCCAAGCAAA CAGGACAGGT AGGAAAGGGG 60  
ACAGAGGAGC CAAGGCCTCT CAGTGCCGAA TTGGGGGCCC AGGAGTCTGG AGGGTCCCCA 120  
CGCAGGAGGG TCCCTGAGCC CTGAGCTGCT CATCGATTCT GCCTCTTCCT TCCCT 175

<210> 89  
<211> 72  
<212> DNA  
<213> Homo sapiens

<400> 89  
GTGAGTGGGG GAAAGGGGAC ACCTGGGTCC CAGGAAGGGG ACCCTGCTGA GTCCTGTCCT 60  
CCCTCCCCTC AG 72

<210> 90  
 <211> 421  
 <212> DNA  
 <213> Homo sapiens

<400> 90  
 CTGGCCCCCT GGCTCAGAAG CGGAATCAGA AAGCCACACC AAACAGTCCT CGGACCCCTC 60  
 TTCCACCAGG TGCTCCCTCC CCAGAATCAA AGAAGAACCA GAAAAAGCAG TATCAGTTGC 120  
 CCAGTTTCCC AGAACCCAAA TCATCCACTC AAGCCCCAGA ATCCCAGGAG AGCCAAGAGG 180  
 AGCTCCATTA TGCCACGCTC AACTTCCCAG GCGTCAGACC CAGGCCTGAG GCCCGGATGC 240  
 CCAAGGGCAC CCAGGCGGAT TATGCAGAAG TCAAGTTCCA ATGAGGGTCT CTTAGGCTTT 300  
 AGGACTGGGA CTTCGGCTAG GGAGGAAGGT AGAGTAAGAG GTTGAAGATA ACAGAGTGCA 360  
 AAGTTTCCTT CTCTCCCTCT CTCTCTCTCT TTCTCTCTCT CTCTCTCTTT CTCTCTCTTT 420  
 T 421

<210> 91  
 <211> 964  
 <212> DNA  
 <213> Homo sapiens

<400> 91  
 AAAAAACAT CTGGCCAGGG CACAGTGGCT CACGCCTGTA ATCCCAGCAC TTTGGGAGGT 60  
 TGAGGTGGGC AGATCGCCTG AGGTGGGGAG TTCGAGACCA GCCTGGCCAA CTTGGTGAAA 120  
 CCCCCTCTCT ACTAAAAATA CAAAAATTAG CTGGGCATGG TGGCAGGCGC CTGTAATCCT 180  
 ACTACTTGGG AAGCTGAGGC AGGAGAATCA CTTGAACCTG GGAGACGGAG GTTGCAGTGA 240  
 GCCAAGATCA CACCATTGCA CGCCAGCTTG GGCAACAAAG CGAGACTCCA TCTCAAAAAA 300  
 AAAATCCTCC AAATGGGTG GGTGTCTGTA ATCCCAGCAC TTTGGGAGGC TAAGGTGGGT 360  
 GGATTGCTTG AGCCCAGGAG TTCGAGACCA GCCTGGGCAA CATGGTGAAA CCCCATCTCT 420  
 ACAAAAAATA CAAAACATAG CTGGGCTTGG TGGTGTGTGC CTGTAGTCCC AGCTGTCAGA 480  
 CATTTAAACC AGAGCAACTC CCATCTGGAA TGGGAGCTGA ATAAAATGAG GCTGAGACCT 540  
 ACTGGGCTGC CATTCTCAGA CAGTGGAGGC CATTCCTAAGT CACAGGATGA GACAGGAGGT 600  
 CCGTACAAGA TACAGGTCAT AAAGACTTTG CTGATAAAAC AGATTGCAGT AAAGAAGCCA 660  
 ACCAAATCCC ACCAAAACCA AGTTGGCCAC GAGAGTGACC TCTGGTCGTC CTCAGTGCTA 720  
 CACTCCTGAC AGCACCATGA CAGTTTACAA ATGCCATGGC AACATCAGGA AGTTACCCGA 780

88

TATGTCCCAA AAGGGGGAGG AATGAATAAT CCACCCCTTG TTTAGCAAAT AAGCAAGAAA 840  
 TAACCATAAA AGTGGGCAAC CAGCAGCTCT AGGCGCTGCT CTTGTCTATG GAGTAGCCAT 900  
 TCTTTTGTTT CTTTACTTTC TTAATAAACT TGCTTTCACC TTAAAAAAAA AAAAAAAAAA 960  
 AAAA 964

<210> 92  
 <211> 364  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 92

Met Pro Leu Leu Leu Leu Leu Pro Leu Leu Trp Ala Gly Ala Leu Ala  
 1 5 10 15  
 Met Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln  
 20 25 30  
 Glu Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro  
 35 40 45  
 Tyr Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly  
 50 55 60  
 Ala Ile Ile Ser Gly Asp Ser Pro Val Ala Thr Asn Lys Leu Asp Gln  
 65 70 75 80  
 Glu Val Gln Glu Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Pro  
 85 90 95  
 Ser Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp  
 100 105 110  
 Asn Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser  
 115 120 125  
 Tyr Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg  
 130 135 140  
 Pro Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn  
 145 150 155 160  
 Leu Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile  
 165 170 175  
 Phe Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr  
 180 185 190  
 His Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr  
 195 200 205  
 Asn Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu  
 210 215 220

89

Arg Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr  
 225 230 235 240  
 Gly Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly  
 245 250 255  
 Val Val His Gly Ala Ile Gly Gly Ala Gly Val Thr Ala Leu Leu Ala  
 260 265 270  
 Leu Cys Leu Cys Leu Ile Phe Phe Ile Val Lys Thr His Arg Arg Lys  
 275 280 285  
 Ala Ala Arg Thr Ala Val Gly Arg Asn Asp Thr His Pro Thr Thr Gly  
 290 295 300  
 Ser Ala Ser Pro Lys His Gln Lys Lys Ser Lys Leu His Gly Pro Thr  
 305 310 315 320  
 Glu Thr Ser Ser Cys Ser Gly Ala Ala Pro Thr Val Glu Met Asp Glu  
 325 330 335  
 Glu Leu His Tyr Ala Ser Leu Asn Phe His Gly Met Asn Pro Ser Lys  
 340 345 350  
 Asp Thr Ser Thr Glu Tyr Ser Glu Val Arg Thr Gln  
 355 360

&lt;210&gt; 93

&lt;211&gt; 397

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (19)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (68)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (148)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (262)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (323)

&lt;223&gt; n equals a,t,g, or c

<220>  
 <221> SITE  
 <222> (361)  
 <223> n equals a,t,g, or c

<220>  
 <221> SITE  
 <222> (386)  
 <223> n equals a,t,g, or c

<220>  
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 <222> (388)  
 <223> n equals a,t,g, or c

<220>  
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 <222> (390)  
 <223> n equals a,t,g, or c

<220>  
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 <222> (392)  
 <223> n equals a,t,g, or c

<220>  
 <221> SITE  
 <222> (394)  
 <223> n equals a,t,g, or c

<400> 93  
 GGCAGAGTGG CCCCCTGGNT CAGAAGCGGA ATCAGAAAGC CACACCAAAC AGTCCTCGGA 60  
 CCCCTCTNCC ACCAGGTGCT CCCTCCCCAG AATCAAAGAA GAACCAGAAA AAGCAGTATC 120  
 AGTTGCCCAG TTTCCCAGAA CCCAAATNAT CCACTCAAGC CCCAGAATCC CAGGAGAGCC 180  
 AAGAGGAGCT CCATTATGCC ACGCTCAACT TCCCAGGCGT CAGACCCAGG CCTGAGGCCG 240  
 GTATGCCCAA GGGCACCCAG GNGGATTATG CAGAAGTCAA GTTCCAATGA GGGTCTCTTA 300  
 GGCTTTAGGA CTGGGACTTC GGNTAGGGAG GAAGGTAGAG TAAGAGGTTG AAGTTAACAG 360  
 NTGCAAATTT CCTTTTTTTC CTTTNTNTN TNNTTT 397

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CAGTGA CTGA GACAACCAAG GGTGCTCCTG TGGCCACAAA CCACCAGAGT CGAGAGGTGG 120  
AAATGAGCAC CCGGGGCCGA TTCCAGCTCA CTGGGGATCC CGCCAAGGGG AACTGCTCCT 180  
TGGTGATCAN AAGACGCGCA GATGCAGGAT GAGTCACAGT ACTTCTTTTCG GGTGGAGAGA 240  
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CTCCGTGTGG CCTATGCCCC CAGAGACCTT GTTATCAGCA TTTCACGTGA CAACACGCCA 180  
GATCCTCCAG AGAACCTGAG AGTGATGGTT TCCCAAGCAA ACAGGACAGT CCTGGAAAAC 240  
CTTGGGAACG GCACGTCTCT CCCAGTACTG GAGGGCCAAA GCCTGTGCCT GGTCTGTGTC 300  
ACACACAGCA GCCCCCAGC CAGGCTGAGC TGGACCCAGA AGGGACANGT TCTGAGCCCC 360  
TCCCAGCCCT CAGANCCCGG GGTCTGAG TGCCTTCGGG TTCAACTGGA GCAACGAAAG 420  
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CGGCACAGCA CGATCCTGGA TTACATCAAT GTGGTCCCGN ACGGACTGGC CCCCTGGCTC 180  
AGAAGCGGNA ATCAGTAAAG CCACACCAAA CAGTCCTCGG NACCCCTCTT GCCACCAGGT 240  
GCTCCCTNCC CCAGGAATGC AAAGAAGAAC CAGAAAAAGG CAGTNATGCA GTTGCCCAAGT 300  
TTGCCCAAGAA CCCAAATCAT TCCATNCAAG CCCCAGAANC CCANGAGAGC CAAGAGGACT 360  
TCCATTAAGG CCAGGTTCAA ANTTTCCCAG GNGTTCTGA 398

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 AGCACGANCA GANAACAGGC CTGTNTCAAG NAGGCCCTGC GCCTCCTATG CGGAGATGCT 120  
 ACTGCNNCTG CTGCTGTCCT CGCTGCTGGG CGGGTCCCAG GNTNTGGATG GGAGATTCTG 180  
 GATNCGAGTG CAGGAGTCAG TGATGGTGCC GGAAGGCCTG TGCATCTCTG TGCCCTGCTC 240  
 TTTCTCCTAC NCCCGN 256

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 CCTGGAACGT CCACGGGGCC CAGAGTGGCT CTGTCTTCCA GCTGCTACCA GGGTGAAGAT 120  
 CTGCAGGAAG GAAGCTCGCA AGAGGGCAGC AGCTGAGCAG GACGTGCCCT CCACCCTGGG 180  
 ACCCATCTCC CAGGGTCACC AGCATGAATG CTCGGCAGGC AGCTCCCAAG ACCACCCGNC 240  
 CCCAGGTGCA GCCACCTACA CCCNNGGGGAA GGGGGAAGAG CAGGAGCTCC ACTATGCCT 299

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 Glu Arg Arg Phe Gln Leu Glu Gly Pro Glu Ser Leu Thr Val Gln Glu  
 20 25 30  
 Gly Leu Cys Val Leu Val Pro Cys Arg Leu Pro Thr Thr Leu Pro Ala  
 35 40 45  
 Ser Tyr Tyr Gly Tyr Gly Tyr Trp Phe Leu Glu Gly Ala Asp Val Pro

50 55 96 60  
 Val Ala Thr Asn Asp Pro Asp Glu Glu Val Gln Glu Glu Thr Arg Gly  
 65 70 75 80  
 Arg Phe His Leu Leu Trp Asp Pro Arg Arg Lys Asn Cys Ser Leu Ser  
 85 90 95  
 Ile Arg Asp Ala Arg Arg Arg Asp Asn Ala Ala Tyr Phe Phe Arg Leu  
 100 105 110  
 Lys Ser Lys Trp Met Lys Tyr Gly Tyr Thr Ser Ser Lys Leu Ser Val  
 115 120 125  
 Arg Val Met Ala Leu Thr His Arg Pro Asn Ile Ser Ile Pro Gly Thr  
 130 135 140  
 Leu Glu Ser Gly His Pro Ser Asn Leu Thr Cys Ser Val Pro Trp Val  
 145 150 155 160  
 Cys Glu Gln Gly Thr Pro Pro Ile Phe Ser Trp Met Ser Ala Ala Pro  
 165 170 175  
 Thr Ser Leu Gly Pro Arg Thr Thr Gln Ser Ser Val Leu Thr Ile Thr  
 180 185 190  
 Pro Arg Pro Gln Asp His Ser Thr Asn Leu Thr Cys Gln Val Thr Phe  
 195 200 205  
 Pro Gly Ala Gly Val Thr Met Glu Arg Thr Ile Gln Leu Asn Val Ser  
 210 215 220  
 Tyr Ala Pro Gln Lys Val Ala Ile Ser Ile Phe Gln Gly Asn Ser Ala  
 225 230 235 240  
 Ala Phe Lys Ile Leu Gln Asn Thr Ser Ser Leu Pro Val Leu Glu Gly  
 245 250 255  
 Gln Ala Leu Arg Leu Leu Cys Asp Ala Asp Gly Asn Pro Pro Ala His  
 260 265 270  
 Leu Ser Trp Phe Gln Gly Phe Pro Ala Leu Asn Ala Thr Pro Ile Ser  
 275 280 285  
 Asn Thr Gly Val Leu Glu Leu Pro Gln Val Gly Ser Ala Glu Glu Gly  
 290 295 300  
 Asp Phe Thr Cys Arg Ala Gln His Pro Leu Gly Ser Leu Gln Ile Ser  
 305 310 315 320  
 Leu Ser Leu Phe Val His Trp Lys Pro Glu Gly Arg Ala Gly Gly Val  
 325 330 335  
 Leu Gly Ala Val Trp Gly Ala Ser Ile Thr Thr Leu Val Phe Leu Cys  
 340 345 350  
 Val Cys Phe Ile Phe Arg Val Lys Thr Arg Arg Lys Lys Ala Ala Gln  
 355 360 365

Pro Val Gln Asn Thr Asp Asp Val Asn Pro Val Met Val Ser Gly Ser  
 370 375 380

Arg Gly His Gln His Gln Phe Gln Thr Gly Ile Val Ser Asp His Pro  
 385 390 395 400

Ala Glu Ala Gly Pro Ile Ser Glu Asp Glu Gln Glu Leu His Tyr Ala  
 405 410 415

Val Leu His Phe His Lys Val Gln Pro Gln Glu Pro Lys Val Thr Asp  
 420 425 430

Thr Glu Tyr Ser Glu Ile Lys Ile His Lys  
 435 440

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AAAATGGAAT TATAAATATG ACCAGCTCTC TGTGAACGTG ACAGACCCTC CTCAGAACTT 180

GACTGTGACT GTNTTNCAAG GAGAAGGCAC AGCATCCACA GCTCTGGGGN ACAGCTCATC 240

TCTTTCAGTC CTAGAGGG 258

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CTCCTTCTCC TACCCAGTGG ACGCCAGACT GNATCTGCAC ACGTTCTGGA TATGGTTCGG 120  
GCNGGAATGA NTNAGCTGG 139

<210> 102  
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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 102

Thr Asn Gly Tyr Gln Lys Thr Gly Asp Val Tyr Lys Cys Pro Val Ile  
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His Gly Asn Cys Thr Lys Leu Asn Leu Gly Arg Val Thr Leu Ser Asn  
 20 25 30

Val

&lt;210&gt; 103

&lt;211&gt; 1151

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 103

Phe Asn Val Asp Val Lys Asn Ser Met Thr Phe Ser Gly Pro Val Glu  
 1 5 10 15

Asp Met Phe Gly Tyr Thr Val Gln Gln Tyr Glu Asn Glu Glu Gly Lys  
 20 25 30

Trp Val Leu Ile Gly Ser Pro Leu Val Gly Gln Pro Lys Asn Arg Thr  
 35 40 45

Gly Asp Val Tyr Lys Cys Pro Val Gly Arg Gly Glu Ser Leu Pro Cys  
 50 55 60

Val Lys Leu Asp Leu Pro Val Asn Thr Ser Ile Pro Asn Val Thr Glu  
 65 70 75 80

Val Lys Glu Asn Met Thr Phe Gly Ser Thr Leu Val Thr Asn Pro Asn  
 85 90 95

Gly Gly Phe Leu Ala Cys Gly Pro Leu Tyr Ala Tyr Arg Cys Gly His  
 100 105 110

Leu His Tyr Thr Thr Gly Ile Cys Ser Asp Val Ser Pro Thr Phe Gln  
 115 120 125

Val Val Asn Ser Ile Ala Pro Val Gln Glu Cys Ser Thr Gln Leu Asp  
 130 135 140

Ile Val Ile Val Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Asp Ser  
 145 150 155 160

Val Thr Ala Phe Leu Asn Asp Leu Leu Lys Arg Met Asp Ile Gly Pro  
 165 170 175

Lys Gln Thr Gln Val Gly Ile Val Gln Tyr Gly Glu Asn Val Thr His  
 180 185 190

Glu Phe Asn Leu Asn Lys Tyr Ser Ser Thr Glu Glu Val Leu Val Ala  
 195 200 205

100

Ala Lys Lys Ile Val Gln Arg Gly Gly Arg Gln Thr Met Thr Ala Leu  
 210 215 220  
 Gly Thr Asp Thr Ala Arg Lys Glu Ala Phe Thr Glu Ala Arg Gly Ala  
 225 230 235 240  
 Arg Arg Gly Val Lys Lys Val Met Val Ile Val Thr Asp Gly Glu Ser  
 245 250 255  
 His Asp Asn His Arg Leu Lys Lys Val Ile Gln Asp Cys Glu Asp Glu  
 260 265 270  
 Asn Ile Gln Arg Phe Ser Ile Ala Ile Leu Gly Ser Tyr Asn Arg Gly  
 275 280 285  
 Asn Leu Ser Thr Glu Lys Phe Val Glu Glu Ile Lys Ser Ile Ala Ser  
 290 295 300  
 Glu Pro Thr Glu Lys His Phe Phe Asn Val Ser Asp Glu Leu Ala Leu  
 305 310 315 320  
 Val Thr Ile Val Lys Thr Leu Gly Glu Arg Ile Phe Ala Leu Glu Ala  
 325 330 335  
 Thr Ala Asp Gln Ser Ala Ala Ser Phe Glu Met Glu Met Ser Gln Thr  
 340 345 350  
 Gly Phe Ser Ala His Tyr Ser Gln Asp Trp Val Met Leu Gly Ala Val  
 355 360 365  
 Gly Ala Tyr Asp Trp Asn Gly Thr Val Val Met Gln Lys Ala Ser Gln  
 370 375 380  
 Ile Ile Ile Pro Arg Asn Thr Thr Phe Asn Val Glu Ser Thr Lys Lys  
 385 390 395 400  
 Asn Glu Pro Leu Ala Ser Tyr Leu Gly Tyr Thr Val Asn Ser Ala Thr  
 405 410 415  
 Ala Ser Ser Gly Asp Val Leu Tyr Ile Ala Gly Gln Pro Arg Tyr Asn  
 420 425 430  
 His Thr Gly Gln Val Ile Ile Tyr Arg Met Glu Asp Gly Asn Ile Lys  
 435 440 445  
 Ile Leu Gln Thr Leu Ser Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser  
 450 455 460  
 Ile Leu Thr Thr Thr Asp Ile Asp Lys Asp Ser Asn Thr Asp Ile Leu  
 465 470 475 480  
 Leu Val Gly Ala Pro Met Tyr Met Gly Thr Glu Lys Glu Glu Gln Gly  
 485 490 495  
 Lys Val Tyr Val Tyr Ala Leu Asn Gln Thr Arg Phe Glu Tyr Gln Met  
 500 505 510

101

Ser Leu Glu Pro Ile Lys Gln Thr Cys Cys Ser Ser Arg Gln His Asn  
515 520 525

Ser Cys Thr Thr Glu Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly  
530 535 540

Thr Ala Ile Ala Ala Val Lys Asp Leu Asn Leu Asp Gly Phe Asn Asp  
545 550 555 560

Ile Val Ile Gly Ala Pro Leu Glu Asp Asp His Gly Gly Ala Val Tyr  
565 570 575

Ile Tyr His Gly Ser Gly Lys Thr Ile Arg Lys Glu Tyr Ala Gln Arg  
580 585 590

Ile Pro Ser Gly Gly Asp Gly Lys Thr Leu Lys Phe Phe Gly Gln Ser  
595 600 605

Ile His Gly Glu Met Asp Leu Asn Gly Asp Gly Leu Thr Asp Val Thr  
610 615 620

Ile Gly Gly Leu Gly Gly Ala Ala Leu Phe Trp Ser Arg Asp Val Ala  
625 630 635 640

Val Val Lys Val Thr Met Asn Phe Glu Pro Asn Lys Val Asn Ile Gln  
645 650 655

Lys Lys Asn Cys His Met Glu Gly Lys Glu Thr Val Cys Ile Asn Ala  
660 665 670

Thr Val Cys Phe Glu Val Lys Leu Lys Ser Lys Glu Asp Thr Ile Tyr  
675 680 685

Glu Ala Asp Leu Gln Tyr Arg Val Thr Leu Asp Ser Leu Arg Gln Ile  
690 695 700

Ser Arg Ser Phe Phe Ser Gly Thr Gln Glu Arg Lys Val Gln Arg Asn  
705 710 715 720

Ile Thr Val Arg Lys Ser Glu Cys Thr Lys His Ser Phe Tyr Met Leu  
725 730 735

Asp Lys His Asp Phe Gln Asp Ser Val Arg Ile Thr Leu Asp Phe Asn  
740 745 750

Leu Thr Asp Pro Glu Asn Gly Pro Val Leu Asp Asp Ser Leu Pro Asn  
755 760 765

Ser Val His Glu Tyr Ile Pro Phe Ala Lys Asp Cys Gly Asn Lys Glu  
770 775 780

Lys Cys Ile Ser Asp Leu Ser Leu His Val Ala Thr Thr Glu Lys Asp  
785 790 795 800

Leu Leu Ile Val Arg Ser Gln Asn Asp Lys Phe Asn Val Ser Leu Thr  
805 810 815

Val Lys Asn Thr Lys Asp Ser Ala Tyr Asn Thr Arg Thr Ile Val His

102

820	825	830
Tyr Ser Pro Asn Leu Val Phe Ser Gly Ile Glu Ala Ile Gln Lys Asp		
835	840	845
Ser Cys Glu Ser Asn His Asn Ile Thr Cys Lys Val Gly Tyr Pro Phe		
850	855	860
Leu Arg Arg Gly Glu Met Val Thr Phe Lys Ile Leu Phe Gln Phe Asn		
865	870	875
Thr Ser Tyr Leu Met Glu Asn Val Thr Ile Tyr Leu Ser Ala Thr Ser		
885	890	895
Asp Ser Glu Glu Pro Pro Glu Thr Leu Ser Asp Asn Val Val Asn Ile		
900	905	910
Ser Ile Pro Val Lys Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala		
915	920	925
Ser Glu Tyr His Ile Ser Ile Ala Ala Asn Glu Thr Val Pro Glu Val		
930	935	940
Ile Asn Ser Thr Glu Asp Ile Gly Asn Glu Ile Asn Ile Phe Tyr Leu		
945	950	955
Ile Arg Lys Ser Gly Ser Phe Pro Met Pro Glu Leu Lys Leu Ser Ile		
965	970	975
Ser Phe Pro Asn Met Thr Ser Asn Gly Tyr Pro Val Leu Tyr Pro Thr		
980	985	990
Gly Leu Ser Ser Ser Glu Asn Ala Asn Cys Arg Pro His Ile Phe Glu		
995	1000	1005
Asp Pro Phe Ser Ile Asn Ser Gly Lys Lys Met Thr Thr Ser Thr Asp		
1010	1015	1020
His Leu Lys Arg Gly Thr Ile Leu Asp Cys Asn Thr Cys Lys Phe Ala		
1030	1035	1040
Thr Ile Thr Cys Asn Leu Thr Ser Ser Asp Ile Ser Gln Val Asn Val		
1045	1050	1055
Ser Leu Ile Leu Trp Lys Pro Thr Phe Ile Lys Ser Tyr Phe Ser Ser		
1060	1065	1070
Leu Asn Leu Thr Ile Arg Gly Glu Leu Arg Ser Glu Asn Ala Ser Leu		
1075	1080	1085
Val Leu Ser Ser Ser Asn Gln Lys Arg Glu Leu Ala Ile Gln Ile Ser		
1090	1095	1100
Lys Asp Gly Leu Pro Gly Arg Val Pro Leu Trp Val Ile Leu Leu Ser		
1110	1115	1120
Ala Phe Ala Gly Leu Leu Leu Leu Met Leu Leu Ile Leu Ala Leu Trp		
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Lys Ile Gly Phe Phe Lys Arg Pro Leu Lys Lys Lys Met Glu Lys  
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TCAGATCAAT GCCAGCCTCC ACTTTGAGCC ATCCAAGATC AACATCTTCC ACAGAGACTG 180  
CAAGCGCAGT GGCAGGGATG CCACCTGCCT GGCCGCCTTC CTCTGCTTCA CGCCCATCTT 240  
CCTGGCACCC CATTTNCAAA CAACAACTGT TGGCATCANA TACAACGCCA CCATGGGATG 300  
ANAGGCGGTN TACACCGAGG GCCCACCTGG ACAAGGCGGG GACCGANTNA CAACAGAACC 360

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<400> 105  
GAATTCGGCA NAGGCAGACA CTGCTCCTTG GGTAGCCATA ACTGTGTCCC CACTTTCCAG 60  
GGTGCCAGAC CTACATGGAC ATCGTCATTG TCCTGGATGG GTCCAACAGC ATCTACCCCT 120  
GGGTGGGGGT TCAGCACTTC CTCATCAACA TCCTGAAAAA GTTTTACATT GGCCCAGGGC 180  
AGATCCAGGT TGGACTTGTG CAGTATGGCG ANGATGTGGT GCATGAGTTT CACCTCAATG 240  
ACTACAGGTC TGTAAGAGAT GTGGTGGNAG CTGNCAGCCA CATTGAGCCN GAGAGGNGGG 300  
ACAGAGACCC GGACCGNATT TGGCATTGGA ATTTGGCACG GTTAAAAAAA AAGTNGGGCC 360  
AAAAAAATTT TTTTGGGTC NCANATGCTT TTGTAGTNAN TCCNNTNGGC TTNNNAACAA 420  
ATTTCCCCAA ATTNNGTNCC CTNGGGCCAT ATTTTTTTAT TNCCNNNAAT TTTGGGGTTT 480  
GNNTGGGTCA A 491

<210> 106  
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CACCTCAAAT ACGAGGCTGA CGTCCTCTTC ACCAGGAGCA GCAGCCTGAG CCACTACGAA 120  
GGTCAAGCTC AACAGCTCGC TGGAGAGATA CGATGGTATC GGGCCTCCCT TCAGCTGCAT 180  
CTTCAGGNTC CAGAACTTGG GCTTGTTCCC CATCCACGGG ATGATGGATG GAAGATCACC 240  
ATTCCCATCG NCACCAGGAG CGGCAACCGC CTTACTGAAG TTGAGGGACT TNCTCAAGGA 300  
CGAGGCGNAC ANGTCCTGTA AACATTNGGG GCAATAGCAT 340

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CTCAAGTACA GATCCATGAA AATNATGGTC AACGCAGCCT TGCAGAGGCA GGTGACACAG 120  
CCCCCTTCATC TTCCGTGAAG GAGGTATCCC AGCCGCCAGA TCGTGTTTGA GAATCTCCAA 180  
GCAAGAGGAC TGGCAGGTCC CCATCTGGAT CATGTAGGC AGCACCTGG GGGGCCTCCT 240  
ACTGCTGGCC CTGCTGGTTC CTGGGCACTG TGGGAAGCTT CGGTTTCTTT AAGAAGTNTC 300  
CAGGTCGCAG NNGGGGTAGC CTGGTTCTGG GACCCNAANC CNNAAAATTG CTGGGT 356

109

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TGGCCTGGGC GCTCANCCTG TGGCCAGGGT TCACGGACAC CTTCAACATG GTACACCAGG 120  
AAGCCCCGGG TCATCCCTGG CTCCAGGACC GCCTTCTTTG GCTACACAGT GCAGCAGCAC 180  
GACATCAGTG GCAATAAGTG GCTGGTCCTT GGGGCNCCCC ACTGGAAACC AATNGCTACA 240  
AAAAAAANGG AAAACTNTNC AA 262

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<220>  
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<222> (326)

111

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 109

GGCAGANCTA CAGCACGGTC CTAAATATCT CGNAGTCAGC AAACCTNCAG TTTCNAGCTT	60
AATCCANAAG GAGGACTCAA ACGGTAGCAT TGAGTGTNTG AACGAGGAGA GGAGGCTCCA	120
GAAGCAAGTT TGCAACGTCA GCTATCCCTT CTNCCGGGCC AAGGCCAAGG TGGCTTTCCG	180
TCTTGNATTT TAAGTTCAGC AAATCCATCT TCCTACACCA CCTGGAGATC GAGCCTCGCT	240
GCAGCAGTGA CAGTAATGNG ATGAGGGGTT AGCCGGGGTT TGNACCCAAG TGNATTTAC	300
ATTGGCCGGA AATTTNAAAA TTTCNC	327

&lt;210&gt; 110

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (71)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (72)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (90)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (194)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (212)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (241)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (245)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

112

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<223> n equals a,t,g, or c

<220>  
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<222> (290)  
<223> n equals a,t,g, or c

<220>  
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AACAGCTGCA NNAAGGGAAT GAAGAAAGAN TCTAAGAATG TGGAGACTGA TGGCCAGGCA 120  
AGTGGGACCA GGATACTGAA CGCTGTCCTG AAGAATGAGA AGGTAGCCGG GCTCTGCACC 180  
CACGTGCATT GCANATTGAA CCGCAACTGA ANACATTCCC CCACCAGCTG CAGCCCCCTTG 240  
NTCTNCAGTT GCCAACCCTC CCGGGTGNA TTTTNTTCCC AGGTACCTTN ATGGGNAAGC 300  
A 301

<210> 111  
<211> 478  
<212> DNA  
<213> Homo sapiens

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TCATCCTCAT TGCAGCCGTT CCAGAAGGGC ACCTGNGCCA GGGAGAGCCA GGTGTGGGCA 120  
GCTGGGTAGG GACCCGCAGC CCCTCGCCCT CAATGTACAC CAGCTCTGTC TCCACCACAC 180  
TAGACATGGG CTGGCTTTCC TGCACGTGCC CCAGACACCA CACTGCTCTG TCTTGTGCTT 240  
TTCCATAGAT GCTTCCCTCT TTAACACGAT GCTCAAAGCT TCAGNTCCTC CTGGCTCCCC 300  
TCCAGTTTCA TGAATGGAGC TGATGGCACA GAACCCCCAA CCCCATTCAA CCAGCAGANG 360  
GTTCTGGTTC AACATTTATT GATCAANAAT GTGTGTGGGG CAAGGGNTTG GTAATGGGGG 420  
TTACAAAACA AGNAAGTTGG CAGTTTTGGC CNTCAGTTCA AGGGGAAANT GGTGTTTG 478

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<211> 224  
<212> DNA  
<213> Homo sapiens

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<220>  
<221> SITE  
<222> (49)

114

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (66)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (176)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (184)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (197)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (212)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (221)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 112

CTATTGCCCC ANATGTTACA NGACGTGTTT GCCTCGTCCG TGTAGGAANT CCCTCAGCTT 60

CAGTANGCGG TTGCCGCTCC TGGTGGCGAG GGAATGGTGA ATCTTCATCA TCATCCCGTG 120

GTATGGGGAA CAAACCCAAG TTCTGGATCC TGAAAAATCA ACTGAAAGGA AGGCCNATAC 180

ATCNTATCTC TCCAACNAAC TGTGGGCTTG ANCTCCTAAT NGTT 224

&lt;210&gt; 113

&lt;211&gt; 126

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (72)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 113

GGCACGAGCT GACATCTCTC TGTCACCTCTG TTGCAGGCAC CAACAAGAAC GAGACCTCCT 60

TTGGGCTGTG GNAGTCACAG ACGGGCTTTT CCTCGCACGT GGTGGAGGTA TGTGGTGGAG 120



115

GTACGG

126

&lt;210&gt; 114

&lt;211&gt; 150

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 114

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Met Leu Phe Ala Cys Ala Leu Leu Ala Leu Leu Gly Leu Ala Thr Ser
  1              5              10              15

Cys Ser Phe Ile Val Pro Arg Ser Glu Trp Arg Ala Leu Pro Ser Glu
          20              25              30

Cys Ser Ser Arg Leu Gly His Pro Val Arg Tyr Val Val Ile Ser His
          35              40              45

Thr Ala Gly Ser Phe Cys Asn Ser Pro Asp Ser Cys Glu Gln Gln Ala
  50              55              60

Arg Asn Val Gln His Tyr His Lys Asn Glu Leu Gly Trp Cys Asp Val
  65              70              75              80

Ala Tyr Asn Phe Leu Ile Gly Glu Asp Gly His Val Tyr Glu Gly Arg
          85              90              95

Gly Trp Asn Ile Lys Gly Asp His Thr Gly Pro Ile Trp Asn Pro Met
          100              105              110

Ser Ile Gly Ile Thr Phe Met Gly Asn Phe Met Asp Arg Val Arg Lys
          115              120              125

Ala Gly Pro Pro Cys Cys Pro Lys Ser Ser Gly Ile Trp Gly Val Ser
          130              135              140

Gly Leu Pro Glu Ile Gln
145              150

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&lt;210&gt; 115

&lt;211&gt; 285

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (18)

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&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (263)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

116

&lt;222&gt; (270)

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&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (273)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (276)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

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&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 115

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AGGTCCAACAT ATGTGCTCAA AGGACACCGG GATGTGCAGC GTACACTCTC TCCAGGCAAC 120

CAGCTCTACC ACCTCATCCA GAATTGGCCA CACTACCGCT CCCCCTGAGG CCCTGCTGAT 180

CCGCACCCCA TTCCTCCCCT CCCATGGCCA AAAACCCAC TGTCTCCTTC TCCAATAAAG 240

ATGTAGCTCA AAAAAAAAAA AANAAAAAAN CCNGGNGGGG GGNCC 285

&lt;210&gt; 116

&lt;211&gt; 457

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;223&gt; n equals a,t,g, or c

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&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

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118

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GCTCTCCCN GCCTNCTTCN ACTCGAAGCG GCTCAGGAGA CAGAAGACCN GGCCTGCTGC 120  
AGCCCCATAG TGCCCCGGA ACAGTGAAG GCCCTGGTAT CAAAGTGCGC CCNGCNCTGA 180  
AGACCTGCCC TTACGCTATG TGGTGGTATC GNACACGGCG GGCAGCAGCT GCAACANCCC 240

CGATTTGTTG	CCAGCAGCAA	GCCCCGGAATG	TGCAGCACTA	CCCACATGAA	GACACTGGGN	300
TGGTGCGAAN	GTGGGGTNAN	AAATTNCTGA	TTTGGGNGAA	AGAAGGGNTT	CTTATAAGAG	360
GGGGCCTTTG	GTTTGGGAAT	T'TAAAGGGTT	GCCCCNTTNA	GGTGAATTTT	TGGGAAACCC	420
TTGTTCCATT	GGGATNAANT	TTCNTGGGCA	NTNACAT			457

&lt;210&gt; 117

&lt;211&gt; 1833

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 117

ACATCCATGG	CTCTAATGCT	CAGTTTGGTT	CTGAGTCTCC	TCAAGCTGGG	ATCAGGGCAG	60
TGGCAGGTGT	T'TGGGCCAGA	CAAGCCTGTC	CAGGCCTTGG	TGGGGGAGGA	CGCAGCATTG	120
TCCTGTTTTCC	TGTCTCCTAA	GACCAATGCA	GAGGCCATGG	AAGTCCGGTT	CTTCAGGGGC	180
CAGTTCTCTA	GCGTGGTCCA	CCTCTACAGG	GACGGGAAGG	ACCAGCCATT	TATGCAGATG	240
CCACAGTATC	AAGGCAGGAC	AAAACCTGGT	AAGGATTCTA	T'TGCGGAGGG	GCGCATCTCT	300
CTGAGGCTGG	AAAACATTAC	TGTGTTGGAT	GCTGGCCTCT	ATGGGTGCAG	GATTAGTTCC	360
CAGTCTTACT	ACCAGAAGGC	CATCTGGGAG	CTACAGGTGT	CAGCACTGGG	CTCAGTTCTT	420
CTCATTTCCTA	TCACGGGATA	TGTTGATAGA	GACATCCAGC	TACTCTGTCA	GTCCTCGGGC	480
TGGT'TCCCCC	GGCCCACAGC	GAAGTGGAAG	GGTCCACAAG	GACAGGATTT	GTCCACAGAC	540
TCCAGGACAA	ACAGAGACAT	GCATGGCCTG	TTTGATGTGG	AGATCTCTCT	GACCGTCCAA	600
GAGAACGCCG	GGAGCATATC	CTGTTCCATG	CGGCATGCTC	ATCTGAGCCG	AGAGGTGGAA	660
TCCAGGGTAC	AGATAGGAGA	TACCTTTTTT	GAGCCTATAT	CGTGGCACCT	GGCTACCAAA	720
GTACTGGGAA	TACTCTGCTG	TGGCCTATTT	TTTGGCATTG	TTGGACTGAA	GATTTTCTTC	780
TCCAAATTCC	AGTGGAATAA	CCAGGCGGAA	CTGGACTGGA	GAAGAAAGCA	CGGACAGGCA	840
GAATTGAGAG	ACGCCCCGAA	ACACGCAGTG	GAGGTGACTC	TGGATCCAGA	GACGGCTCAC	900
CCGAAGCTCT	GCGTTTCTGA	TCTGAAAAC	GTAACCCATA	GAAAAGCTCC	CCAGGAGGTG	960
CCTCACTCTG	AGAAGAGATT	TACAAGGAAG	AGTGTGGTGG	CTTCTCAGAG	TTTCCAAGCA	1020
GGGAAACATT	ACTGGGAGGT	GGACGGAGGA	CACAATAAAA	GGTGGCGCGT	GGGAGTGTGC	1080
CGGGATGATG	TGGACAGGAG	GAAGGAGTAC	GTGACTTTGT	CTCCCGATCA	TGGGTACTGG	1140
GTCTTCAGAC	TGAATGGAGA	ACATTTGTAT	TTCACATTAA	ATCCCCGTTT	TATCAGCGTC	1200
TTCCCCAGGA	CCCCACCTAC	AAAAATAGGG	GTCTTCCTGG	ACTATGAGTG	TGGGACCATC	1260

TCCTTCTTCA	ACATAAAATGA	CCAGTCCCTT	ATTTATACCC	TGACATGTCG	GTTTGAAGGC	1320
TTATTGAGGC	CCTACATTGA	GTATCCCTCC	TATAATGAGC	AAAATGGAAC	TCCCAGAGAC	1380
AAGCAACAGT	GAGTCCTCCT	CACAGGCAAC	CACGCCCTTC	CTCCCCAGGG	GTGAAATGTA	1440
GGATGAATCA	CATCCCACAT	TCTTCTTTAG	GGATATTAAG	GTCTCTCTCC	CAGATCCAAA	1500
GTCCCGCAGC	AGCCGGCCAA	GGTGGCTTCC	AGATGAAGGG	GGACTGGCCT	GTCCACATGG	1560
GAGTCAGGTG	TCATGGCTGC	CCTGAGCTGG	GAGGGAAGAA	GGCTGACATT	ACATTTAGTT	1620
TGCTCTCACT	CCATCTGGCT	AAGTGATCTT	GAAATACCAC	CTCTCAGGTG	AAGAACCGTC	1680
AGGAATTCCC	ATCTCACAGG	CTGTGGTGTA	GATTAAGTAG	ACAAGGAATG	TGAATAATGC	1740
TTAGATCTTA	TTGATGACAG	AGTGTATCCT	AATGGTTTGT	TCATTATATT	ACACTTTCAG	1800
TAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAA			1833

&lt;210&gt; 118

&lt;211&gt; 1386

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 118

ATGGCTCTAA	TGCTCAGTTT	GGTTCTGAGT	CTCCTCAAGC	TGGGATCAGG	GCAGTGGCAG	60
GTGTTTGGGC	CAGACAAGCC	TGTCCAGGCC	TTGGTGGGGG	AGGACGCAGC	ATTCTCCTGT	120
TTCTGTCTC	CTAAGACCAA	TGCAGAGGCC	ATGGAAGTGC	GGTTCTTCAG	GGGCCAGTTC	180
TCTAGCGTGG	TCCACCTCTA	CAGGGACGGG	AAGGACCAGC	CATTTATGCA	GATGCCACAG	240
TATCAAGGCA	GGACAAAAC	GGTGAAGGAT	TCTATTGCGG	AGGGGCGCAT	CTCTCTGAGG	300
CTGGAAAACA	TTACTGTGTT	GGATGCTGGC	CTCTATGGGT	GCAGGATTAG	TTCCCAGTCT	360
TACTACCAGA	AGGCCATCTG	GGAGCTACAG	GTGTCAGCAC	TGGGCTCAGT	TCCTCTCAT	420
TCCATCACGG	GATATGTTGA	TAGAGACATC	CAGCTACTCT	GTCAGTCCTC	GGGCTGGTTC	480
CCCCGGCCCA	CAGCGAAGTG	GAAAGGTCCA	CAAGGACAGG	ATTTGTCCAC	AGACTCCAGG	540
ACAAACAGAG	ACATGCATGG	CCTGTTTGAT	GTGGAGATCT	CTCTGACCGT	CCAAGAGAAC	600
GCCGGGAGCA	TATCCTGTTC	CATGCGGCAT	GCTCATCTGA	GCCGAGAGGT	GGAATCCAGG	660
GTACAGATAG	GAGATACCTT	TTTCGAGCCT	ATATCGTGCC	ACCTGGCTAC	CAAAGTACTG	720
GGAATACTCT	GCTGTGGCCT	ATTTTGTGGC	ATTGTTGGAC	TGAAGATTTT	CTTCTCCAAA	780
TTCCAGTGGA	AAATCCAGGC	GGAAGTGGAC	TGGAGAAGAA	AGCACGGACA	GGCAGAATTG	840
AGAGACGCCC	GGAAACACGC	AGTGGAGGTG	ACTCTGGATC	CAGAGACGGC	TCACCCGAAG	900

121

CTCTGCGTTT CTGATCTGAA AACTGTAACC CATAGAAAAG CTCCCCAGGA GGTGCCTCAC 960  
TCTGAGAAGA GATTTACAAG GAAGAGTGTG GTGGCTTCTC AGAGTTTCCA AGCAGGGAAA 1020  
CATTACTGGG AGGTGGACGG AGGACACAAT AAAAGGTGGC GCGTGGGAGT GTGCCGGGAT 1080  
GATGTGGACA GGAGGAAGGA GTACGTGACT TTGTCTCCCG ATCATGGGTA CTGGGTCCTC 1140  
AGACTGAATG GAGAACATTT GTATTTTACA TTAAATCCCC GTTTTATCAG CGTCTTCCCC 1200  
AGGACCCAC CTACAAAAAT AGGGGTCTTC CTGGACTATG AGTGTGGGAC CATCTCCTTC 1260  
TTCAACATAA ATGACCAGTC CCTTATTTAT ACCCTGACAT GTCGGTTTGA AGGCTTATTG 1320  
AGGCCCTACA TTGAGTATCC GTCCTATAAT GAGCAAAATG GAACTCCCAG AGACAAGCAA 1380  
CAGTGA 1386

&lt;210&gt; 119

&lt;211&gt; 461

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 119

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly Ser  
1 5 10 15

Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala Leu Val  
20 25 30

Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys Thr Asn Ala  
35 40 45

Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe Ser Ser Val Val  
50 55 60

His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe Met Gln Met Pro Gln  
65 70 75 80

Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp Ser Ile Ala Glu Gly Arg  
85 90 95

Ile Ser Leu Arg Leu Glu Asn Ile Thr Val Leu Asp Ala Gly Leu Tyr  
100 105 110

Gly Cys Arg Ile Ser Ser Gln Ser Tyr Tyr Gln Lys Ala Ile Trp Glu  
115 120 125

Leu Gln Val Ser Ala Leu Gly Ser Val Pro Leu Ile Ser Ile Thr Gly  
130 135 140

Tyr Val Asp Arg Asp Ile Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe  
145 150 155 160

Pro Arg Pro Thr Ala Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser

<210> 120



123

<211> 1152

<212> DNA

<213> Homo sapiens

<400> 120

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ACCTTTTTCG AGCCTATATC GTGGCACCTG GCTACCAAAG TACTGGGAAT ACTCTGCTGT      60
GGCCTATTTT TTGGCATTGT TGGACTGAAG ATTTTCTTCT CCAAATTCCA GTGGAAAAATC      120
CAGGCGGAAC TGGACTGGAG AAGAAAGCAC GGACAGGCAG AATTGAGAGA CGCCCGGAAA      180
CACGCAGTGG AGGTGACTCT GGATCCAGAG ACGGCTCACC CGAAGCTCTG CGTTTCTGAT      240
CTGAAAAC TGTAACCCATAG AAAAGCTCCC CAGGAGGTGC CTCACTCTGA GAAGAGATTT      300
ACAAGGAAGA GTGTGGTGGC TTCTCAGAGT TTCCAAGCAG GGAAACATTA CTGGGAGGTG      360
GACGGAGGAC ACAATAAAAG GTGGCGCGTG GGAGTGTGCC GGGATGATGT GGACAGGAGG      420
AAGGAGTACG TGACTTTGTC TCCCAGTCAT GGGTACTGGG TCCTCAGACT GAATGCAGAA      480
CATTTGTATT TCACATTAAA TCCCCGTTTT ATCAGCGTCT TCCCAGGAC CCCACCTACA      540
AAAATAGGGG TCTTCCTGGA CTATGAGTGT GGGACCATCT CCTTCTTCAA CATAAATGAC      600
CAGTCCCTTA TTTATACCCT GACATGTCGG TTTGAAGGCT TATTGAGGCC CTACATTGAG      660
TATCCGTCCT ATAATGAGCA AAATGGAAC CCCAGAGACA AGCAACAGTG AGTCCTCCTC      720
ACAGGCAACC ACGCCCTTCC TCCCCAGGGG TGAAATGTAG GATGAATCAC ATCCCACATT      780
CTTCTTTAGG GATATTAAGG TCTCTCTCCC AGATCCAAAG TCCCGCAGCA GCCGGCCAAG      840
GTGGCTTCCA GATGAAGGGG GACTGGCCTG TCCACATGGG AGTCAGGTGT CATGGCTGCC      900
CTGAGCTGGG AGGGAAGAAG GCTGACATTA CATTTAGTTT GCTCTCACTC CATCTGGCTA      960
AGTGATCTTG AAATACCACC TCTCAGGTGA AGAACCGTCA GGAATTCCCA TCTCACAGGC     1020
TGTGGTGTAG ATTAAGTAGA CAAGGAATGT GAATAATGCT TAGATCTTAT TGATGACAGA     1080
GTGTATCCTA ATGGTTTGTT CATTATATTA CACTTTCAGT AAAAAAAAAA AAAAAAAAAA     1140
AAAAAAAAAA AA                                                                1152

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<210> 121

<211> 526

<212> PRT

<213> Homo sapiens

<400> 121

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Met Ala Val Phe Pro Asn Ser Cys Leu Ala Gly Cys Leu Leu Ile Phe
  1              5              10              15
Ile Leu Leu Gln Leu Pro Lys Leu Asp Ser Ala Pro Phe Asp Val Ile
      20              25              30

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124

Gly Pro Gln Glu Pro Ile Leu Ala Val Val Gly Glu Asp Ala Glu Leu  
 35 40 45  
 Pro Cys Arg Leu Ser Pro Asn Val Ser Ala Lys Gly Met Glu Leu Arg  
 50 55 60  
 Trp Phe Arg Glu Lys Val Ser Pro Ala Val Phe Val Ser Arg Glu Gly  
 65 70 75 80  
 Gln Glu Gln Glu Gly Glu Glu Met Ala Glu Tyr Arg Gly Arg Val Ser  
 85 90 95  
 Leu Val Glu Asp His Ile Ala Glu Gly Ser Val Ala Val Arg Ile Gln  
 100 105 110  
 Glu Val Lys Ala Ser Asp Asp Gly Glu Tyr Arg Cys Phe Phe Arg Gln  
 115 120 125  
 Asp Glu Asn Tyr Glu Glu Ala Ile Val His Leu Lys Val Ala Ala Leu  
 130 135 140  
 Gly Ser Asp Pro His Ile Ser Met Lys Val Gln Glu Ser Gly Glu Ile  
 145 150 155 160  
 Gln Leu Glu Cys Thr Ser Val Gly Trp Tyr Pro Glu Pro Gln Val Gln  
 165 170 175  
 Trp Arg Thr His Arg Gly Glu Glu Phe Pro Ser Met Ser Glu Ser Arg  
 180 185 190  
 Asn Pro Asp Glu Glu Gly Leu Phe Thr Val Arg Ala Ser Val Ile Ile  
 195 200 205  
 Arg Asp Ser Ser Met Lys Asn Val Ser Cys Cys Ile Arg Asn Leu Leu  
 210 215 220  
 Leu Gly Gln Glu Lys Asp Val Glu Val Ser Ile Pro Ala Ser Phe Phe  
 225 230 235 240  
 Pro Arg Leu Thr Pro Trp Met Val Ala Val Ala Val Ile Leu Val Val  
 245 250 255  
 Leu Gly Leu Leu Thr Ile Gly Ser Ile Phe Phe Thr Trp Arg Leu Tyr  
 260 265 270  
 Lys Glu Arg Ser Arg Gln Arg Arg Asn Glu Phe Ser Ser Lys Glu Lys  
 275 280 285  
 Leu Leu Glu Glu Leu Lys Trp Lys Arg Ala Thr Leu His Ala Val Asp  
 290 295 300  
 Val Thr Leu Asp Pro Asp Thr Ala His Pro His Leu Phe Leu Tyr Glu  
 305 310 315 320  
 Asp Ser Lys Ser Val Arg Leu Glu Asp Ser Arg Gln Lys Leu Pro Glu  
 325 330 335

125  
 Lys Pro Glu Arg Phe Asp Ser Trp Pro Cys Val Met Gly Arg Glu Ala  
 340 345 350  
 Phe Thr Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly Asp Arg Thr  
 355 360 365  
 Asp Trp Ala Ile Gly Val Cys Arg Glu Asn Val Met Lys Lys Gly Phe  
 370 375 380  
 Asp Pro Met Thr Pro Glu Asn Gly Phe Trp Ala Val Glu Leu Tyr Gly  
 385 390 395 400  
 Asn Gly Tyr Trp Ala Leu Thr Pro Leu Arg Thr Pro Leu Pro Leu Ala  
 405 410 415  
 Gly Pro Pro Arg Arg Val Gly Val Phe Leu Asp Tyr Glu Ser Gly Asp  
 420 425 430  
 Ile Phe Phe Tyr Asn Met Thr Asp Gly Ser His Ile Tyr Thr Phe Ser  
 435 440 445  
 Lys Ala Ser Phe Ser Gly Pro Leu Arg Pro Phe Phe Cys Leu Trp Ser  
 450 455 460  
 Cys Gly Lys Lys Pro Leu Thr Ile Cys Pro Val Thr Asp Gly Leu Glu  
 465 470 475 480  
 Gly Val Met Val Val Ala Asp Ala Lys Asp Ile Ser Lys Glu Ile Pro  
 485 490 495  
 Leu Ser Pro Met Gly Glu Asp Ser Ala Ser Gly Asp Ile Glu Thr Leu  
 500 505 510  
 His Ser Lys Leu Ile Pro Leu Gln Pro Ser Gln Gly Val Pro  
 515 520 525

&lt;210&gt; 122

&lt;211&gt; 469

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (63)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (289)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (338)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

126

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<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

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GGCAGAGCCT GTCATCCGTT TCCATGCCGT GAGGTCCATT CACAGAACAC ATCCATGGCT  
CTNATGCTCA GTTTGTTCT GAGTCTCCTC AAGCTGGGAT CAGGGCAGTG GCAGGTGTTT

60

120

GGGCCAGACA AGCCTGTCCA GGCCTTGGTG GGGGAGGACG CAGCATTCTC CTGTTTCCTG	180
TCTCCTAAGA ACCAATGCAG AGGCCATGGT AAGTGCGGTT CTTCAGGGGC CAGTTTCTCT	240
AGCGTGGTCC ACCTCTTACA GGGACGGGAA GGACCAGCCC ATTTTATGNC AGATGGCCAC	300
AGTATTCAAG GCCAGGACAA AAAATGGGTG GAAGGTTNCT ATTTGCGGAG GGGCGCNNTT	360
TNTNTTGAGG GTGGGAAAAA NATTTACTNT NTTTGATTG CTGGGCCCCCT TATGGGTGCC	420
AGGGTTAAGT TTCCCANTTT TTAATTNACC CGANAGGNCC ATTTGGGGG	469

&lt;210&gt; 123

&lt;211&gt; 368

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (81)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (109)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (133)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (210)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (228)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (242)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (245)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (249)

128

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (251)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (268)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (329)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (335)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (339)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (353)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (362)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 123

GGCAGAGAGG ATTTGTCCAC AGACTCCAGG ACAAACAGAG ACATGCATGG CCTGTTTGAT 60

GTGGAGATCT CTCTGACCGT NCAAGAGAAC GCCGGGAGCA TATCCTGTNC CATGCGGCAT 120

GCTCATCTAA GCNCGAGAAG GTGGGAATCC AGGGTACAGA TAGGAGATAC CTTTTCGAAG 180

CCTATATCGT GGCACCTGGC TACCAAAGTN CTGGGAAATA CTCTGCTNGT GGCCTATTTT 240

TNGGNATTNT NGGACTAAAG ATATTTTNCT CCAAATTCCA GTGTAAGCAA GGGAGAAGGG 300

GCATGGGCCC GTGCCTTATT CCATGGTTNC CAGCNGGGNC AGGATCAGAG ATNGCTCCCA 360

CNTCCAGT 368

&lt;210&gt; 124

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

129

&lt;400&gt; 124

Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile  
 1 5 10 15

His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln  
 20 25

&lt;210&gt; 125

&lt;211&gt; 413

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 125

Gly Thr Arg Gly Gln Ala Trp Glu Pro Arg Ala Leu Ser Arg Arg Pro  
 1 5 10 15

His Leu Ser Glu Arg Arg Ser Glu Pro Arg Pro Gly Arg Ala Ala Arg  
 20 25 30

Arg Gly Thr Val Leu Gly Met Ala Gly Ile Pro Gly Leu Leu Phe Leu  
 35 40 45

Leu Phe Phe Leu Leu Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala  
 50 55 60

Pro Trp Lys Pro Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro  
 65 70 75 80

Gln Ser Thr Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys  
 85 90 95

Leu Glu Val Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro  
 100 105 110

Leu Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu  
 115 120 125

Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu  
 130 135 140

Ser Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser Ser Gly  
 145 150 155 160

Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser  
 165 170 175

Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val  
 180 185 190

Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val Ala Glu Lys His Val  
 195 200 205

Leu Thr Ala Ala His Cys Ile His Asp Gly Lys Thr Tyr Val Lys Gly  
 210 215 220

Thr Gln Lys Leu Arg Val Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly

WO 00/29435

PCT/US99/25031

225 230 130 235 240  
 Gly Arg Gly Ala Asn Asp Ser Thr Ser Ala Met Pro Glu Gln Met Lys  
 245 250 255  
 Phe Gln Trp Ile Arg Val Lys Arg Thr His Val Pro Lys Gly Trp Ile  
 260 265 270  
 Lys Gly Asn Ala Asn Asp Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu  
 275 280 285  
 Glu Leu Lys Lys Pro His Lys Arg Lys Phe Met Lys Ile Gly Val Ser  
 290 295 300  
 Pro Pro Ala Lys Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr  
 305 310 315 320  
 Asp Asn Asp Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys  
 325 330 335  
 Asp Glu Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ser Gln Pro Gly  
 340 345 350  
 Ala Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln His Gln  
 355 360 365  
 Lys Trp Glu Arg Lys Ile Ile Gly Met Ile Ser Gly His Gln Trp Val  
 370 375 380  
 Asp Met Asp Gly Ser Pro Gln Glu Phe Thr Arg Gly Cys Ser Glu Ile  
 385 390 395 400  
 Thr Pro Leu Gln Tyr Ile Pro Asp Ile Ser Ile Gly Val  
 405 410

<210> 126

<211> 383

<212> PRT

<213> Homo sapiens

<400> 126

Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys  
 1 5 10 15  
 Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp  
 20 25 30  
 Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu  
 35 40 45  
 Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser  
 50 55 60  
 Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu  
 65 70 75 80  
 Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg



<210> 127

132

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

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Met Ile Arg Thr Leu Leu Leu Ser Thr Leu Val Ala Gly Ala Leu Ser
 1             5             10             15

Cys Gly Asp Pro Thr Tyr Pro Pro Tyr Val Thr Arg Val Val Gly Gly
      20             25             30

Glu Glu Ala Arg Pro Asn Ser Trp Pro Trp Gln Val Ser Leu Gln Tyr
      35             40             45

Ser Ser Asn Gly Lys Trp Tyr His Thr Cys Gly Gly Ser Leu Ile Ala
 50             55             60

Asn Ser Trp Val Leu Thr Ala Ala His Cys Ile Ser Ser Ser Arg Thr
 65             70             75             80

Tyr Arg Val Gly Leu Gly Arg His Asn Leu Tyr Val Ala Glu Ser Gly
      85             90             95

Ser Leu Ala Val Ser Val Ser Lys Ile Val Val His Lys Asp Trp Asn
      100             105             110

Ser Asn Gln Ile Ser Lys Gly Asn Asp Ile Ala Leu Leu Lys Leu Ala
      115             120             125

Asn Pro Val Ser Leu Thr Asp Lys Ile Gln Leu Ala Cys Leu Pro Pro
      130             135             140

Ala Gly Thr Ile Leu Pro Asn Asn Tyr Pro Cys Tyr Val Thr Gly Trp
      145             150             155             160

Gly Arg Leu Gln Thr Asn Gly Ala Val Pro Asp Val Leu Gln Gln Gly
      165             170             175

Arg Leu Leu Val Val Asp Tyr Ala Thr Cys Ser Ser Ser Ala Trp Trp
      180             185             190

Gly Ser Ser Val Lys Thr Ser Met Ile Val Ala Gly Gly Asp Gly Val
      195             200             205

Ile Ser Ser Cys Asn Gly Asp Ser Gly Gly Pro Leu Asn Cys Gln Ala
      210             215             220

Ser Asp Gly Arg Trp Gln Val His Gly Ile Val Ser Phe Gly Ser Arg
      225             230             235             240

Leu Gly Cys Asn Tyr Tyr His Lys Pro Ser Val Phe Thr Arg Val Ser
      245             250             255

Asn Tyr Ile Asp Trp Ile Asn Ser Val Ile Ala Asn Asn
      260             265

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&lt;210&gt; 128

133

<211> 328  
<212> DNA  
<213> Homo sapiens

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<220>  
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ATTATGATTA TGCCCTCCTG GAACTCAAAA AGCCCCACAA GAGAAAATTT ATGAAGATTG 120  
GGGTGAGCCC TCCTGCTAAG CAGCTGCCAG GGGGCAGAAT TCACTTCTCT GGTATGACA 180  
ATGACCGACC AGGCAATTTG GTGTATCGCT TCTGTNACGT CAAAGACGAG ACCTATGACT 240  
TGCTCTACCA GCAATGCGAT GCCCAGCCAG GGGCCAGCGG GTCTGGGGTC TATGTTAGGA 300  
TGTGGGAGAG ACAGCAGCAT GAAGTGGG 328

<210> 129  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (23)  
<223> n equals a,t,g, or c

<220>  
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<220>  
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<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

<220>  
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<223> n equals a,t,g, or c

<220>  
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 GCAGATTTAT GGCTATGACA GCAGGTTTCAG CATTTTTTGGG AAGGACTTCC TGCTCAACTA 120  
 CCCTTTCTCA ACATCAGTGA AGTTATCCAC GGGCTGCACC GGCACCCTGG TGGGCAGAGA 180  
 AGCATGTCCT CACAGCTGCC CACTGCATAC ACGATGGAAA AACCTATGTG AAAGGAACCC 240  
 AGAAGCTTCG AGTGGGCTTN CTAAAGCCCA AGTTTAAAGA TGGTGGTCTGA NGGGNCAACG 300  
 ACTTNCACCT CAGCCATGNC CGAGCAGATG NATTTTCAGT GGGTCCGGTG GNAAGGAACC 360  
 CTGNTGCCCA AGGGTTTGGG TTCAGGGGGN ATGGCATGAN CNAGGNATGG GTTTATGATT 420  
 ATGCCTCNNG GGAATTCAAA AGGCCCANAA GGGGAAATTT NTNANGGTNN GGGTGNGGCC 480  
 TNCTGTTANG AAAT'T 495

<210> 130  
<211> 288  
<212> DNA  
<213> Homo sapiens

<220>  
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GTTGGGCAAG TAAGCCCTTA CAGTGCCCCC TGGAACCCA CTTGGCC'TGC ATACCGCCTC 180  
CCTGTCGTCT TGCCCCAGTN TACCCTCAAT TTAGCCAAGC CAGACTTTGG AGCCGAAGCC 240  
AAATTAGAAG TATCTTCTTC ATGTGGACCC CAGTGTGATA AGGGAAC 288

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138

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&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (396)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (405)

&lt;223&gt; n equals a,t,g, or c

&lt;400&gt; 131

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NCAGTGGATC CGGGTGAANG CACCCATGTN GCCAAGGGTT GGATCAAGGG CAATGCCAAT 120

GAACATCGGC ATGGATTATG AATTATGCCC CTCCTGGGAA CTGCAAAAAG CCCCACAAGA 180

GAAAATTTAT GAAAGATTGG GGTGGAGCCC TCCTGCTTAA GCANCTGCCA GGGGGCAGAA 240

TTGCACTTCT NTGGTTATGA ACAATGAACC GNCCAGGGCA ATTTGGTGTG ATCGCTTCTN 300

TGAACGTNCA AAGANGAGGA CCTATGGACT TGGTCTTAC CCAGCAATGG GGATTGCCCC 360

AGNCCAGGGG GCCANCGGGG TTTGGGGGGT TTTTNTTTT AAGNTTTT GGAAGGGGG 420

CCA 423

&lt;210&gt; 132

&lt;211&gt; 145

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (66)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

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&lt;222&gt; (76)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

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&lt;222&gt; (104)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;



139

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AATCTNCACG TTTTNCAAA CTTTGGATTT TTATTTTCATC TGANCTTGTT TNAAAGATTT 120  
ATATTAAATA TTTNGCATAC AAGAG 145

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GGTCCCCCAC AGGATTTCAA CGTGGCTGTC AGAATCACTC CTCTCAAATA TGCCAGATT 120  
TGCTATTGGA TTAAAGGAAA CTACCTGGAT TGTAGGGAGG GGTGACACAG TGTTCCTCC 180  
TGGCAGCAAT TAAGGGTCTT CATGTTCTTA TTTTAGGAGA GGCCAAATTG TTTTTGTCA 240  
TTGGCGTGCA CACGTGTGTN TGGTGTGTGT GGTGTGTGTG TAAAGGTGTC TTATNAATCT 300  
TTTACCCAT TTNNTTACAA TTGCAAGATG ACTGGCTTTA 340

140

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CCGGGCGGGC TGCTCGGCNC GGAACAGTGC TCGGCATGG 99

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 CCTTACAGTT GCCCACTGTA AACCCACTTG GNCTGNNTAC C 161

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 20 25 30  
 Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe  
 35 40 45  
 Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys  
 50 55 60  
 Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn  
 65 70 75 80

142

Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg  
 85 90 95  
 Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr  
 100 105 110  
 Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr  
 115 120 125  
 Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro  
 130 135 140  
 Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu  
 145 150 155 160  
 Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr  
 165 170 175  
 Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val  
 180 185 190  
 Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys  
 195 200 205  
 Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His  
 210 215 220  
 Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln  
 225 230 235 240  
 Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu  
 245 250 255  
 Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys  
 260 265 270  
 Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro  
 275 280 285  
 Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn  
 290 295 300  
 Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly  
 305 310 315 320  
 Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr  
 325 330 335  
 Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr  
 340 345 350  
 Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Ser  
 355 360 365  
 Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val Val Ala Val Val  
 370 375 380

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143  
Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala  
385 390 395 400  
Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp  
405 410 415  
Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn  
420 425 430  
Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile  
435 440

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<213> Homo sapiens

<400> 137

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ACAGGTGATG GGCAGAACTCT GTTTACGAAA GACGTGACAG TGATCGAGGG AGAGGTTGCC	180
ACCATCAGTT GCCAAGTCAA TAAGAGTGAC GACTCTGTGA TTCAGCTACT GAATCCCAAC	240
AGGCAGACCA TTTATTTTCAG GGAATTTCAGG CCTTTGAAGG ACAGCAGGTT TCAGTTGCTG	300
AATTTTCTA GCAGTGAAC TAAAGTATCA TTGACAAACG TCTCAATTC TGATGAAGGA	360
AGATACTTTT GCCAGCTCTA TACCGATCCC CCACAGGAAA GTTACACCAC CATCACAGTC	420
CTGGTCCCAC CACGTAATCT GATGATCGAT ATCCAGAAAG AACTGCGGT GGAAGGTGAG	480
GAGATTGAAG TCAACTGCAC TGCTATGGCC AGCAAGCCAG CCACGACTAT CAGGTGGTTC	540
AAAGGGAACA CAGAGCTAAA AGGCAAATCG GAGGTGGAAG AGTGGTCAGA CATGTACACT	600
GTGACCAGTC AGCTGATGCT GAAGGTGCAC AAGGAGGACG ATGGGGTCCC AGTGATCTGC	660
CAGGTGGAGC ACCCTGCGGT CACTGGAAAC CTGCAGACCC AGCGGTATCT AGAAGTACAG	720
TATAAGCCTC AAGTGCACAT TCAGATGACT TATCCTCTAC AAGGCTTAAC CCGGGAAGGG	780
GACGCGCTTG AGTTAACATG TGAAGCCATC GGAAGCCCC AGCCTGTGAT GGTAACCTGG	840
GTGAGAGTCG ATGATGAAAT GCCTCAACAC GCCGTACTGT CTGGGCCCCA CCTGTTTCATC	900
AATAACCTAA AAAAAACAGA TAATGGTACA TACCGCTGTG AAGCTTCAAA CATAGTGGGG	960
AAAGCTCACT CGGATTATAT GCTGTATGTA TACGATCCCC CCACAACTAT CCTCCTCCC	1020
ACAACAACCA CCACCACCAC CACCACCACC ACCACCACCA TCCTTACCAT CATCACAGAT	1080
TCCCCGAGCAG GTGAAGAAGG CTCGATCAGG GCAGTGGATC ATGCCGTGAT CCGTGGCGTC	1140
GTGGCGGTGG TGGTGTTCGC CATGCTGTGC TTGCTCATCA TTCTGGGGCG CTATTTTGCC	1200

AGACATAAAG GTACATACTT CACTCATGAA GCCAAAGGAG CCGATGACGC AGCAGACGCA 1260  
 GACACAGCTA TAATCAATGC AGAAGGAGGA CAGAACAACCT CCGAAGAAAA GAAAGAGTAC 1320  
 TTCATCTAG 1329

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<400> 138

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 20 25 30  
 Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly Gly  
 35 40 45  
 Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu Tyr  
 50 55 60  
 Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His Gln  
 65 70 75 80  
 Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser Pro  
 85 90 95  
 Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser Thr  
 100 105 110  
 Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu His  
 115 120 125  
 Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala Thr  
 130 135 140  
 Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile Ala  
 145 150 155 160  
 Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln Asp  
 165 170 175  
 Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro Ala  
 180 185 190  
 Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr Gln  
 195 200 205  
 Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe Thr  
 210 215 220  
 Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys Val

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										145											
225					230					235					240						
Glu	His	Glu	Ser	Phe	Glu	Glu	Pro	Ala	Leu	Ile	Pro	Val	Thr	Leu	Ser						
				245					250					255							
Val	Arg	Tyr	Pro	Pro	Glu	Val	Ser	Ile	Ser	Gly	Tyr	Asp	Asp	Asn	Trp						
				260					265					270							
Tyr	Leu	Gly	Arg	Thr	Asp	Ala	Thr	Leu	Ser	Cys	Asp	Val	Arg	Ser	Asn						
				275					280					285							
Pro	Glu	Pro	Thr	Gly	Tyr	Asp	Trp	Ser	Thr	Thr	Ser	Gly	Thr	Phe	Pro						
				290					295					300							
Thr	Ser	Ala	Val	Ala	Gln	Gly	Ser	Gln	Leu	Val	Ile	His	Ala	Val	Asp						
305					310					315					320						
Ser	Leu	Phe	Asn	Thr	Thr	Phe	Val	Cys	Thr	Val	Thr	Asn	Ala	Val	Gly						
				325					330					335							
Met	Gly	Arg	Ala	Glu	Gln	Val	Ile	Phe	Val	Arg	Glu	Thr	Pro	Asn	Thr						
				340					345					350							
Ala	Gly	Ala	Gly	Ala	Thr	Gly	Gly	Ile	Ile	Gly	Gly	Ile	Ile	Ala	Ala						
				355					360					365							
Ile	Ile	Ala	Thr	Ala	Val	Ala	Ala	Thr	Gly	Ile	Leu	Ile	Cys	Arg	Gln						
				370					375					380							
Gln	Arg	Lys	Glu	Gln	Thr	Leu	Gln	Gly	Ala	Glu	Glu	Asp	Glu	Asp	Leu						
385					390					395					400						
Glu	Gly	Pro	Pro	Ser	Tyr	Lys	Pro	Pro	Thr	Pro	Lys	Ala	Lys	Leu	Glu						
				405					410					415							
Ala	Gln	Glu	Met	Pro	Ser	Gln	Leu	Phe	Thr	Leu	Gly	Ala	Ser	Glu	His						
				420					425					430							
Ser	Pro	Leu	Lys	Thr	Pro	Tyr	Phe	Asp	Ala	Gly	Ala	Ser	Cys	Thr	Glu						
				435					440					445							
Gln	Glu	Met	Pro	Arg	Tyr	His	Glu	Leu	Pro	Thr	Leu	Glu	Glu	Arg	Ser						
				450					455					460							
Gly	Pro	Leu	His	Pro	Gly	Ala	Thr	Ser	Leu	Gly	Ser	Pro	Ile	Pro	Val						
465					470					475					480						
Pro	Pro	Gly	Pro	Pro	Ala	Val	Glu	Asp	Val	Ser	Leu	Asp	Leu	Glu	Asp						
				485					490					495							
Glu	Glu	Gly	Glu	Glu	Glu	Glu	Glu	Tyr	Leu	Asp	Lys	Ile	Asn	Pro	Ile						
				500					505					510							
Tyr	Asp	Ala	Leu	Ser	Tyr	Ser	Ser	Pro	Ser	Asp	Ser	Tyr	Gln	Gly	Lys						
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Gly	Phe	Val	Met	Ser	Arg	Ala	Met	Tyr	Val												
				530					535												

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147

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 GATGCTGAAG GTGCANAAGG AGGACGATGG GGTCCCAGTG ATCTGCCAGG TGGAGCACCC 120  
 TGCGGTCACT GGAAACCTGC AGACCCAGCG GTATCTAGAA GTACAGTATA AGCCTCAAGT 180  
 GCACATTNAG ATGACTTATC CTNTACAAGG CTTAACCCGG GAAGGGGACG CGCTTGANTT 240  
 AACATGTGAA GCCATCGGGA AGCCCCAGCC TGTGAATGGT AAAC TTGGGT GAGAAGTGCG 300  
 ATGATGAAAT GCCTCAACAC GCCGTACTGT TTGGGCCCAA CNTGTTNCAT TCATTAAACNT 360  
 AAACAAAACA GTTAATGGTA CNTACCGTTG TGNANGTTTC AAACNNAGTG GGGGAAAGTT 420

CATTCGGGTT NTATGCTGTN TGTNTNAGNT TCCCCCACA ATTTTCCTNC NTCCCACAAC 480  
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TTCTGCATTG ATTATAGCTG TGTCTGCGTC TNCNGCGTCA TCGGCTCCTT TGGCTTCATG 180  
AGTGAAGTAT GTACCTTTAT GTCTGGCAAA ATAGCGCCCC AGAATGATGA GCAAGCACAG 240  
CATGG 245

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149

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&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (148)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (256)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

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&lt;222&gt; (316)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (317)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

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&lt;222&gt; (322)

&lt;223&gt; n equals a,t,g, or c

&lt;220&gt;

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ACTGTGAACC AGTCAGCTGA TGCTGAAGGT GCANAAGGAG GACGATGGGG TCCCAGTGAA 120

TCTGCCAGGT GGAGCACCTT GCGGTCANTG GAAACCTGCA GACCCAGCGG TATCTAGAAG 180

TACAGTATAA GCCTCAAGTG CACATTTTCAG ATGACTTATC CTGTACAAGG CTTAACCCGG 240

AAGGGGACGC GCTTTNAGTT TAACATGTGA AGCCATCGGG GAAGCCCCCA GCCTGTGAAT 300

GGTAAATTTG GGTANNAGT CNGN 324

&lt;210&gt; 142

&lt;211&gt; 468

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (89)

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&lt;220&gt;

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TTCTCCGCCG CGGCACTGAT CCCACAGGT GATGGGCAGA ATCTGTTTAC GAAAGACGTG 180  
ACAGTGATCG AGGGAGAGGT TGCGACCATC AGTTGCCAAG TCAATNAAGA GTGACGACTC 240  
TNTGNATTCA GCTACTGAAT CCCAACAGGC AGACCATTTA TTTCAGGGGA CTTTCAGGNCT 300  
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ATATGCTGTA TGTATACGAT CCCCCACAA CTATCCCTCC TCCCACAACA ACCACCACCA	180
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Thr Leu Thr Leu Lys Cys Val Thr Ser Leu Arg Lys Asn Ser Ser Leu
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Gln Trp Leu Thr Pro Ser Gly Phe Thr Ile Phe Leu Asn Glu Tyr Pro
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Ala Leu Lys Asn Ser Lys Tyr Gln Leu Leu His His Ser Ala Asn Gln
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Leu Ser Ile Thr Val Pro Asn Val Thr Leu Gln Asp Glu Gly Val Tyr
      85              90              95

Lys Cys Leu His Tyr Ser Asp Ser Val Ser Thr Lys Glu Val Lys Val
      100              105              110

Ile Val Leu Ala Thr Pro Phe Lys Pro Ile Leu Glu Ala Ser Val Ile
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Arg Lys Gln Asn Gly Glu Glu His Val Val Leu Met Cys Ser Thr Met
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Arg Ser Lys Pro Pro Pro Gln Ile Thr Trp Leu Leu Gly Asn Ser Met
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Glu Val Ser Gly Gly Thr Leu His Glu Phe Glu Thr Asp Gly Lys Lys
      165              170              175

Cys Asn Thr Thr Ser Thr Leu Ile Ile Leu Ser Tyr Gly Lys Asn Ser
      180              185              190

Thr Val Asp Cys Ile Ile Arg His Arg Gly Leu Gln Gly Arg Lys Leu
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Val Ala Pro Phe Arg Phe Glu Asp Leu Val Thr Asp Glu Glu Thr Ala
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Ser Asp Ala Leu Glu Arg Asn Ser Leu Ser Thr Gln Asp Pro Gln Gln
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Pro Thr Ser Thr Val Ser Val Thr Glu Asp Ser Ser Thr Ser Glu Ile
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Asp Lys Glu Glu Lys Glu Gln Thr Thr Gln Asp Pro Asp Leu Thr Thr
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Glu Ala Asn Pro Gln Tyr Leu Gly Leu Ala Arg Lys Lys Ser Gly Ile
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Leu Leu Leu Thr Leu Val Ser Phe Leu Ile Phe Ile Leu Phe Ile Ile

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 Ser Asn Asn Glu Glu Thr Ser Ser Glu Glu Lys Asn Gly Gln Ser Ser  
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 Leu Pro Met Arg Cys Met Asn Tyr Ile Thr Lys Leu Tyr Ser Glu Ala  
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Gly Asp Pro Pro Arg Pro Val Leu Glu Asp Gly Ser Glu Ser Leu Glu
      35              40              45

Tyr Leu Ser Ser Ser Asn Leu Lys Glu Val Leu Ala Cys Arg Gly Ser
 50              55              60

Leu His Gly Trp Ala Gln Leu Val His Leu Pro Phe Ser Ala Tyr Ala
 65              70              75              80

Gly Tyr Ser Ser Glu Pro Gly Thr Leu Leu Ser Ala Glu Leu Lys Leu
      85              90              95

His Thr Met Val Leu Trp Pro Gln Phe Tyr Arg Ser Ile Leu Tyr Leu
      100              105              110

Leu Tyr Trp Leu Leu Arg Gly Arg Arg Asn Asn Thr Lys Pro Lys Pro
      115              120              125

Phe Cys Cys Asp His Pro Pro Ser Tyr Pro Leu His Phe Arg Leu Tyr
      130              135              140

Gln Met Glu Lys Thr Leu Ser Gly Asp Val His His Gln Tyr Tyr His
      145              150              155              160

Gln Asp Phe Ser Arg Lys Tyr Tyr His Pro Gly Ile Cys Trp Leu Gln
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Leu Leu Leu Leu Ser Ala Pro Phe His Ser Ile Asn Met Leu Arg Glu
      180              185              190

Phe Ala Ile Leu Ser Asn Ile Leu Met His Ser His Lys Leu Gln Cys
      195              200              205

Asn Ser Leu Leu Phe Met Tyr Lys Val Arg Asn Leu Cys Leu Leu Pro
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Cys Trp His Leu Pro Leu Lys Ser Lys Ser Lys Cys Ser Tyr Ala Arg
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Glu Ser Arg Val Thr Leu Phe Tyr Gly Ser Cys Ser
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&lt;211&gt; 369

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GGAGGAAGAA	AGATTTTCAGT	TAAGGAGAAT	GNAAGTTTCT	CCTGAAATGA	AAGGAAGAAA	180
ACCAGGATAG	TGCCATGCAA	AGGAAGGTGT	TTCAAAGAGG	AGGAAGAGAT	TAACAGTGCC	240
AAATGCGACT	NCGANTGTCA	AAGAAGTTTG	AAAGAAATAA	GGGTTNTCCT	GGGTAGCCTT	300
NGTTAGAGTA	GTTCTGGTGG	AATGGTAGAC	ATGGGAGTTA	CCTTTNTATN	GGTTGGGAAG	360
GAAAGGGNG						369

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US99/25031

<b>A. CLASSIFICATION OF SUBJECT MATTER</b> IPC(7) :C07K 14/435; C12N 15/12 US CL :530/350; 536/23.5 According to International Patent Classification (IPC) or to both national classification and IPC		
<b>B. FIELDS SEARCHED</b> Minimum documentation searched (classification system followed by classification symbols) U.S. : 530/350; 536/23.5 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) EMBL, Genbank, EMBLest, Genbankest, USPAT issued search terms: sequences corresponding to SEQ ID NOS: 11-20		
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database Genbank on STN, National Center for Biotechnology Information (Bethesda, MD), Accession Number AF076483, positions 22-690 relevant to positions 9-677 of instant SEQ ID NO:18, 15 August 1998.	1, 7-11, 14-16
X	Database Genbank on STN, National Center for Biotechnology Information (Bethesda, MD), Accession Number AJ001016, positions 1-1312 relevant to positions 8-1316 of instant SEQ ID NO: 13, 05 June 1998.	1, 7-11, 14-16
X	EP 0 869 178 A1 (SMITHKLINE BEECHAM CORPORATION) 07 October 1998, see SEQ ID NO:1 on page 14, positions 1-1501 relevant to positions 18-1518 of instant SEQ ID NO: 16.	1, 7-11, 14-16
<input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family	
Date of the actual completion of the international search 12 FEBRUARY 2000		Date of mailing of the international search report 07 MAR 2000
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230		Authorized officer JOHN S. BRUSCA Telephone No. (703) 308-0196

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US99/25031

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1-12, 14-16

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US99/25031

### BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1-12, 14-16, drawn to nucleic acids, polypeptides encoded by the nucleic acids, vectors and cells comprising the nucleic acids, and methods of using the cells to express polypeptides encoded by the nucleic acids.  
Group II, claim(s) 13, drawn to antibodies specific to the polypeptide encoded by the nucleic acids of Group I.  
Group III, claim(s) 17, drawn to a therapeutic method of using the nucleic acids or encoded polypeptides of Group I.  
Group IV, claim(s) 18, drawn to a diagnostic method using the nucleic acids of Group I.  
Group V, claim(s) 19, drawn to a diagnostic method of detecting the proteins of Group I.  
Group VI, claim(s) 20, drawn to an assay of a binding partner of the polypeptides of Group I.  
Group VII, claim(s) 21, drawn to a complete gene corresponding to the nucleic acids of Group I.  
Group VIII, claim(s) 22, drawn to a method of determining the activity of the polypeptides of Group I.  
Group IX, claim(s) 23, drawn to a binding partner of the polypeptides of Group I.

The inventions listed as Groups I-IX do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Groups II-IX correspond to the second product, the second through fifth method of using, the third product, the sixth method of using, and the fourth product, respectively of the nucleic acids and polypeptides of Group I. PCT Rule 13.1 and Annex B do not provide for unity of invention between a first and second product, or method of use.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows:

The twelve nucleic acid sequences and corresponding polypeptide sequences depicted in Table XIII.

The claims are deemed to correspond to the species listed above in the following manner:

All claims are drawn to the species indicated above.

The following claims are generic: 1-23.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: Each species is drawn to a different nucleic acid or corresponding polypeptide. There is no disclosed relationship between the sequences of each individual species.

Restriction to a single species has been waived sua sponte and the Applicants are permitted to have ten species examined without payment of additional fees. The Applicant's representative Kenley Hoover elected telephonically on 02 February 2000 to have the sequences corresponding to SEQ ID NOS: 11-20 examined.